sequences of DPYSL2 BINDING SITE, designated SEQ ID:7064, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68150] Another function of VGAM1960 is therefore inhibition of Dihydropyrimidinase-like 2 (DPYSL2, Accession NM_001386), a gene which is a member of the dihydropyrimidinase family. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPYSL2. The function of DPYSL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM217.E2F Transcription Factor 3 (E2F3, Accession NM_001949) is another VGAM1960 host target gene. E2F3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by E2F3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of E2F3 BINDING SITE, designated SEQ ID:7668, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68151] Another function of VGAM1960 is therefore inhibition of E2F Transcription Factor 3 (E2F3, Accession NM_001949), a gene which binds dna and controls cell-cycle progression from g1 to s phase. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with E2F3. The function of E2F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM475.Coagulation Factor II (thrombin) Receptor (F2R, Accession NM_001992) is another VGAM1960 host target gene. F2R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by F2R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of F2R BINDING SITE, designated SEQ ID:7723, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68152] Another function of VGAM1960 is therefore inhibition of Coagulation Factor II (thrombin) Receptor (F2R, Accession NM_001992), a gene which Thrombin receptor; G protein-coupled receptor involved in platelet activation. Accord-

ingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F2R. The function of F2R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM140.F-box and Leucine-rich Repeat Protein 2 (FBXL2, Accession NM_012157) is another VGAM1960 host target gene. FBXL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXL2 BINDING SITE, designated SEQ ID:14454, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68153] Another function of VGAM1960 is therefore inhibition of F-box and Leucine-rich Repeat Protein 2 (FBXL2, Accession NM_012157). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXL2. Glypican 1 (GPC1, Accession NM_002081) is another VGAM1960 host target gene. GPC1 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by GPC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPC1 BINDING SITE, designated SEQ ID:7875, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68154] Another function of VGAM1960 is therefore inhibition of Glypican 1 (GPC1, Accession NM_002081), a gene which may play a role in growth control and differentation. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPC1. The function of GPC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM125.Hemochromatosis (HFE, Accession NM_000410) is another VGAM1960 host target gene. HFE BINDING SITE1 and HFE BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HFE, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the comple-

mentarity of the nucleotide sequences of HFE BINDING SITE1 and HFE BINDING SITE2, designated SEQ ID:5985 and SEQ ID:29099 respectively, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68155] Another function of VGAM1960 is therefore inhibition of Hemochromatosis (HFE, Accession NM_000410). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HFE. Kinesin Family Member 5C (KIF5C, Accession NM_004522) is another VGAM1960 host target gene. KIF5C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIF5C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIF5C BINDING SITE, designated SEQ ID:10855, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68156] Another function of VGAM1960 is therefore inhibition of Kinesin Family Member 5C (KIF5C, Accession NM_004522). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with KIF5C. Leucine Zipper-EF-hand Containing Transmembrane Protein 1 (LETM1, Accession NM_012318) is another VGAM1960 host target gene. LETM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LETM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LETM1 BINDING SITE, designated SEQ ID:14698, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68157] Another function of VGAM1960 is therefore inhibition of Leucine Zipper-EF-hand Containing Transmembrane Protein 1 (LETM1, Accession NM_012318). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LETM1. Leukocyte Immunoglobulin-like Receptor, Subfamily B (with TM and ITIM domains), Member 4 (LILRB4, Accession NM_006847) is another VGAM1960 host target gene. LILRB4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LILRB4, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LILRB4 BINDING SITE, designated SEQ ID:13717, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68158] Another function of VGAM1960 is therefore inhibition of Leukocyte Immunoglobulin-like Receptor, Subfamily B (with TM and ITIM domains), Member 4 (LILRB4, Accession NM_006847). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LILRB4. MAD, Mothers Against Decapentaplegic Homolog 4 (Drosophila) (MADH4, Accession NM_005359) is another VGAM1960 host target gene. MADH4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MADH4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MADH4 BINDING SITE, designated SEQ ID:11834, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68159] Another function of VGAM1960 is therefore inhibition of MAD, Mothers Against Decapentaplegic Homolog 4 (Drosophila) (MADH4, Accession NM_005359), a gene which common mediator of signal transduction by tgf-beta (transforming growth factor) superfamily; smad4 is the common smad (co-smad). promotes binding of the smad2/smad4/fast-1 complex to dna and provides an activation function required for smad1 or smad2 to stimulate transcription. may act as a tumor suppressor. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADH4. The function of MADH4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM217.Maltase-glucoamylase (alpha-glucosidase) (MGAM, Accession XM_051351) is another VGAM1960 host target gene. MGAM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGAM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGAM BINDING SITE, des-

ignated SEQ ID:35827, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68160] Another function of VGAM1960 is therefore inhibition of Maltase-glucoamylase (alpha-glucosidase) (MGAM, Accession XM_051351), a gene which plays a role in the final steps of digestion of starch. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGAM. The function of MGAM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM791.Neuroepithelial Cell Transforming Gene 1 (NET1, Accession NM_005863) is another VGAM1960 host target gene. NET1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NET1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NET1 BINDING SITE, designated SEQ ID:12474, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68161] Another function of VGAM1960 is therefore inhibition of Neuroepithelial Cell Transforming Gene 1 (NET1, Accession NM_005863), a gene which is induced morphologic alterations and conferred a malignant phenotype in vitro and in nude mice. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NET1. The function of NET1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1333.Neurotrophic Tyrosine Kinase, Receptor, Type 2 (NTRK2, Accession NM_006180) is another VGAM1960 host target gene. NTRK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NTRK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NTRK2 BINDING SITE, designated SEQ ID:12847, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68162] Another function of VGAM1960 is therefore inhibition of Neurotrophic Tyrosine Kinase, Receptor, Type 2 (NTRK2,

Accession NM_006180), a gene which is involved in the development and/or maintenance of the nervous system. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTRK2. The function of NTRK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM341.Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), Alpha Polypeptide I (P4HA1, Accession NM_000917) is another VGAM1960 host target gene. P4HA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P4HA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P4HA1 BINDING SITE, designated SEQ ID:6625, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68163] Another function of VGAM1960 is therefore inhibition of Procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), Alpha Polypeptide I (P4HA1, Ac-

cession NM_000917), a gene which catalyzes the formation of 4-hydroxyproline in collagen. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P4HA1. The function of P4HA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM260.PDL2 (Accession NM_025239) is another VGAM1960 host target gene. PDL2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PDL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDL2 BINDING SITE, designated SEQ ID:24923, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68164] Another function of VGAM1960 is therefore inhibition of PDL2 (Accession NM_025239), a gene which is a second ligand for PD-1 and inhibits T cell activation. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDL2. The function of PDL2 has been established by

previous studies. The costimulatory B7 molecules (e.g., B7-1, or CD80; 112203) signal through CD28 (OMIM Ref. No. 186760) family molecules such as CD28, CTLA4 (OMIM Ref. No. 123890), ICOS (OMIM Ref. No. 604558), and programmed cell death-1 (PDCD1, or PD1; 600244). Ctla4-deficient mice are prone to a fatal lymphoproliferative disorder, suggesting that CTLA4 plays a critical regulatory and immunoinhibitory function, and Pdcd1-deficient mice develop lupus-like autoimmune diseases, including arthritis and cardiomyopathy. By searching EST databases with mouse Pd1 ligand-1 (Pdl1, or B7H1; 605402), Latchman et al. (2001) identified cDNAs encoding mouse Pdl2 and human PDL2, which they cloned from a placenta cDNA library. Sequence analysis predicted that the 273-amino acid PDL2 protein, which is 70% identical to the mouse Pdl2 protein, contains a signal sequence, IgV- and IgC-like domains, a transmembrane region, and a cytoplasmic region. Flow cytometric analysis showed that the IgV region of mouse Pdl2, like Pdl1, binds to human PDCD1 but not to CTLA4, CD28, or ICOS. Northern blot analysis detected wide expression of PDL2, with highest levels in placenta, heart, pancreas, lung, and liver, and lower levels in spleen, lymph nodes, and thy-

mus. Stimulation with gamma-interferon (IFNG; 147570) was required to detect expression in monocytes. Stimulation of mouse T cells with anti-CD3 (see OMIM Ref. No. 186740) and Pdl2 or Pdl1 resulted in inhibition of proliferation and cytokine production, and Pdl2 could inhibit T-cell receptor (see OMIM Ref. No. 186880)-CD28 signals at low antigen concentrations. Latchman et al. (2001) proposed that blocking of the PDL-PDCD1 pathway may enhance antitumor immunity, whereas stimulating this pathway may help downregulate graft rejection and autoimmune and allergic reactions. By screening a subtractive dendritic cell-activated macrophage cDNA library, Tseng et al. (2001) isolated mouse and human cDNAs encoding PDL2, which they termed B7DC. Northern blot analysis detected Pdl2 transcripts in mouse dendritic cells but not in primary macrophages or macrophage cell lines. Expression was also detected in human dendritic cells but not in placenta. Functional analysis showed that in the presence of low concentrations of anti-CD3, mouse Pdl2 preferentially costimulates CD4 (OMIM Ref. No. 186940)-positive (Th1) T-cell proliferation and Ifng production to a greater level than does B7.1.

[68165] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[68166] Latchman, Y.; Wood, C. R.; Chernova, T.; Chaudhary, D.; Borde, M.; Chernova, I.; Iwai, Y.; Long, A. J.; Brown, J. A.; Nunes, R.; Greenfield, E. A.; Bourque, K. : PD-L2 is a second ligand for PD-1 and inhibits T cell activation. Nature Immun. 2: 261-268, 2001. ; and

[68167] Tseng, B. S.-Y.; Otsuji, M.; Gorski, K.; Huang, X.; Slansky, J. E.; Pai, S. I.; Shalabi, A.; Shin, T.; Pardoll, D. M.; Tsuchiya, H. : B7-DC, a new dendritic cell molecule with potent c.

[68168] Further studies establishing the function and utilities of PDL2 are found in John Hopkins OMIM database record ID 605723, and in sited publications numbered 681 and 6909 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Pleckstrin Homology, Sec7 and Coiled/coil Domains, Binding Protein (PSCDBP, Accession NM_004288) is another VGAM1960 host target gene. PSCDBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSCDBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of PSCDBP BINDING SITE, designated SEQ ID:10500, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68169] Another function of VGAM1960 is therefore inhibition of Pleckstrin Homology, Sec7 and Coiled/coil Domains, Binding Protein (PSCDBP, Accession NM_004288), a gene which Protein that contains leucine zipper domains and a nuclear targeting sequence. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSCDBP. The function of PSCDBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1924.Secreted Frizzled-related Protein 1 (SFRP1, Accession NM_003012) is another VGAM1960 host target gene. SFRP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFRP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRP1 BINDING SITE, designated SEQ ID:8935, to the nucleotide sequence of

VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68170] Another function of VGAM1960 is therefore inhibition of Secreted Frizzled-related Protein 1 (SFRP1, Accession NM_003012), a gene which is a receptor for wnt proteins that may have an anti-apoptotic function. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRP1. The function of SFRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM250.Tissue Inhibitor of Metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3, Accession NM_000362) is another VGAM1960 host target gene. TIMP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIMP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIMP3 BINDING SITE, designated SEQ ID:5930, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68171] Another function of VGAM1960 is therefore inhibition of Tissue Inhibitor of Metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3, Accession NM_000362). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIMP3. Tropomyosin 4 (TPM4, Accession NM_003290) is another VGAM1960 host target gene. TPM4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TPM4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TPM4 BINDING SITE, designated SEQ ID:9301, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68172] Another function of VGAM1960 is therefore inhibition of Tropomyosin 4 (TPM4, Accession NM_003290), a gene which plays a central role, in association with the troponin complex, in the calcium dependent regulation of vertebrate striated muscle contraction. Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TPM4.

The function of TPM4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM744.Zinc Finger Protein 14 (KOX 6) (ZNF14, Accession NM_021030) is another VGAM1960 host target gene. ZNF14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF14 BINDING SITE, designated SEQ ID:22018, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68173] Another function of VGAM1960 is therefore inhibition of Zinc Finger Protein 14 (KOX 6) (ZNF14, Accession NM_021030). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF14. ADP-ribosylation Factor GTPase Activating Protein 3 (ARFGAP3, Accession NM_014570) is another VGAM1960 host target gene. ARFGAP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARF-

GAP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARFGAP3 BINDING SITE, designated SEQ ID:15924, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68174] Another function of VGAM1960 is therefore inhibition of ADP-ribosylation Factor GTPase Activating Protein 3 (ARFGAP3, Accession NM_014570). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARFGAP3. B7-H1 (Accession NM_014143) is another VGAM1960 host target gene. B7-H1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by B7-H1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B7-H1 BINDING SITE, designated SEQ ID:15424, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68175] Another function of VGAM1960 is therefore inhibition of

B7-H1 (Accession NM_014143). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B7-H1. Chromosome 1 Open Reading Frame 17 (C1orf17, Accession XM_042965) is another VGAM1960 host target gene. C1orf17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf17 BINDING SITE, designated SEQ ID:33855, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68176] Another function of VGAM1960 is therefore inhibition of Chromosome 1 Open Reading Frame 17 (C1orf17, Accession XM_042965). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf17. Calcium Channel, Voltage-dependent, Gamma Subunit 4 (CACNG4, Accession NM_014405) is another VGAM1960 host target gene. CACNG4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

CACNG4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CACNG4 BINDING SITE, designated SEQ ID:15746, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68177] Another function of VGAM1960 is therefore inhibition of Calcium Channel, Voltage-dependent, Gamma Subunit 4 (CACNG4, Accession NM_014405). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNG4. COE2 (Accession XM_034639) is another VGAM1960 host target gene. COE2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COE2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COE2 BINDING SITE, designated SEQ ID:32129, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68178] Another function of VGAM1960 is therefore inhibition of

COE2 (Accession XM_034639). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COE2. Cysteine and Tyrosine-rich 1 (CYYR1, Accession NM_052954) is another VGAM1960 host target gene. CYYR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYYR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYYR1 BINDING SITE, designated SEQ ID:27513, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68179] Another function of VGAM1960 is therefore inhibition of Cysteine and Tyrosine-rich 1 (CYYR1, Accession NM_052954). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYYR1. DKFZp434C0328 (Accession NM_017577) is another VGAM1960 host target gene. DKFZp434C0328 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434C0328, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434C0328 BINDING SITE, designated SEQ ID:19017, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68180] Another function of VGAM1960 is therefore inhibition of DKFZp434C0328 (Accession NM_017577). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434C0328. DKFZp434K1210 (Accession NM_017606) is another VGAM1960 host target gene. DKFZp434K1210 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434K1210, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434K1210 BINDING SITE, designated SEQ ID:19103, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68181] Another function of VGAM1960 is therefore inhibition of DKFZp434K1210 (Accession NM_017606). Accordingly,

utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434K1210. Eukaryotic Translation Initiation Factor 4B (EIF4B, Accession XM_071605) is another VGAM1960 host target gene. EIF4B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF4B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF4B BINDING SITE, designated SEQ ID:37400, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68182] Another function of VGAM1960 is therefore inhibition of Eukaryotic Translation Initiation Factor 4B (EIF4B, Accession XM_071605). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF4B. FLJ20094 (Accession NM_017665) is another VGAM1960 host target gene. FLJ20094 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20094, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20094 BINDING SITE, designated SEQ ID:19209, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68183] Another function of VGAM1960 is therefore inhibition of FLJ20094 (Accession NM_017665). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20094. FLJ21106 (Accession NM_025097) is another VGAM1960 host target gene. FLJ21106 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21106, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21106 BINDING SITE, designated SEQ ID:24738, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68184] Another function of VGAM1960 is therefore inhibition of FLJ21106 (Accession NM_025097). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ21106. Fucose-1-phosphate Guanylyltransferase (FPGT, Accession NM_003838) is another VGAM1960 host target gene. FPGT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FPGT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FPGT BINDING SITE, designated SEQ ID:9930, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68185] Another function of VGAM1960 is therefore inhibition of Fucose-1-phosphate Guanylyltransferase (FPGT, Accession NM_003838). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FPGT. KIAA0368 (Accession XM_036708) is another VGAM1960 host target gene. KIAA0368 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0368, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0368 BINDING SITE, designated SEQ ID:32488, to the nucleotide sequence of VGAM1960

RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68186] Another function of VGAM1960 is therefore inhibition of KIAA0368 (Accession XM_036708). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0368. KIAA0427 (Accession NM_014772) is another VGAM1960 host target gene. KIAA0427 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0427, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0427 BINDING SITE, designated SEQ ID:16579, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68187] Another function of VGAM1960 is therefore inhibition of KIAA0427 (Accession NM_014772). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0427. KIAA0534 (Accession XM_049349) is another VGAM1960 host target gene. KIAA0534 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA0534, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0534 BINDING SITE, designated SEQ ID:35387, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68188] Another function of VGAM1960 is therefore inhibition of KIAA0534 (Accession XM_049349). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0534. KIAA0644 (Accession NM_014817) is another VGAM1960 host target gene. KIAA0644 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0644, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0644 BINDING SITE, designated SEQ ID:16785, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68189] Another function of VGAM1960 is therefore inhibition of KIAA0644 (Accession NM_014817). Accordingly, utilities

of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0644. KIAA0961 (Accession NM_014898) is another VGAM1960 host target gene. KIAA0961 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0961, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0961 BINDING SITE, designated SEQ ID:17075, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68190] Another function of VGAM1960 is therefore inhibition of KIAA0961 (Accession NM_014898). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0961. KIAA0984 (Accession XM_037557) is another VGAM1960 host target gene. KIAA0984 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0984, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0984 BINDING SITE, designated SEQ ID:32644, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68191] Another function of VGAM1960 is therefore inhibition of KIAA0984 (Accession XM_037557). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0984. KIAA1136 (Accession XM_166110) is another VGAM1960 host target gene. KIAA1136 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1136, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1136 BINDING SITE, designated SEQ ID:43883, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68192] Another function of VGAM1960 is therefore inhibition of KIAA1136 (Accession XM_166110). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1136. KIAA1300 (Accession XM_031744) is another VGAM1960 host target gene. KIAA1300 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1300, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1300 BINDING SITE, designated SEQ ID:31481, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68193] Another function of VGAM1960 is therefore inhibition of KIAA1300 (Accession XM_031744). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1300. KIAA1598 (Accession NM_018330) is another VGAM1960 host target gene. KIAA1598 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1598, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1598 BINDING SITE, designated SEQ ID:20331, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68194] Another function of VGAM1960 is therefore inhibition of

KIAA1598 (Accession NM_018330). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1598. KIAA1676 (Accession XM_167612) is another VGAM1960 host target gene. KIAA1676 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1676, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1676 BINDING SITE, designated SEQ ID:44727, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68195] Another function of VGAM1960 is therefore inhibition of KIAA1676 (Accession XM_167612). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1676. KIAA1889 (Accession XM_056298) is another VGAM1960 host target gene. KIAA1889 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1889, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1889 BINDING SITE, designated SEQ ID:36389, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68196] Another function of VGAM1960 is therefore inhibition of KIAA1889 (Accession XM_056298). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1889. l(3)mbt-like 2 (Drosophila) (L3MBTL2, Accession XM_114201) is another VGAM1960 host target gene. L3MBTL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by L3MBTL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of L3MBTL2 BINDING SITE, designated SEQ ID:42791, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68197] Another function of VGAM1960 is therefore inhibition of l(3)mbt-like 2 (Drosophila) (L3MBTL2, Accession XM_114201). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with L3MBTL2. LIN-7-C (Accession NM_018362) is another VGAM1960 host target gene. LIN-7-C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIN-7-C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIN-7-C BINDING SITE, designated SEQ ID:20372, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68198] Another function of VGAM1960 is therefore inhibition of LIN-7-C (Accession NM_018362). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIN-7-C. Mesoderm Development Candidate 1 (MESDC1, Accession NM_022566) is another VGAM1960 host target gene. MESDC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MESDC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MESDC1 BINDING SITE, designated SEQ

ID:22885, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68199] Another function of VGAM1960 is therefore inhibition of Mesoderm Development Candidate 1 (MESDC1, Accession NM_022566). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MESDC1. MGC12335 (Accession NM_032744) is another VGAM1960 host target gene. MGC12335 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC12335, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC12335 BINDING SITE, designated SEQ ID:26478, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68200] Another function of VGAM1960 is therefore inhibition of MGC12335 (Accession NM_032744). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12335. Ring Finger Protein 38 (RNF38, Accession

NM_022781) is another VGAM1960 host target gene. RNF38 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNF38, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF38 BINDING SITE, designated SEQ ID:23064, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68201] Another function of VGAM1960 is therefore inhibition of Ring Finger Protein 38 (RNF38, Accession NM_022781). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF38. Solute Carrier Family 6 (neurotransmitter transporter), Member 14 (SLC6A14, Accession NM_007231) is another VGAM1960 host target gene. SLC6A14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC6A14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC6A14 BINDING SITE, designated SEQ

ID:14101, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68202] Another function of VGAM1960 is therefore inhibition of Solute Carrier Family 6 (neurotransmitter transporter), Member 14 (SLC6A14, Accession NM_007231). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A14. Synovial Sarcoma Translocation Gene On Chromosome 18-like 1 (SS18L1, Accession XM_037202) is another VGAM1960 host target gene. SS18L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SS18L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SS18L1 BINDING SITE, designated SEQ ID:32567, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68203] Another function of VGAM1960 is therefore inhibition of Synovial Sarcoma Translocation Gene On Chromosome 18-like 1 (SS18L1, Accession XM_037202). Accordingly,

utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SS18L1. Signal Transducing Adaptor Molecule (SH3 domain and ITAM motif) 2 (STAM2, Accession NM_005843) is another VGAM1960 host target gene. STAM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STAM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAM2 BINDING SITE, designated SEQ ID:12460, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68204] Another function of VGAM1960 is therefore inhibition of Signal Transducing Adaptor Molecule (SH3 domain and ITAM motif) 2 (STAM2, Accession NM_005843). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAM2. TRAP150 (Accession NM_005119) is another VGAM1960 host target gene. TRAP150 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TRAP150, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRAP150 BINDING SITE, designated SEQ ID:11603, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68205] Another function of VGAM1960 is therefore inhibition of TRAP150 (Accession NM_005119). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAP150. Ubiquitin Specific Protease 8 (USP8, Accession NM_005154) is another VGAM1960 host target gene. USP8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP8 BINDING SITE, designated SEQ ID:11631, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68206] Another function of VGAM1960 is therefore inhibition of Ubiquitin Specific Protease 8 (USP8, Accession NM_005154). Accordingly, utilities of VGAM1960 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with USP8. Zinc Finger Protein 294 (ZNF294, Accession XM_047829) is another VGAM1960 host target gene. ZNF294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF294 BINDING SITE, designated SEQ ID:35058, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68207] Another function of VGAM1960 is therefore inhibition of Zinc Finger Protein 294 (ZNF294, Accession XM_047829). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF294. Zinc Finger Protein 33a (KOX 31) (ZNF33A, Accession XM_166119) is another VGAM1960 host target gene. ZNF33A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF33A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of ZNF33A BINDING SITE, designated SEQ ID:43899, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68208] Another function of VGAM1960 is therefore inhibition of Zinc Finger Protein 33a (KOX 31) (ZNF33A, Accession XM_166119). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF33A. LOC112616 (Accession NM_138410) is another VGAM1960 host target gene. LOC112616 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC112616, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112616 BINDING SITE, designated SEQ ID:28776, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68209] Another function of VGAM1960 is therefore inhibition of LOC112616 (Accession NM_138410). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC112616. LOC113763 (Accession NM_138434) is another VGAM1960 host target gene. LOC113763 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC113763, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC113763 BINDING SITE, designated SEQ ID:28804, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68210] Another function of VGAM1960 is therefore inhibition of LOC113763 (Accession NM_138434). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113763. LOC134266 (Accession XM_059701) is another VGAM1960 host target gene. LOC134266 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC134266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC134266 BINDING SITE, designated SEQ ID:37070, to the nucleotide sequence of VGAM1960 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4671.

[68211] Another function of VGAM1960 is therefore inhibition of LOC134266 (Accession XM_059701). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC134266. LOC139673 (Accession XM_071645) is another VGAM1960 host target gene. LOC139673 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC139673, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC139673 BINDING SITE, designated SEQ ID:37405, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68212] Another function of VGAM1960 is therefore inhibition of LOC139673 (Accession XM_071645). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139673. LOC144747 (Accession XM_084954) is another VGAM1960 host target gene. LOC144747 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144747, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144747 BINDING SITE, designated SEQ ID:37785, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68213] Another function of VGAM1960 is therefore inhibition of LOC144747 (Accession XM_084954). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144747. LOC146856 (Accession XM_096086) is another VGAM1960 host target gene. LOC146856 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146856, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146856 BINDING SITE, designated SEQ ID:40299, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68214] Another function of VGAM1960 is therefore inhibition of LOC146856 (Accession XM_096086). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC146856. LOC147990 (Accession XM_097358) is another VGAM1960 host target gene. LOC147990 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147990, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147990 BINDING SITE, designated SEQ ID:40863, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68215] Another function of VGAM1960 is therefore inhibition of LOC147990 (Accession XM_097358). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147990. LOC152018 (Accession XM_098156) is another VGAM1960 host target gene. LOC152018 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152018, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152018 BINDING SITE, designated SEQ ID:41421, to

the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68216] Another function of VGAM1960 is therefore inhibition of LOC152018 (Accession XM_098156). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152018. LOC157798 (Accession XM_098827) is another VGAM1960 host target gene. LOC157798 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157798, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157798 BINDING SITE, designated SEQ ID:41850, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68217] Another function of VGAM1960 is therefore inhibition of LOC157798 (Accession XM_098827). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157798. LOC158709 (Accession XM_088648) is another VGAM1960 host target gene. LOC158709 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC158709, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158709 BINDING SITE, designated SEQ ID:39882, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68218] Another function of VGAM1960 is therefore inhibition of LOC158709 (Accession XM_088648). Accordingly, utilities of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158709. LOC203365 (Accession XM_114690) is another VGAM1960 host target gene. LOC203365 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203365, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203365 BINDING SITE, designated SEQ ID:43034, to the nucleotide sequence of VGAM1960 RNA, herein designated VGAM RNA, also designated SEQ ID:4671.

[68219] Another function of VGAM1960 is therefore inhibition of LOC203365 (Accession XM_114690). Accordingly, utilities

of VGAM1960 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203365. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1961 (VGAM1961) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[68220] VGAM1961 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1961 was detected is described hereinabove with reference to Figs. 1-8.

[68221] VGAM1961 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM1961 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[68222] VGAM1961 gene encodes a VGAM1961 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1961 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM1961 precursor RNA is designated SEQ ID:1947, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1947 is located at position 16323 relative to the genome of Camelpox Virus.

[68223] VGAM1961 precursor RNA folds onto itself, forming VGAM1961 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[68224] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1961 folded precursor RNA into VGAM1961 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1961 RNA is designated SEQ ID:4672, and

is provided hereinbelow with reference to the sequence listing part.

[68225] VGAM1961 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1961 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1961 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[68226] VGAM1961 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1961 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1961 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM1961 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1961 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[68227] The complementary binding of VGAM1961 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1961 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1961 host target RNA into VGAM1961 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[68228] It is appreciated that VGAM1961 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1961 host target genes. The mRNA of each one of this plurality of VGAM1961 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1961 RNA, herein designated VGAM RNA, and which when bound by VGAM1961 RNA causes inhibition of translation of respective one or more VGAM1961 host target proteins.

[68229] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1961 gene, herein designated VGAM GENE, on one or more VGAM1961 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[68230] It is yet further appreciated that a function of VGAM1961 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1961 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM1961 correlate with, and may be deduced from, the identity of the host target genes which VGAM1961 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[68231] Nucleotide sequences of the VGAM1961 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1961 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1961 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1961 are further described hereinbelow with reference to Table 1.

[68232] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1961 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1961 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[68233] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM1961 gene, herein designated VGAM is inhibition of expression of VGAM1961 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1961 correlate with, and may be deduced from, the identity of the target genes which VGAM1961 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[68234] Inositol 1,4,5-triphosphate Receptor, Type 1 (ITPR1, Accession NM_002222) is a VGAM1961 host target gene. ITPR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITPR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITPR1 BINDING SITE, designated SEQ ID:7985, to the nucleotide sequence of VGAM1961 RNA, herein designated VGAM RNA, also designated SEQ ID:4672.

[68235] A function of VGAM1961 is therefore inhibition of Inositol 1,4,5-triphosphate Receptor, Type 1 (ITPR1, Accession NM_002222), a gene which couples cell membrane receptors to Ca2+ signal transduction pathways. Accordingly, utilities of VGAM1961 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with ITPR1. The function of ITPR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM106.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1962 (VGAM1962) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[68236] VGAM1962 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1962 was detected is described hereinabove with reference to Figs. 1-8.

[68237] VGAM1962 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM1962 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[68238] VGAM1962 gene encodes a VGAM1962 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1962 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1962 precursor RNA is designated SEQ ID:1948, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1948 is located at position 16962 relative to the genome of Camelpox Virus.

[68239] VGAM1962 precursor RNA folds onto itself, forming VGAM1962 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[68240] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1962 folded precursor RNA into VGAM1962 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide se-

quence of VGAM1962 RNA is designated SEQ ID:4673, and is provided hereinbelow with reference to the sequence listing part.

[68241] VGAM1962 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1962 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1962 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[68242] VGAM1962 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1962 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1962 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM1962 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1962 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[68243] The complementary binding of VGAM1962 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1962 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1962 host target RNA into VGAM1962 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[68244] It is appreciated that VGAM1962 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1962 host target genes. The mRNA of each one of this plurality of VGAM1962 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1962 RNA, herein designated VGAM RNA, and which when bound by VGAM1962 RNA causes inhibition of translation of respective one or more VGAM1962 host target proteins.

[68245] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1962 gene, herein designated VGAM GENE, on one or more VGAM1962 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[68246] It is yet further appreciated that a function of VGAM1962

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1962 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM1962 correlate with, and may be deduced from, the identity of the host target genes which VGAM1962 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[68247] Nucleotide sequences of the VGAM1962 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1962 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1962 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1962 are further described hereinbelow with reference to Table 1.

[68248] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1962 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1962 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[68249] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1962 gene, herein designated VGAM is inhibition of expression of VGAM1962 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1962 correlate with, and may be deduced from, the identity of the target genes which VGAM1962 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[68250] A Kinase (PRKA) Anchor Protein 10 (AKAP10, Accession NM_007202) is a VGAM1962 host target gene. AKAP10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKAP10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP10 BINDING SITE, designated SEQ ID:14056, to the nucleotide sequence of VGAM1962 RNA, herein designated VGAM RNA, also designated SEQ ID:4673.

[68251] A function of VGAM1962 is therefore inhibition of A Kinase (PRKA) Anchor Protein 10 (AKAP10, Accession NM_007202). Accordingly, utilities of VGAM1962 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP10. Chromosome 11

Open Reading Frame 23 (C11orf23, Accession NM_018312) is another VGAM1962 host target gene. C11orf23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf23 BINDING SITE, designated SEQ ID:20304, to the nucleotide sequence of VGAM1962 RNA, herein designated VGAM RNA, also designated SEQ ID:4673.

[68252] Another function of VGAM1962 is therefore inhibition of Chromosome 11 Open Reading Frame 23 (C11orf23, Accession NM_018312). Accordingly, utilities of VGAM1962 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf23. C20orf180 (Accession NM_018431) is another VGAM1962 host target gene. C20orf180 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf180, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf180 BINDING

SITE, designated SEQ ID:20494, to the nucleotide sequence of VGAM1962 RNA, herein designated VGAM RNA, also designated SEQ ID:4673.

[68253] Another function of VGAM1962 is therefore inhibition of C20orf180 (Accession NM_018431). Accordingly, utilities of VGAM1962 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf180. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1963 (VGAM1963) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[68254] VGAM1963 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1963 was detected is described hereinabove with reference to Figs. 1-8.

[68255] VGAM1963 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM1963 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[68256] VGAM1963 gene encodes a VGAM1963 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1963 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1963 precursor RNA is designated SEQ ID:1949, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1949 is located at position 17595 relative to the genome of Camelpox Virus.

[68257] VGAM1963 precursor RNA folds onto itself, forming VGAM1963 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[68258] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1963 folded precursor RNA into VGAM1963 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1963 RNA is designated SEQ ID:4674, and is provided hereinbelow with reference to the sequence listing part.

[68259] VGAM1963 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1963 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1963 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[68260] VGAM1963 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1963 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1963 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1963 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1963 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[68261] The complementary binding of VGAM1963 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1963 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1963 host target RNA into VGAM1963 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[68262] It is appreciated that VGAM1963 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1963 host target genes. The mRNA of each one of this plurality of VGAM1963 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1963 RNA, herein designated VGAM RNA, and which when bound by VGAM1963 RNA causes inhibition of translation of respective one or more VGAM1963 host target proteins.

[68263] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1963 gene, herein designated VGAM GENE, on one or more VGAM1963 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[68264] It is yet further appreciated that a function of VGAM1963 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1963 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM1963 correlate with, and may be deduced from, the identity of the host target genes which VGAM1963 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[68265] Nucleotide sequences of the VGAM1963 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1963 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1963 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1963 are further described hereinbelow with reference to Table 1.

[68266] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1963 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM1963 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[68267] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1963 gene, herein designated VGAM is inhibition of expression of VGAM1963 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1963 correlate with, and may be deduced from, the identity of the target genes which VGAM1963 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[68268] Retinitis Pigmentosa 2 (X-linked recessive) (RP2, Accession NM_006915) is a VGAM1963 host target gene. RP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RP2 BINDING SITE, designated SEQ ID:13790, to the nucleotide sequence of VGAM1963 RNA, herein designated VGAM RNA, also designated SEQ ID:4674.

[68269] A function of VGAM1963 is therefore inhibition of Retinitis

Pigmentosa 2 (X-linked recessive) (RP2, Accession NM_006915). Accordingly, utilities of VGAM1963 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RP2. caspr5 (Accession NM_130773) is another VGAM1963 host target gene. caspr5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by caspr5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of caspr5 BINDING SITE, designated SEQ ID:28267, to the nucleotide sequence of VGAM1963 RNA, herein designated VGAM RNA, also designated SEQ ID:4674.

[68270] Another function of VGAM1963 is therefore inhibition of caspr5 (Accession NM_130773). Accordingly, utilities of VGAM1963 include diagnosis, prevention and treatment of diseases and clinical conditions associated with caspr5. FLJ11252 (Accession XM_041702) is another VGAM1963 host target gene. FLJ11252 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11252, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11252 BINDING SITE, designated SEQ ID:33566, to the nucleotide sequence of VGAM1963 RNA, herein designated VGAM RNA, also designated SEQ ID:4674.

[68271] Another function of VGAM1963 is therefore inhibition of FLJ11252 (Accession XM_041702). Accordingly, utilities of VGAM1963 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11252. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1964 (VGAM1964) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[68272] VGAM1964 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1964 was detected is described hereinabove with reference to Figs. 1-8.

[68273] VGAM1964 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM1964 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[68274] VGAM1964 gene encodes a VGAM1964 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1964 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1964 precursor RNA is designated SEQ ID:1950, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1950 is located at position 87983 relative to the genome of Rana Tigrina Ranavirus.

[68275] VGAM1964 precursor RNA folds onto itself, forming VGAM1964 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[68276] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1964 folded precursor RNA into VGAM1964

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1964 RNA is designated SEQ ID:4675, and is provided hereinbelow with reference to the sequence listing part.

[68277] VGAM1964 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1964 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1964 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[68278] VGAM1964 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1964 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1964 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1964 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1964 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[68279] The complementary binding of VGAM1964 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1964 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1964 host target RNA into VGAM1964 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[68280] It is appreciated that VGAM1964 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1964 host target genes. The mRNA of each one of this plurality of VGAM1964 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1964 RNA, herein designated VGAM RNA, and which when bound by VGAM1964 RNA causes inhibition of translation of respective one or more VGAM1964 host target proteins.

[68281] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1964 gene, herein designated VGAM GENE, on one or more VGAM1964 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[68282] It is yet further appreciated that a function of VGAM1964 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1964 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM1964 correlate with, and may be deduced from, the identity of the host target genes which VGAM1964 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[68283] Nucleotide sequences of the VGAM1964 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1964 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1964 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1964 are further described hereinbelow with reference to Table 1.

[68284] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1964 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1964 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[68285] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1964 gene, herein designated VGAM is inhibition of expression of VGAM1964 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1964 correlate with, and may be deduced from, the identity of the target genes which VGAM1964 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[68286] UDP-GlcNAc:betaGal Beta-1,3-N-acetylglucosaminyltransferase 3 (B3GNT3, Accession NM_014256) is a VGAM1964 host target gene. B3GNT3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by B3GNT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B3GNT3 BINDING SITE, designated SEQ

ID:15533, to the nucleotide sequence of VGAM1964 RNA, herein designated VGAM RNA, also designated SEQ ID:4675.

[68287] A function of VGAM1964 is therefore inhibition of UDP-GlcNAc:betaGal Beta-1,3-N-acetylglucosaminyltransferase 3 (B3GNT3, Accession NM_014256). Accordingly, utilities of VGAM1964 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B3GNT3. Microtubule-associated Protein 7 (MAP7, Accession NM_003980) is another VGAM1964 host target gene. MAP7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP7 BINDING SITE, designated SEQ ID:10118, to the nucleotide sequence of VGAM1964 RNA, herein designated VGAM RNA, also designated SEQ ID:4675.

[68288] Another function of VGAM1964 is therefore inhibition of Microtubule-associated Protein 7 (MAP7, Accession NM_003980), a gene which Microtubule-associated protein 7; stabilizes microtubules, may help establish epithelial cell polarity. Accordingly, utilities of VGAM1964 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP7. The function of MAP7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1373.Retinal Pigment Epithelium-specific Protein 65kDa (RPE65, Accession NM_000329) is another VGAM1964 host target gene. RPE65 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPE65, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPE65 BINDING SITE, designated SEQ ID:5872, to the nucleotide sequence of VGAM1964 RNA, herein designated VGAM RNA, also designated SEQ ID:4675.

[68289] Another function of VGAM1964 is therefore inhibition of Retinal Pigment Epithelium-specific Protein 65kDa (RPE65, Accession NM_000329), a gene which May play a role in vitamin-A metabolism of the retina. Accordingly, utilities of VGAM1964 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPE65. The function of RPE65 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM66.ERp44 (Accession XM_088476) is another VGAM1964 host target gene. ERp44 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERp44, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERp44 BINDING SITE, designated SEQ ID:39722, to the nucleotide sequence of VGAM1964 RNA, herein designated VGAM RNA, also designated SEQ ID:4675.

[68290] Another function of VGAM1964 is therefore inhibition of ERp44 (Accession XM_088476). Accordingly, utilities of VGAM1964 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERp44.

KIAA0266 (Accession NM_021645) is another VGAM1964 host target gene. KIAA0266 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0266 BINDING SITE, designated SEQ ID:22309, to the nucleotide sequence of VGAM1964 RNA, herein designated VGAM RNA, also designated SEQ ID:4675.

[68291] Another function of VGAM1964 is therefore inhibition of KIAA0266 (Accession NM_021645). Accordingly, utilities of VGAM1964 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0266. LOC113523 (Accession XM_054378) is another VGAM1964 host target gene. LOC113523 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC113523, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC113523 BINDING SITE, designated SEQ ID:36152, to the nucleotide sequence of VGAM1964 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4675.

[68292] Another function of VGAM1964 is therefore inhibition of LOC113523 (Accession XM_054378). Accordingly, utilities of VGAM1964 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113523. LOC145786 (Accession XM_096860) is another VGAM1964 host target gene. LOC145786 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145786 BINDING SITE, designated SEQ ID:40591, to the nucleotide sequence of VGAM1964 RNA, herein designated VGAM RNA, also designated SEQ ID:4675.

[68293] Another function of VGAM1964 is therefore inhibition of LOC145786 (Accession XM_096860). Accordingly, utilities of VGAM1964 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145786. LOC146332 (Accession XM_085413) is another VGAM1964 host target gene. LOC146332 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146332, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146332 BINDING SITE, designated SEQ ID:38128, to the nucleotide sequence of VGAM1964 RNA, herein designated VGAM RNA, also designated SEQ ID:4675.

[68294] Another function of VGAM1964 is therefore inhibition of LOC146332 (Accession XM_085413). Accordingly, utilities of VGAM1964 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146332. LOC158527 (Accession XM_088594) is another VGAM1964 host target gene. LOC158527 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158527, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158527 BINDING SITE, designated SEQ ID:39865, to the nucleotide sequence of VGAM1964 RNA, herein designated VGAM RNA, also designated SEQ ID:4675.

[68295] Another function of VGAM1964 is therefore inhibition of LOC158527 (Accession XM_088594). Accordingly, utilities of VGAM1964 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC158527. LOC91408 (Accession XM_038290) is another VGAM1964 host target gene. LOC91408 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91408, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91408 BINDING SITE, designated SEQ ID:32792, to the nucleotide sequence of VGAM1964 RNA, herein designated VGAM RNA, also designated SEQ ID:4675.

[68296] Another function of VGAM1964 is therefore inhibition of LOC91408 (Accession XM_038290). Accordingly, utilities of VGAM1964 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91408. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1965 (VGAM1965) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[68297] VGAM1965 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1965 was detected is described hereinabove with reference to Figs. 1-8.

[68298] VGAM1965 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM1965 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[68299] VGAM1965 gene encodes a VGAM1965 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1965 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1965 precursor RNA is designated SEQ ID:1951, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1951 is located at position 100137 relative to the genome of Rana Tigrina Ranavirus.

[68300] VGAM1965 precursor RNA folds onto itself, forming VGAM1965 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[68301] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1965 folded precursor RNA into VGAM1965 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1965 RNA is designated SEQ ID:4676, and is provided hereinbelow with reference to the sequence listing part.

[68302] VGAM1965 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1965 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1965 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[68303] VGAM1965 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1965 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1965 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1965 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1965 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[68304] The complementary binding of VGAM1965 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1965 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1965 host target RNA into VGAM1965 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[68305] It is appreciated that VGAM1965 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1965 host target genes. The mRNA of each one of this plurality of VGAM1965 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1965 RNA, herein designated VGAM RNA, and which when bound by VGAM1965 RNA causes inhibition of translation of respective one or more VGAM1965 host target proteins.

[68306] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1965 gene, herein designated VGAM GENE, on one or more VGAM1965 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[68307] It is yet further appreciated that a function of VGAM1965 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM1965 correlate with, and may be deduced from, the identity of the host target genes which VGAM1965 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[68308] Nucleotide sequences of the VGAM1965 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM1965 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1965 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1965 are further described hereinbelow with reference to Table 1.

[68309] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1965 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1965 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[68310] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1965 gene, herein designated VGAM is inhibition of expression of VGAM1965 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1965 correlate with, and may be deduced from, the identity of the target genes which VGAM1965 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[68311] ATP-binding Cassette, Sub-family D (ALD), Member 4 (ABCD4, Accession NM_020323) is a VGAM1965 host target gene. ABCD4 BINDING SITE1 through ABCD4 BINDING

SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ABCD4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCD4 BINDING SITE1 through ABCD4 BINDING SITE4, designated SEQ ID:21583, SEQ ID:21585, SEQ ID:21588 and SEQ ID:21591 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68312] A function of VGAM1965 is therefore inhibition of ATP-binding Cassette, Sub-family D (ALD), Member 4 (ABCD4, Accession NM_020323), a gene which Putative peroxisomal ATP binding cassette transporter. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCD4. The function of ABCD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1924.Acid Phosphatase, Testicular (ACPT, Accession NM_080790) is another VGAM1965 host target gene. ACPT BINDING SITE1 and ACPT BINDING SITE2 are HOST TARGET binding sites found in untranslated re-

gions of mRNA encoded by ACPT, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACPT BINDING SITE1 and ACPT BINDING SITE2, designated SEQ ID:28049 and SEQ ID:35054 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68313] Another function of VGAM1965 is therefore inhibition of Acid Phosphatase, Testicular (ACPT, Accession NM_080790). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACPT. Adenylate Cyclase 6 (ADCY6, Accession NM_015270) is another VGAM1965 host target gene. ADCY6 BINDING SITE1 and ADCY6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ADCY6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADCY6 BINDING SITE1 and ADCY6 BINDING SITE2, designated SEQ ID:17592 and SEQ ID:43182 respectively, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[68314] Another function of VGAM1965 is therefore inhibition of Adenylate Cyclase 6 (ADCY6, Accession NM_015270), a gene which this a membrane-bound, ca(2+)-inhibitable adenylyl cyclase (by similarity). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY6. The function of ADCY6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM22.S-adenosylmethionine Decarboxylase 1 (AMD1, Accession NM_001634) is another VGAM1965 host target gene. AMD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AMD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AMD1 BINDING SITE, designated SEQ ID:7346, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68315] Another function of VGAM1965 is therefore inhibition of S-adenosylmethionine Decarboxylase 1 (AMD1, Accession

NM_001634), a gene which catalyzes the removal of the carboxylate group of S-adenosylmethionine in the polyamine biosynthesis pathway. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMD1. The function of AMD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1016.Aminomethyltransferase (glycine cleavage system protein T) (AMT, Accession NM_000481) is another VGAM1965 host target gene. AMT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AMT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AMT BINDING SITE, designated SEQ ID:6091, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68316] Another function of VGAM1965 is therefore inhibition of Aminomethyltransferase (glycine cleavage system protein T) (AMT, Accession NM_000481). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with AMT. Ankyrin Repeat Domain 3 (ANKRD3, Accession NM_020639) is another VGAM1965 host target gene. ANKRD3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANKRD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANKRD3 BINDING SITE, designated SEQ ID:21798, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68317] Another function of VGAM1965 is therefore inhibition of Ankyrin Repeat Domain 3 (ANKRD3, Accession NM_020639). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKRD3. Adaptor-related Protein Complex 1, Beta 1 Subunit (AP1B1, Accession NM_001127) is another VGAM1965 host target gene. AP1B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP1B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of AP1B1 BINDING SITE, designated SEQ ID:6798, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68318] Another function of VGAM1965 is therefore inhibition of Adaptor-related Protein Complex 1, Beta 1 Subunit (AP1B1, Accession NM_001127), a gene which plays a role in protein sorting in the late-golgi/trans-golgi network (tgn) and/or endosomes. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1B1. The function of AP1B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1048.Adenomatosis Polyposis Coli (APC, Accession NM_000038) is another VGAM1965 host target gene. APC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APC BINDING SITE, designated SEQ ID:5479, to the nucleotide sequence of VGAM1965 RNA, herein designated

VGAM RNA, also designated SEQ ID:4676.

[68319] Another function of VGAM1965 is therefore inhibition of Adenomatosis Polyposis Coli (APC, Accession NM_000038). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APC. APPL (Accession NM_012096) is another VGAM1965 host target gene. APPL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APPL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APPL BINDING SITE, designated SEQ ID:14401, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68320] Another function of VGAM1965 is therefore inhibition of APPL (Accession NM_012096). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APPL. Archain 1 (ARCN1, Accession NM_001655) is another VGAM1965 host target gene. ARCN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARCN1, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARCN1 BINDING SITE, designated SEQ ID:7368, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68321] Another function of VGAM1965 is therefore inhibition of Archain 1 (ARCN1, Accession NM_001655), a gene which plays a fundamental role in eukaryotic cell biology. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARCN1. The function of ARCN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1226.ADP-ribosylation Factor 3 (ARF3, Accession NM_001659) is another VGAM1965 host target gene. ARF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARF3 BINDING SITE, designated SEQ ID:7380, to the nucleotide sequence of

VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68322] Another function of VGAM1965 is therefore inhibition of ADP-ribosylation Factor 3 (ARF3, Accession NM_001659). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARF3. Rho Guanine Nucleotide Exchange Factor (GEF) 7 (ARHGEF7, Accession NM_003899) is another VGAM1965 host target gene. ARHGEF7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHGEF7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGEF7 BINDING SITE, designated SEQ ID:9986, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68323] Another function of VGAM1965 is therefore inhibition of Rho Guanine Nucleotide Exchange Factor (GEF) 7 (ARHGEF7, Accession NM_003899), a gene which acts as a rac1 guanine nucleotide exchange factor (gef) and can induce membrane ruffling. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with ARHGEF7. The function of ARHGEF7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM297.ATP10C (Accession NM_024490) is another VGAM1965 host target gene. ATP10C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP10C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP10C BINDING SITE, designated SEQ ID:23688, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68324] Another function of VGAM1965 is therefore inhibition of ATP10C (Accession NM_024490), a gene which is phosphorylated in their intermediate state, drives uphill transport of ions across membranes. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP10C. The function of ATP10C and its association with various diseases and clinical conditions, has been estab-

lished by previous studies, as described hereinabove with reference to VGAM801.ATPase, Class VI, Type 11A (ATP11A, Accession XM_085028) is another VGAM1965 host target gene. ATP11A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP11A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP11A BINDING SITE, designated SEQ ID:37799, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68325] Another function of VGAM1965 is therefore inhibition of ATPase, Class VI, Type 11A (ATP11A, Accession XM_085028). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP11A. ATPase, Ca++ Transporting, Type 2C, Member 1 (ATP2C1, Accession NM_014382) is another VGAM1965 host target gene. ATP2C1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP2C1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of ATP2C1 BINDING SITE, designated SEQ ID:15718, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68326] Another function of VGAM1965 is therefore inhibition of ATPase, Ca++ Transporting, Type 2C, Member 1 (ATP2C1, Accession NM_014382). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP2C1. ATPase, Class I, Type 8B, Member 2 (ATP8B2, Accession XM_036933) is another VGAM1965 host target gene. ATP8B2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP8B2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP8B2 BINDING SITE, designated SEQ ID:32519, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68327] Another function of VGAM1965 is therefore inhibition of ATPase, Class I, Type 8B, Member 2 (ATP8B2, Accession

XM_036933). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8B2. Arginine Vasopressin Receptor 1A (AVPR1A, Accession NM_000706) is another VGAM1965 host target gene. AVPR1A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AVPR1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AVPR1A BINDING SITE, designated SEQ ID:6376, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68328] Another function of VGAM1965 is therefore inhibition of Arginine Vasopressin Receptor 1A (AVPR1A, Accession NM_000706), a gene which mediates cell contraction and proliferation, platelet aggregation, release of coagulation factor, and glycogenolysis. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AVPR1A. The function of AVPR1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to VGAM549.Beta-site APP-cleaving Enzyme (BACE, Accession NM_138971) is another VGAM1965 host target gene. BACE BINDING SITE1 and BACE BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by BACE, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BACE BINDING SITE1 and BACE BINDING SITE2, designated SEQ ID:29089 and SEQ ID:14421 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68329] Another function of VGAM1965 is therefore inhibition of Beta-site APP-cleaving Enzyme (BACE, Accession NM_138971), a gene which is responsible for the proteolytic processing of the amyloid precursor protein. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BACE. The function of BACE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM173.Bromodomain Adjacent to Zinc Finger Domain, 2B (BAZ2B, Accession

NM_013450) is another VGAM1965 host target gene. BAZ2B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BAZ2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAZ2B BINDING SITE, designated SEQ ID:15125, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68330] Another function of VGAM1965 is therefore inhibition of Bromodomain Adjacent to Zinc Finger Domain, 2B (BAZ2B, Accession NM_013450). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAZ2B. BCL2-like 2 (BCL2L2, Accession NM_004050) is another VGAM1965 host target gene. BCL2L2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL2L2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL2L2 BINDING SITE, designated SEQ ID:10264, to the nucleotide se-

quence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68331] Another function of VGAM1965 is therefore inhibition of BCL2-like 2 (BCL2L2, Accession NM_004050), a gene which promotes cell survival. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL2L2. The function of BCL2L2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM431.B-cell CLL/lymphoma 7A (BCL7A, Accession NM_020993) is another VGAM1965 host target gene. BCL7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL7A BINDING SITE, designated SEQ ID:21993, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68332] Another function of VGAM1965 is therefore inhibition of B-cell CLL/lymphoma 7A (BCL7A, Accession NM_020993).

Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL7A. BCRP2 (Accession XM_031102) is another VGAM1965 host target gene. BCRP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCRP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCRP2 BINDING SITE, designated SEQ ID:31274, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68333] Another function of VGAM1965 is therefore inhibition of BCRP2 (Accession XM_031102). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCRP2. Bone Morphogenetic Protein Receptor, Type IA (BMPR1A, Accession NM_004329) is another VGAM1965 host target gene. BMPR1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BMPR1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of BMPR1A BINDING SITE, designated SEQ ID:10529, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68334] Another function of VGAM1965 is therefore inhibition of Bone Morphogenetic Protein Receptor, Type IA (BMPR1A, Accession NM_004329). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BMPR1A. Bassoon (presynaptic cytomatrix protein) (BSN, Accession NM_003458) is another VGAM1965 host target gene. BSN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BSN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BSN BINDING SITE, designated SEQ ID:9522, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68335] Another function of VGAM1965 is therefore inhibition of Bassoon (presynaptic cytomatrix protein) (BSN, Accession NM_003458), a gene which may be involved in cytomatrix

organization at the site of neurotransmitter release. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BSN. The function of BSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM638.B-cell Translocation Gene 1, Anti-proliferative (BTG1, Accession NM_001731) is another VGAM1965 host target gene. BTG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTG1 BINDING SITE, designated SEQ ID:7466, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68336] Another function of VGAM1965 is therefore inhibition of B-cell Translocation Gene 1, Anti-proliferative (BTG1, Accession NM_001731), a gene which is a member of a new family of antiproliferative proteins. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTG1.

The function of BTG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1296.Chromosome 11 Open Reading Frame 8 (C11orf8, Accession NM_001584) is another VGAM1965 host target gene. C11orf8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf8 BINDING SITE, designated SEQ ID:7303, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68337] Another function of VGAM1965 is therefore inhibition of Chromosome 11 Open Reading Frame 8 (C11orf8, Accession NM_001584), a gene which May function in brain development. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf8. The function of C11orf8 has been established by previous studies. Schwartz et al. (1994) identified a gene, which they designated 239FB, from the 11p13-p14 region between PAX6

(OMIM Ref. No. 607108) and FSHB (OMIM Ref. No. 136530) known as the WAGR region (Wilms tumor, aniridia, genitourinary abnormalities, and mental retardation). Schwartz et al. (1995) showed that the predicted 294-amino acid protein shares regions of significant identity to a gene identified in an 8.5-day chicken embryo library and 2 C. elegans loci of unknown function. The gene consists of 6 exons spanning about 87 kb. A CpG island occurs at the 5-prime end of the gene. Northern blots detected a 3.1-kb transcript in fetal brain RNA. The extensive conservation of sequence places 239FB among a group of proteins that contains ancient conserved regions (Green et al., 1993) and is, presumably, functionally important. See also 239AB (OMIM Ref. No. 602112), a related human gene identified in adult brain.

[68338] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68339] Green, P.; Lipman, D.; Hillier, L.; Waterston, R.; States, D.; Claverie, J.-M. : Ancient conserved regions in new gene sequences and the protein databases. Science 259: 1711-1716, 1993. ; and

[68340] Schwartz, F.; Eisenman, R.; Knoll, J.; Gessler, M.; Bruns, G.

: cDNA sequence, genomic organization, and evolutionary conservation of a novel gene from the WAGR region. Genomics 29: 526-.

[68341] Further studies establishing the function and utilities of C11orf8 are found in John Hopkins OMIM database record ID 600911, and in sited publications numbered 9607-9609 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.C1D (Accession NM_006333) is another VGAM1965 host target gene. C1D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1D BINDING SITE, designated SEQ ID:13033, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68342] Another function of VGAM1965 is therefore inhibition of C1D (Accession NM_006333), a gene which is similar to murine C1D and may be a component of nuclear hormone receptor complexes. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1D. The function

of C1D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM78.Complement Component 5 Receptor 1 (C5a ligand) (C5R1, Accession NM_001736) is another VGAM1965 host target gene. C5R1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C5R1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5R1 BINDING SITE, designated SEQ ID:7475, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68343] Another function of VGAM1965 is therefore inhibition of Complement Component 5 Receptor 1 (C5a ligand) (C5R1, Accession NM_001736), a gene which has a nonredundant function and is required for mucosal host cell defense in the lung. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5R1. The function of C5R1 and its association with various diseases and clinical conditions, has been established by previous studies, as de-

scribed hereinabove with reference to VGAM484.Calumenin (CALU, Accession NM_001219) is another VGAM1965 host target gene. CALU BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CALU, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CALU BINDING SITE, designated SEQ ID:6887, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68344] Another function of VGAM1965 is therefore inhibition of Calumenin (CALU, Accession NM_001219), a gene which binds 7 calcium ions with a low affinity with unidtified function. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CALU. The function of CALU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM253.Caspase 3, Apoptosis-related Cysteine Protease (CASP3, Accession NM_032991) is another VGAM1965 host target gene. CASP3 BINDING SITE1 and CASP3 BINDING SITE2 are HOST

TARGET binding sites found in untranslated regions of mRNA encoded by CASP3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASP3 BINDING SITE1 and CASP3 BINDING SITE2, designated SEQ ID:26872 and SEQ ID:10541 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68345] Another function of VGAM1965 is therefore inhibition of Caspase 3, Apoptosis-related Cysteine Protease (CASP3, Accession NM_032991), a gene which is one apoptosis-related cysteine protease and is important for the initiation of apoptotic cell death. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP3. The function of CASP3 has been established by previous studies. Nicholson et al. (1995) developed a potent peptide aldehyde inhibitor and showed that it prevents apoptotic events in vitro, suggesting that apopain/CPP32 is important for the initiation of apoptotic cell death.Apoptosis of human endothelial cells after growth factor deprivation is associated with rapid and dramatic upregulation of cyclin

A-associated cyclin-dependent kinase-2 (CDK2; 116953) activity. Levkau et al. (1998) showed that in apoptotic cells the carboxyl termini of the CDK inhibitors CDKN1A (OMIM Ref. No. 116899) and CDKN1B (OMIM Ref. No. 600778) are truncated by specific cleavage. The enzyme involved in this cleavage is CASP3 and/or a CASP3-like caspase. After cleavage, CDKN1A loses its nuclear localization sequence and exits the nucleus. Cleavage of CDKN1A and CDKN1B resulted in a substantial reduction in their association with nuclear cyclin-CDK2 complexes, leading to a dramatic induction of CDK2 activity. Dominant-negative CDK2, as well as a mutant CDKN1A resistant to caspase cleavage, partially suppressed apoptosis. These data suggested that CDK2 activation, through caspase-mediated cleavage of CDK inhibitors, may be instrumental in the execution of apoptosis following caspase activation. Animal model experiments lend further support to the function of CASP3. To analyze the function of CPP32 in vivo, Kuida et al. (1996) generated CPP32-deficient mice by homologous recombination. These mice, born at a frequency lower than expected by mendelian genetics, were smaller than their littermates and died at 1 to 3 weeks of age. Although their thymocytes retained normal susceptibility to various

apoptotic stimuli, brain development in CPP32-deficient mice was profoundly affected, and discernible by embryonic day 12, resulting in a variety of hypoplasias and disorganized cell deployment. These supernumerary cells were postmitotic and terminally differentiated by the postnatal stage. Pyknotic clusters at sites of major morphogenetic change during normal brain development were not observed in the mutant embryos, indicating increased apoptosis in the absence of CPP32. Thus, CPP32 was shown by Kuida et al. (1996) to play a critical role during morphogenetic cell death in the mammalian brain.

[68346] It is appreciated that the abovementioned animal model for CASP3 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[68347] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68348] Kuida, K.; Zheng, T. S.; Na, S.; Kuan, C.; Yang, D.; Karasuyama, H.; Rakio, P.; Flavell, R. A. : Decreased apoptosis in the brain and premature lethality in CPP32-deficient mice. Nature 384: 368-372, 1996. ; and

[68349] Nicholson, D. W.; Ali, A.; Thornberry, N. A.; Vaillancourt, J.

P.; Ding, C. K.; Gallant, M.; Gareau, Y.; Griffin, P. R.; Labelle, M.; Lazebnik, Y. A.; Munday, N. A.; Raju, S. M.; Smulso.

[68350] Further studies establishing the function and utilities of CASP3 are found in John Hopkins OMIM database record ID 600636, and in sited publications numbered 7119-7121, 1211, 7122-7124, 462, 712 and 7128-7127 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.CD28 Antigen (Tp44) (CD28, Accession NM_006139) is another VGAM1965 host target gene. CD28 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD28, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD28 BINDING SITE, designated SEQ ID:12782, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68351] Another function of VGAM1965 is therefore inhibition of CD28 Antigen (Tp44) (CD28, Accession NM_006139), a gene which possibly involved in t-cell activation. Accordingly, utilities of VGAM1965 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with CD28. The function of CD28 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM281.CD69 Antigen (p60, early T-cell activation antigen) (CD69, Accession NM_001781) is another VGAM1965 host target gene. CD69 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD69, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD69 BINDING SITE, designated SEQ ID:7539, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68352] Another function of VGAM1965 is therefore inhibition of CD69 Antigen (p60, early T-cell activation antigen) (CD69, Accession NM_001781), a gene which is involved in lymphocyte proliferation and functions as a signal transmitting receptor. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD69. The function of CD69 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to VGAM1888.Cadherin 2, Type 1, N-cadherin (neuronal) (CDH2, Accession NM_001792) is another VGAM1965 host target gene. CDH2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDH2 BINDING SITE, designated SEQ ID:7543, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68353] Another function of VGAM1965 is therefore inhibition of Cadherin 2, Type 1, N-cadherin (neuronal) (CDH2, Accession NM_001792), a gene which may be involved in neuronal recognition mechanism. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH2. The function of CDH2 has been established by previous studies. may be involved in neuronal recognition mechanism.

[68354] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[68355] Tanaka, H.; Shan, W.; Phillips, G. R.; Arndt, K.; Bozdagi, O.; Shapiro, L.; Huntley, G. W.; Benson, D. L.; Colman, D. R. : Molecular modification of N-cadherin in response to synaptic activity. Neuron 25: 93-107, 2000. ; and

[68356] Miyatani, S.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N. A.; Takeichi, M. : Genomic structure and chromosomal mapping of the mouse N-cadherin gene. Proc. Nat. Acad. Sci. 89: 8443-844.

[68357] Further studies establishing the function and utilities of CDH2 are found in John Hopkins OMIM database record ID 114020, and in sited publications numbered 334 and 11647-11653 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Cadherin 6, Type 2, K-cadherin (fetal kidney) (CDH6, Accession NM_004932) is another VGAM1965 host target gene. CDH6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDH6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDH6 BINDING SITE, designated SEQ ID:11377,

to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68358] Another function of VGAM1965 is therefore inhibition of Cadherin 6, Type 2, K-cadherin (fetal kidney) (CDH6, Accession NM_004932), a gene which is a calcium dependent cell adhesion protein. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH6. The function of CDH6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM60.Cyclin-dependent Kinase Inhibitor 1A (p21, Cip1) (CDKN1A, Accession NM_078467) is another VGAM1965 host target gene. CDKN1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDKN1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDKN1A BINDING SITE, designated SEQ ID:27784, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68359] Another function of VGAM1965 is therefore inhibition of

Cyclin-dependent Kinase Inhibitor 1A (p21, Cip1) (CDKN1A, Accession NM_078467), a gene which inhibits cyclin-kinase activity and probably serves as the effector of p53 cell cycle control. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKN1A. The function of CDKN1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1912.Carcinoembryonic Antigen-related Cell Adhesion Molecule 6 (non-specific cross reacting antigen) (CEACAM6, Accession NM_002483) is another VGAM1965 host target gene. CEACAM6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CEACAM6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CEACAM6 BINDING SITE, designated SEQ ID:8311, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68360] Another function of VGAM1965 is therefore inhibition of Carcinoembryonic Antigen-related Cell Adhesion Molecule

6 (non-specific cross reacting antigen) (CEACAM6, Accession NM_002483), a gene which Non-specific cross reacting antigen (. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEACAM6. The function of CEACAM6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM286.Centaurin, Delta 1 (CENTD1, Accession NM_139182) is another VGAM1965 host target gene. CENTD1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CENTD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CENTD1 BINDING SITE, designated SEQ ID:29198, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68361] Another function of VGAM1965 is therefore inhibition of Centaurin, Delta 1 (CENTD1, Accession NM_139182), a gene which is nvolved in cell signaling/communication. Accordingly, utilities of VGAM1965 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with CENTD1. The function of CENTD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM445.CERD4 (Accession NM_012074) is another VGAM1965 host target gene. CERD4 BINDING SITE1 and CERD4 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CERD4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CERD4 BINDING SITE1 and CERD4 BINDING SITE2, designated SEQ ID:14352 and SEQ ID:14353 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68362] Another function of VGAM1965 is therefore inhibition of CERD4 (Accession NM_012074). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CERD4. Cholinergic Receptor, Nicotinic, Alpha Polypeptide 4 (CHRNA4, Accession NM_000744) is another VGAM1965 host target gene. CHRNA4 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by CHRNA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHRNA4 BINDING SITE, designated SEQ ID:6399, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68363] Another function of VGAM1965 is therefore inhibition of Cholinergic Receptor, Nicotinic, Alpha Polypeptide 4 (CHRNA4, Accession NM_000744), a gene which binds acetylcholine and opens an ion-conducting channel across the plasma membrane. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRNA4. The function of CHRNA4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1649.Cholinergic Receptor, Nicotinic, Alpha Polypeptide 5 (CHRNA5, Accession XM_007577) is another VGAM1965 host target gene. CHRNA5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CHRNA5, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHRNA5 BINDING SITE, designated SEQ ID:30057, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68364] Another function of VGAM1965 is therefore inhibition of Cholinergic Receptor, Nicotinic, Alpha Polypeptide 5 (CHRNA5, Accession XM_007577). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRNA5. Cholinergic Receptor, Nicotinic, Beta Polypeptide 2 (neuronal) (CHRNB2, Accession NM_000748) is another VGAM1965 host target gene. CHRNB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHRNB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHRNB2 BINDING SITE, designated SEQ ID:6403, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68365] Another function of VGAM1965 is therefore inhibition of

Cholinergic Receptor, Nicotinic, Beta Polypeptide 2 (neuronal) (CHRNB2, Accession NM_000748), a gene which mediates fast signal transmission at synapses. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRNB2. The function of CHRNB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM166.Cytoplasmic Linker Associated Protein 1 (CLASP1, Accession XM_037105) is another VGAM1965 host target gene. CLASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLASP1 BINDING SITE, designated SEQ ID:32542, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68366] Another function of VGAM1965 is therefore inhibition of Cytoplasmic Linker Associated Protein 1 (CLASP1, Accession XM_037105), a gene which plays a role in the local

regulation of microtubule dynamics . Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLASP1. The function of CLASP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM298.Cytoplasmic Linker Associated Protein 2 (CLASP2, Accession XM_035453) is another VGAM1965 host target gene. CLASP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLASP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLASP2 BINDING SITE, designated SEQ ID:32271, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68367] Another function of VGAM1965 is therefore inhibition of Cytoplasmic Linker Associated Protein 2 (CLASP2, Accession XM_035453), a gene which is involved in the regional regulation of microtubule dynamics in motile fibroblasts. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with CLASP2. The function of CLASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM897.Ceroid-lipofuscinosis, Neuronal 2, Late Infantile (Jansky-Bielschowsky disease) (CLN2, Accession NM_000391) is another VGAM1965 host target gene. CLN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLN2 BINDING SITE, designated SEQ ID:5963, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68368] Another function of VGAM1965 is therefore inhibition of Ceroid-lipofuscinosis, Neuronal 2, Late Infantile (Jansky-Bielschowsky disease) (CLN2, Accession NM_000391). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLN2. 2',3'-cyclic Nucleotide 3' Phosphodiesterase (CNP, Accession NM_033133) is another VGAM1965 host target gene. CNP

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNP BINDING SITE, designated SEQ ID:26978, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68369] Another function of VGAM1965 is therefore inhibition of 2',3'-cyclic Nucleotide 3' Phosphodiesterase (CNP, Accession NM_033133), a gene which can link tubulin to membranes and may regulate cytoplasmic microtubule distribution. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNP. The function of CNP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM443.Collagen, Type IV, Alpha 1 (COL4A1, Accession NM_001845) is another VGAM1965 host target gene. COL4A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL4A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL4A1 BINDING SITE, designated SEQ ID:7579, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68370] Another function of VGAM1965 is therefore inhibition of Collagen, Type IV, Alpha 1 (COL4A1, Accession NM_001845), a gene which is a member of a subfamily of collagen extracellular matrix proteins. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A1. The function of COL4A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1645.Carboxypeptidase D (CPD, Accession NM_001304) is another VGAM1965 host target gene. CPD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CPD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPD BINDING SITE, designated SEQ ID:6986, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[68371] Another function of VGAM1965 is therefore inhibition of Carboxypeptidase D (CPD, Accession NM_001304), a gene which is a membrane-bound metalloprotease. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPD. The function of CPD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM596.Carboxypeptidase N, Polypeptide 1, 50kD (CPN1, Accession NM_001308) is another VGAM1965 host target gene. CPN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CPN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPN1 BINDING SITE, designated SEQ ID:6991, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68372] Another function of VGAM1965 is therefore inhibition of Carboxypeptidase N, Polypeptide 1, 50kD (CPN1, Accession NM_001308), a gene which cleaves basic amino acid

residues from the C terminal of peptides and proteins. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPN1. The function of CPN1 has been established by previous studies. Carboxypeptidase N (arginine carboxypeptidase, EC 3.4.17.3) cleaves basic amino acid residues from the C terminal of peptides and proteins. The enzyme plays a central role in regulating the biologic activity of peptides such as kinins and anaphylatoxins, and therefore is also known as kininase-1 and anaphylatoxin inactivator. Carboxypeptidase N is a 280-kD tetrameric complex consisting of 2 identical 83-kD regulatory subunits (OMIM Ref. No. 603104) and 2 identical 50-kD catalytic subunits Skidgel et al. (1988) and Gebhard et al. (1989) each purified carboxypeptidase N and determined a partial sequence of the catalytic subunit. By screening a liver cDNA library with an oligonucleotide probe based on the protein sequence, Gebhard et al. (1989) isolated a cDNA encoding the catalytic subunit, CPN1. The predicted protein is 458 amino acids long. Riley et al. (1998) stated that carboxypeptidase N is a member of the regulatory B-type carboxypeptidase group (see OMIM Ref. No. CPD, 603102).

[68373] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68374] Gebhard, W.; Schube, M.; Eulitz, M. : cDNA cloning and complete primary structure of the small, active subunit of human carboxypeptidase N (kininase 1). Eur. J. Biochem. 178: 603-607, 1989. ; and

[68375] Skidgel, R. A.; Bennett, C. D.; Schilling, J. W.; Tan, F.; Weerasinghe, D. K.; Erdos, E. G. : Amino acid sequence of the N-terminus and selected tryptic peptides of the active subunit of.

[68376] Further studies establishing the function and utilities of CPN1 are found in John Hopkins OMIM database record ID 603103, and in sited publications numbered 849 and 8493 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.CAMP Responsive Element Binding Protein-like 2 (CREBL2, Accession NM_001310) is another VGAM1965 host target gene. CREBL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CREBL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of CREBL2 BINDING SITE, designated SEQ ID:6996, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68377] Another function of VGAM1965 is therefore inhibition of CAMP Responsive Element Binding Protein-like 2 (CREBL2, Accession NM_001310). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CREBL2. Connective Tissue Growth Factor (CTGF, Accession NM_001901) is another VGAM1965 host target gene. CTGF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CTGF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTGF BINDING SITE, designated SEQ ID:7625, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68378] Another function of VGAM1965 is therefore inhibition of Connective Tissue Growth Factor (CTGF, Accession NM_001901), a gene which promotes proliferation and differentiation of chondrocytes. Accordingly, utilities of

VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTGF. The function of CTGF has been established by previous studies. Bradham et al. (1991) described a new mitogen produced by human umbilical vein endothelial cells, which they termed connective tissue growth factor. The protein, related to platelet-derived growth factor (see OMIM Ref. No. 190040), was predicted from its cDNA to be a 349-amino acid, 38-kD cysteine-rich secreted protein. Martinerie et al. (1992) identified a locus sharing homology with the nov protooncogene overexpressed in avian nephroblastoma and corresponding to the CTGF gene. They assigned the CTGF gene to 6q23.1 by a combination of study of mouse/human somatic cell hybrids and fluorescence in situ hybridization. They showed that CTGF is situated proximal to MYB (OMIM Ref. No. 189990). By analysis of Northern blots, Kim et al. (1997) found that CTGF is expressed as a 2.4-kb mRNA in a broad spectrum of human tissues. Sequence comparison revealed that CTGF belongs to a group known as the immediate-early genes, which are expressed after induction by growth factors or certain oncogenes (see OMIM Ref. No. 164958). The immediate-early genes have significant sequence ho-

mology to the insulin-like growth factor-binding proteins (OMIM Ref. No. IGFBPs) and contain the conserved N-terminal IGFBP motif (see OMIM Ref. No. IGFBP7, 602867). CTGF shares 28 to 38% amino acid identity with IGFBPs 1-6. Kim et al. (1997) demonstrated that CTGF specifically bound insulin-like growth factors (IGFs), although with relatively low affinity. They proposed that the immediate-early genes, together with IGFBP7, constitute a subfamily of IGFBP genes whose products bind IGFs with low affinity Animal model experiments lend further support to the function of CTGF. Nakanishi et al. (2001) generated transgenic mice that overexpressed CTGF under the control of the mouse type XI collagen (see OMIM Ref. No. 120280) promoter. Embryonic and neonatal growth occurred normally, but transgenic mice showed dwarfism within a few months after birth. X-ray analysis revealed that their bone density was decreased compared with that of normal mice. Nakanishi et al. (2001) concluded that overexpression of CTGF affects certain steps of endochondral ossification. In addition, the testes were much smaller than normal and fertility was affected in transgenic mice, indicating that CTGF may also regulate the embryonic development of the testis

[68379] It is appreciated that the abovementioned animal model for CTGF is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[68380] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68381] Martinerie, C.; Viegas-Pequignot, E.; Guenard, I.; Dutrillaux, B.; Nguyen, V. C.; Bernheim, A.; Perbal, B. : Physical mapping of human loci homologous to the chicken nov proto-oncogene. Oncogene 7: 2529-2534, 1992. ; and

[68382] Nakanishi, T.; Yamaai, T.; Asano, M.; Nawachi, K.; Suzuki, M.; Sugimoto, T.; Takigawa, M. : Overexpression of connective tissue growth factor/hypertrophic chondrocyte-specific gene produc.

[68383] Further studies establishing the function and utilities of CTGF are found in John Hopkins OMIM database record ID 121009, and in sited publications numbered 497 and 11958-11960 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Chromosome X Open Reading Frame 6 (CXorf6, Accession NM_005491) is another VGAM1965 host target gene. CXorf6 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by CXorf6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CXorf6 BINDING SITE, designated SEQ ID:11995, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68384] Another function of VGAM1965 is therefore inhibition of Chromosome X Open Reading Frame 6 (CXorf6, Accession NM_005491). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXorf6. Deleted In Azoospermia (DAZ, Accession NM_004081) is another VGAM1965 host target gene. DAZ BINDING SITE1 through DAZ BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DAZ, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAZ BINDING SITE1 through DAZ BINDING SITE3, designated SEQ ID:10283, SEQ ID:39946 and SEQ ID:39945 respectively, to the nucleotide sequence of VGAM1965 RNA,

herein designated VGAM RNA, also designated SEQ ID:4676.

[68385] Another function of VGAM1965 is therefore inhibition of Deleted In Azoospermia (DAZ, Accession NM_004081), a gene which may play a role in the germ-cell-specific patterns of RNA splicing and storage. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAZ. The function of DAZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Dynactin 1 (p150, glued homolog, Drosophila) (DCTN1, Accession NM_004082) is another VGAM1965 host target gene. DCTN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DCTN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCTN1 BINDING SITE, designated SEQ ID:10286, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68386] Another function of VGAM1965 is therefore inhibition of

Dynactin 1 (p150, glued homolog, Drosophila) (DCTN1, Accession NM_004082), a gene which is a microtubule-based biologic motor protein. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCTN1. The function of DCTN1 has been established by previous studies. Cytoplasmic dynein is a microtubule-based biologic motor protein. Holzbaur and Tokito (1996) noted that dyneins were initially discovered as enzymes that couple ATP hydrolysis to provide a force for cellular motility in eukaryotic cilia and flagella. A distinct cytoplasmic form of dynein (OMIM Ref. No. 600112) was subsequently characterized and thought to be responsible for the intracellular retrograde motility of vesicles and organelles along microtubules (Holzbaur and Vallee, 1994). A large macromolecular complex, dynactin, is required for the cytoplasmic dynein-driven movement of organelles along microtubules. Dynactin is composed of 10 distinct polypeptides of 150, 135, 62, 50, 45, 42, 37, 32, 27, and 24 kD, with a combined mass of 10 million daltons. The largest polypeptide of the dynactin complex, p150(Glued), binds directly to microtubules and to cytoplasmic dynein. The binding of dynactin to dynein is critical for neuronal

function, as antibodies that specifically disrupt this binding block vesicle motility along microtubules in extruded squid axoplasm. Holzbaur and Tokito (1996) stated that the dynein-dynactin interaction is probably a key component of the mechanism of axonal transport of vesicles and organelles. Further evidence for a critical role for dynactin in vivo comes from the analysis of mutations in the homologous gene in Drosophila. Mutant alleles of the 'glued' gene induced disruption of the neurons of the optic lobe and compound eye in heterozygotes; null mutations are lethal.

[68387] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68388] Holzbaur, E. L. F.; Tokito, M. K. : Localization of the DCTN1 gene encoding p150(Glued) to human chromosome 2p13 by fluorescence in situ hybridization. Genomics 31: 398-399, 1996. ; and

[68389] Holzbaur, E. L. F.; Vallee, R. B. : Dyneins: molecular structure and cellular function. Ann. Rev. Cell Biol. 10: 339-372, 1994.

[68390] Further studies establishing the function and utilities of DCTN1 are found in John Hopkins OMIM database record

ID 601143, and in sited publications numbered 2850-2855 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.DNA Fragmentation Factor, 40kDa, Beta Polypeptide (caspase-activated DNase) (DFFB, Accession XM_113366) is another VGAM1965 host target gene. DFFB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DFFB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DFFB BINDING SITE, designated SEQ ID:42244, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68391] Another function of VGAM1965 is therefore inhibition of DNA Fragmentation Factor, 40kDa, Beta Polypeptide (caspase-activated DNase) (DFFB, Accession XM_113366), a gene which induces DNA fragmentation and chromatin condensation during apoptosis. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DFFB. The function of DFFB and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to VGAM74.Diacylglycerol Kinase, Gamma 90kDa (DGKG, Accession NM_001346) is another VGAM1965 host target gene. DGKG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DGKG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGKG BINDING SITE, designated SEQ ID:7027, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68392] Another function of VGAM1965 is therefore inhibition of Diacylglycerol Kinase, Gamma 90kDa (DGKG, Accession NM_001346), a gene which may convert diacylglycerol to phosphatidic acid. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGKG. The function of DGKG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM451.24-dehydrocholesterol Reductase (DHCR24, Accession NM_014762) is another VGAM1965 host target gene. DHCR24 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by DHCR24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DHCR24 BINDING SITE, designated SEQ ID:16526, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68393] Another function of VGAM1965 is therefore inhibition of 24-dehydrocholesterol Reductase (DHCR24, Accession NM_014762), a gene which catalyzes the reduction of sterol intermediates. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DHCR24. The function of DHCR24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM235.Dihydrofolate Reductase (DHFR, Accession NM_000791) is another VGAM1965 host target gene. DHFR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DHFR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of DHFR BINDING SITE, designated SEQ ID:6446, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68394] Another function of VGAM1965 is therefore inhibition of Dihydrofolate Reductase (DHFR, Accession NM_000791), a gene which converts dihydrofolate into tetrahydrofolate. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DHFR. The function of DHFR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM826.Discs, Large (Drosophila) Homolog 3 (neuroendocrine-dlg) (DLG3, Accession NM_021120) is another VGAM1965 host target gene. DLG3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DLG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLG3 BINDING SITE, designated SEQ ID:22095, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68395] Another function of VGAM1965 is therefore inhibition of Discs, Large (Drosophila) Homolog 3 (neuroendocrine-dlg) (DLG3, Accession NM_021120), a gene which may interact with the cytoplasmic tail of the nmda receptor subunit nr2b . Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLG3. The function of DLG3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM782.Discs, Large (Drosophila) Homolog 5 (DLG5, Accession XM_096398) is another VGAM1965 host target gene. DLG5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DLG5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLG5 BINDING SITE, designated SEQ ID:40342, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68396] Another function of VGAM1965 is therefore inhibition of Discs, Large (Drosophila) Homolog 5 (DLG5, Accession XM_096398), a gene which may transmit extracellular sig-

nals to inhibit cell proliferation. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLG5. The function of DLG5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM444.Dihydropyrimidine Dehydrogenase (DPYD, Accession XM_017469) is another VGAM1965 host target gene. DPYD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DPYD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DPYD BINDING SITE, designated SEQ ID:30319, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68397] Another function of VGAM1965 is therefore inhibition of Dihydropyrimidine Dehydrogenase (DPYD, Accession XM_017469). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPYD. Dopamine Receptor D2 (DRD2, Accession NM_000795) is another VGAM1965 host target gene. DRD2 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by DRD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DRD2 BINDING SITE, designated SEQ ID:6467, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68398] Another function of VGAM1965 is therefore inhibition of Dopamine Receptor D2 (DRD2, Accession NM_000795), a gene which has a key role in the control of movement. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRD2. The function of DRD2 has been established by previous studies. Bunzow et al. (1988) cloned the rat gene for D2 dopamine receptor. Grandy et al. (1989) cloned the human gene from a pituitary cDNA library. The deduced protein sequence is 96% identical to that of the rat receptor with 1 major difference: the human receptor contains an additional 29 amino acids in its putative third cytoplasmic loop. Southern blot analysis demonstrated the presence of only 1 human DRD2 gene. The coding sequence is interrupted by 6 introns. The ad-

ditional amino acids present in the human pituitary receptor are encoded by a single exon of 87 basepairs. Eubanks et al. (1992) found that the DRD2 gene extends over 270 kb and includes an intron of approximately 250 kb separating the putative first exon from the exons encoding the receptor protein. They prepared a physical map spanning more than 1.5 Mb of chromosome 11q23, which demonstrated that the neural cell adhesion molecule gene (NCAM; 116930) is located 150 kb 3-prime of the DRD2 gene and is transcribed from the same DNA strand. High resolution fluorescence in situ suppression hybridization using cosmid and YAC clones localized these genes between the APOA1 and STMY genes at the interface of 11q22.3 and 11q23.1. In situ hybridization studies showed, furthermore, that the DRD2/NCAM complex resides telomeric to the STMY1 gene and centromeric of the APOA1 gene. Animal model experiments lend further support to the function of DRD2. Balk et al. (1995) used homologous recombination to generate D2-receptor-deficient mice. Absence of D2 receptors led to animals that were akinetic and bradykinetic in behavioral tests and showed significantly reduced spontaneous movements. The phenotype resembled Parkinson disease.

Maldonado et al. (1997) studied the behavior of DRD2 knockout mice and showed that there was a total suppression of rewarding behavior with morphine. In contrast, these animals showed normal responses when food was used as a reward.

[68399] It is appreciated that the abovementioned animal model for DRD2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[68400] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68401] Eubanks, J. H.; Djabali, M.; Selleri, L.; Grandy, D. K.; Civelli, O.; McElligott, D. L.; Evans, G. A. : Structure and linkage of the D2 dopamine receptor and neural cell adhesion molecule genes on human chromosome 11q23. Genomics 14: 1010-1018, 1992. ; and

[68402] Maldonado, R.; Salardi, A.; Valverde, O.; Samad, T. A.; Roques, B. P.; Borrelli, E. : Absence of opiate rewarding effects in mice lacking dopamine D2 receptors. Nature 388: 586-589, 19.

[68403] Further studies establishing the function and utilities of DRD2 are found in John Hopkins OMIM database record ID

126450, and in sited publications numbered 11895-11899, 11886, 1190 and 11786-11804 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Desmocollin 3 (DSC3, Accession NM_024423) is another VGAM1965 host target gene. DSC3 BINDING SITE1 and DSC3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DSC3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DSC3 BINDING SITE1 and DSC3 BINDING SITE2, designated SEQ ID:23662 and SEQ ID:7651 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68404] Another function of VGAM1965 is therefore inhibition of Desmocollin 3 (DSC3, Accession NM_024423), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC3. The function of DSC3 and its association with various diseases and clinical conditions, has been established by previous studies, as de-

scribed hereinabove with reference to VGAM230.Endothelin 3 (EDN3, Accession NM_000114) is another VGAM1965 host target gene. EDN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EDN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EDN3 BINDING SITE, designated SEQ ID:5582, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68405] Another function of VGAM1965 is therefore inhibition of Endothelin 3 (EDN3, Accession NM_000114). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDN3. Endothelin Receptor Type A (EDNRA, Accession XM_034331) is another VGAM1965 host target gene. EDNRA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EDNRA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EDNRA BINDING SITE, designated SEQ

ID:32057, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68406] Another function of VGAM1965 is therefore inhibition of Endothelin Receptor Type A (EDNRA, Accession XM_034331), a gene which binds endothelins, and induces intracellular calcium flux and arachidonic acid accumulation. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDNRA. The function of EDNRA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM441.Eukaryotic Translation Initiation Factor 1A (EIF1A, Accession XM_114147) is another VGAM1965 host target gene. EIF1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF1A BINDING SITE, designated SEQ ID:42725, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ

ID:4676.

[68407] Another function of VGAM1965 is therefore inhibition of Eukaryotic Translation Initiation Factor 1A (EIF1A, Accession XM_114147), a gene which seems to be required for maximal rate of protein biosynthesis. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF1A. The function of EIF1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM120.Eukaryotic Translation Initiation Factor 2, Subunit 3 Gamma, 52kDa (EIF2S3, Accession NM_001415) is another VGAM1965 host target gene. EIF2S3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF2S3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF2S3 BINDING SITE, designated SEQ ID:7113, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68408] Another function of VGAM1965 is therefore inhibition of Eukaryotic Translation Initiation Factor 2, Subunit 3

Gamma, 52kDa (EIF2S3, Accession NM_001415), a gene which functions in the early steps of protein synthesis. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF2S3. The function of EIF2S3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1254.V-erb-a Erythroblastic Leukemia Viral Oncogene Homolog 4 (avian) (ERBB4, Accession NM_005235) is another VGAM1965 host target gene. ERBB4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERBB4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERBB4 BINDING SITE, designated SEQ ID:11747, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68409] Another function of VGAM1965 is therefore inhibition of V-erb-a Erythroblastic Leukemia Viral Oncogene Homolog 4 (avian) (ERBB4, Accession NM_005235), a gene which may function in growth/differentiation of normal and

transformed cells. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERBB4. The function of ERBB4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Exostoses (multiple) 2 (EXT2, Accession NM_000401) is another VGAM1965 host target gene. EXT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EXT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EXT2 BINDING SITE, designated SEQ ID:5976, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68410] Another function of VGAM1965 is therefore inhibition of Exostoses (multiple) 2 (EXT2, Accession NM_000401). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EXT2. Fatty-acid-Coenzyme A Ligase, Long-chain 3 (FACL3, Accession NM_004457) is another VGAM1965 host target gene. FACL3 BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by FACL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FACL3 BINDING SITE, designated SEQ ID:10759, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68411] Another function of VGAM1965 is therefore inhibition of Fatty-acid-Coenzyme A Ligase, Long-chain 3 (FACL3, Accession NM_004457), a gene which is required for lipid synthesis and fatty acid degradation. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FACL3. The function of FACL3 has been established by previous studies. See FACL1 (OMIM Ref. No. 152425) and FACL2 (OMIM Ref. No. 152426). An initial reaction in fatty acid metabolism in eukaryotic cells is activation of fatty acids catalyzed by acyl-CoA synthetase (ACS; EC 6.2.1.3). Fujino et al. (1996) identified a member of the ACS family by PCR of rat brain cDNAs using primers based on the conserved region of the ACS protein, and designated it ACS3. The 720-amino acid, approximately 80-kd rat pro-

tein preferentially utilizes myristate, laurate, arachidonate, and eicosapentaenoate, and is expressed primarily in brain. Minekura et al. (1997) used rat ACS3 cDNA as a probe to isolate a human ACS3 clone from a placental cDNA library. The predicted 720-amino acid human protein is 92% identical to that of rat ACS3. Minekura et al. (1997) used PCR of somatic cell hybrids and fluorescence in situ hybridization to map the ACS3 gene to 2q34-q35.

[68412] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68413] Fujino, T.; Kang, M.-J.; Suzuki, H.; Iijima, H.; Yamamoto, T. : Molecular characterization and expression of rat acyl-CoA synthetase 3. J. Biol. Chem. 271: 16748-16752, 1996. ; and

[68414] Minekura, H.; Fujino, T.; Kang, M.-J.; Fujita, T.; Endo, Y.; Yamamoto, T. T. : Human acyl-coenzyme A synthetase 3 cDNA and localization of its gene (ACS3) to chromosome band 2q34-q35. G.

[68415] Further studies establishing the function and utilities of FACL3 are found in John Hopkins OMIM database record ID 602371, and in sited publications numbered 8939-8940 listed in the bibliography section hereinbelow,

which are also hereby incorporated by reference.Ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2, Accession NM_015839) is another VGAM1965 host target gene. FCN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FCN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FCN2 BINDING SITE, designated SEQ ID:17955, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68416] Another function of VGAM1965 is therefore inhibition of Ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2, Accession NM_015839), a gene which is involved in phagocytosis of pathogens. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCN2. The function of FCN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM493.Ferredoxin 1 (FDX1, Accession XM_016467) is another VGAM1965 host target gene.

FDX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FDX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FDX1 BINDING SITE, designated SEQ ID:30260, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68417] Another function of VGAM1965 is therefore inhibition of Ferredoxin 1 (FDX1, Accession XM_016467), a gene which tcytochromes P450 involved in steroid, vitamin D, and bile acid metabolism. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FDX1. The function of FDX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM203.Frizzled Homolog 7 (Drosophila) (FZD7, Accession NM_003507) is another VGAM1965 host target gene. FZD7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FZD7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of FZD7 BINDING SITE, designated SEQ ID:9599, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68418] Another function of VGAM1965 is therefore inhibition of Frizzled Homolog 7 (Drosophila) (FZD7, Accession NM_003507), a gene which enhances beta-catenin mediated signaling. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FZD7. The function of FZD7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1063.G2A (Accession NM_013345) is another VGAM1965 host target gene. G2A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by G2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of G2A BINDING SITE, designated SEQ ID:14989, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68419] Another function of VGAM1965 is therefore inhibition of

G2A (Accession NM_013345), a gene which may mediate some of the effects of extracellular atp on insulin secretion. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G2A. The function of G2A has been established by previous studies. G2A belongs to a subfamily of GPCRs that bind to various glycolipids. Kabarowski et al. (2001) determined that expression of G2A induces signaling responses after exposure to lysophosphatidylcholine (LPC) and to sphingosylphosphorylcholine (SPC), a high-affinity ligand for OGR1 (GPR68; 601404). Scatchard analysis indicated that G2A binds LPC with high affinity and SPC with low affinity. Western blot analysis showed that both LPC and SPC activated ERK mitogen-activated protein kinase (see OMIM Ref. No. MAP3K4; 602425) in G2A-expressing CHO cells. LPC, but not SPC, stimulated transmigration of G2A-expressing T lymphocytes. The authors proposed that G2A may act as a sensor of LPC levels at sites of inflammation to limit the expansion of tissue-infiltrating cells promoting overt autoimmune disease. Animal model experiments lend further support to the function of G2A. Le et al. (2001) showed that mice with a targeted disruption of G2a, apart

from enhanced in vitro T-cell proliferative responses, initially appeared normal. With age, however, they developed a progressive secondary lymphoid organ enlargement associated with an abnormal polyclonal lymphocyte expansion. Older animals succumbed to a late-onset autoimmune wasting syndrome

[68420] It is appreciated that the abovementioned animal model for G2A is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[68421] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68422] Kabarowski, J. H. S.; Zhu, K.; Le, L. Q.; Witte, O. N.; Xu, Y. : Lysophosphatidylcholine as a ligand for the immunoregulatory receptor G2A. Science 293: 702-705, 2001. ; and

[68423] Le, L. Q.; Kabarowski, J. H. S.; Weng, Z.; Satterthwaite, A. B.; Harvill, E. T.; Jensen, E. R.; Miller, J. F.; Witte, O. N. : Mice lacking the orphan G protein-coupled receptor G2A de.

[68424] Further studies establishing the function and utilities of G2A are found in John Hopkins OMIM database record ID 606167, and in sited publications numbered 6994 listed

in the bibliography section hereinbelow, which are also hereby incorporated by reference.GRB2-associated Binding Protein 2 (GAB2, Accession NM_012296) is another VGAM1965 host target gene. GAB2 BINDING SITE1 and GAB2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GAB2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAB2 BINDING SITE1 and GAB2 BINDING SITE2, designated SEQ ID:14655 and SEQ ID:27850 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68425] Another function of VGAM1965 is therefore inhibition of GRB2-associated Binding Protein 2 (GAB2, Accession NM_012296), a gene which act as adapters for transmitting various signals. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAB2. The function of GAB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM53.GA Binding Protein Transcription Factor, Beta

Subunit 1, 53kDa (GABPB1, Accession NM_005254) is another VGAM1965 host target gene. GABPB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABPB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABPB1 BINDING SITE, designated SEQ ID:11762, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68426] Another function of VGAM1965 is therefore inhibition of GA Binding Protein Transcription Factor, Beta Subunit 1, 53kDa (GABPB1, Accession NM_005254), a gene which activates adenovirus E4 gene transcription. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABPB1. The function of GABPB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM191.UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3) (GALNT3, Accession NM_004482) is another VGAM1965

host target gene. GALNT3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GALNT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALNT3 BINDING SITE, designated SEQ ID:10805, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68427] Another function of VGAM1965 is therefore inhibition of UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 3 (GalNAc-T3) (GALNT3, Accession NM_004482), a gene which initiates O-glycosylation of serine and threonine residues. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNT3. The function of GALNT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1565.UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7, Accession NM_054110) is another VGAM1965

host target gene. GALNT7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GALNT7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALNT7 BINDING SITE, designated SEQ ID:27652, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68428] Another function of VGAM1965 is therefore inhibition of UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7, Accession NM_054110). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNT7. Growth Arrest-specific 7 (GAS7, Accession NM_003644) is another VGAM1965 host target gene. GAS7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GAS7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAS7 BINDING SITE, designated SEQ ID:9718,

to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68429] Another function of VGAM1965 is therefore inhibition of Growth Arrest-specific 7 (GAS7, Accession NM_003644), a gene which may play a role in promoting maturation and morphological differentiation of cerebellar neurons. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAS7. The function of GAS7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM232.Glioblastoma Amplified Sequence (GBAS, Accession NM_001483) is another VGAM1965 host target gene. GBAS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GBAS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GBAS BINDING SITE, designated SEQ ID:7227, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68430] Another function of VGAM1965 is therefore inhibition of

Glioblastoma Amplified Sequence (GBAS, Accession NM_001483), a gene which might be involved in vesicular transport. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GBAS. The function of GBAS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM859.GEMIN5 (Accession XM_114471) is another VGAM1965 host target gene. GEMIN5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GEMIN5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GEMIN5 BINDING SITE, designated SEQ ID:42973, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68431] Another function of VGAM1965 is therefore inhibition of GEMIN5 (Accession XM_114471). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GEMIN5. Gamma-glutamyl Carboxylase (GGCX, Accession

NM_000821) is another VGAM1965 host target gene. GGCX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GGCX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GGCX BINDING SITE, designated SEQ ID:6482, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68432] Another function of VGAM1965 is therefore inhibition of Gamma-glutamyl Carboxylase (GGCX, Accession NM_000821). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGCX. Gap Junction Protein, Beta 3, 31kDa (connexin 31) (GJB3, Accession NM_024009) is another VGAM1965 host target gene. GJB3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GJB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GJB3 BINDING SITE, designated SEQ ID:23442, to the nucleotide sequence of VGAM1965 RNA, herein designated

VGAM RNA, also designated SEQ ID:4676.

[68433] Another function of VGAM1965 is therefore inhibition of Gap Junction Protein, Beta 3, 31kDa (connexin 31) (GJB3, Accession NM_024009). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GJB3. Guanine Nucleotide Binding Protein (G protein), Alpha Inhibiting Activity Polypeptide 1 (GNAI1, Accession NM_002069) is another VGAM1965 host target gene. GNAI1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNAI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNAI1 BINDING SITE, designated SEQ ID:7842, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68434] Another function of VGAM1965 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Alpha Inhibiting Activity Polypeptide 1 (GNAI1, Accession NM_002069), a gene which is involved as modulators or transducers in various transmembrane signaling systems. Accordingly, utilities of VGAM1965 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with GNAI1. The function of GNAI1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM57.Guanine Nucleotide Binding Protein (G protein), Gamma 2 (GNG2, Accession XM_170743) is another VGAM1965 host target gene. GNG2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GNG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNG2 BINDING SITE, designated SEQ ID:45502, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68435] Another function of VGAM1965 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Gamma 2 (GNG2, Accession XM_170743), a gene which is involved as a modulator or transducer in various transmembrane signaling systems. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNG2. The function of GNG2 has been established by previous studies. Modar-

ressi et al. (2000) identified GNG2 by differential display RT-PCR of normal testis RNA and RNA from the testis of infertile and azoospermic patients. The full-length cDNA, obtained by 5-prime RACE, encodes a deduced 71-amino acid protein that is 100% homologous with the bovine, mouse, and rat GNG2 proteins. RT-PCR revealed expression in adult testis, adrenals, brain, white blood cells, and lung, but no or undetectable expression in testis from infertile or azoospermic patients, or in adult liver, muscle, or prostate. PCR of fetal tissues revealed highest expression in sternum and brain, intermediate expression in limbs, stomach, intestine, and kidney, and lowest expression in testis, heart, spleen, and lung. High expression was also found in tumor tissues from thyroid and parotid glands, in a squamous cell carcinoma, and in a lymphoid cell line, with little detected in granulation tissue. Yu et al. (2001) independently cloned human GNG2 from a 22-week fetal liver cDNA library.

[68436] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68437] Modarressi, M. H.; Taylor, K. E.; Wolfe, J. : Cloning, characterization, and mapping of the gene encoding the hu-

man G protein gamma-2 subunit. Biochem. Biophys. Res. Commun. 272: 610-615, 2000. ; and

[68438] Yu, Y.; Zhang, C.; Zhou, G.; Wu, S.; Qu, X.; Wei, H.; Xing, G.; Dong, C.; Zhai, Y.; Wan, J.; Ouyang, S.; Li, L., Zhang, S.; Zhou, K.; Zhang, Y.; Wu, C.; He, F. : Gene expression profil.

[68439] Further studies establishing the function and utilities of GNG2 are found in John Hopkins OMIM database record ID 606981, and in sited publications numbered 5526-5528 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Glypican 1 (GPC1, Accession NM_002081) is another VGAM1965 host target gene. GPC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPC1 BINDING SITE, designated SEQ ID:7876, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68440] Another function of VGAM1965 is therefore inhibition of Glypican 1 (GPC1, Accession NM_002081), a gene which may play a role in growth control and differentation. Ac-

cordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPC1. The function of GPC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM125.G Protein-coupled Receptor 85 (GPR85, Accession NM_018970) is another VGAM1965 host target gene. GPR85 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GPR85, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR85 BINDING SITE, designated SEQ ID:21044, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68441] Another function of VGAM1965 is therefore inhibition of G Protein-coupled Receptor 85 (GPR85, Accession NM_018970). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR85. Glucocorticoid Receptor DNA Binding Factor 1 (GRLF1, Accession XM_085943) is another VGAM1965 host target gene.

GRLF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRLF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRLF1 BINDING SITE, designated SEQ ID:38417, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68442] Another function of VGAM1965 is therefore inhibition of Glucocorticoid Receptor DNA Binding Factor 1 (GRLF1, Accession XM_085943), a gene which inhibits transcription of the glucocorticoid receptor gene. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRLF1. The function of GRLF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Glutamate Receptor, Metabotropic 6 (GRM6, Accession NM_000843) is another VGAM1965 host target gene. GRM6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRM6, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRM6 BINDING SITE, designated SEQ ID:6511, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68443] Another function of VGAM1965 is therefore inhibition of Glutamate Receptor, Metabotropic 6 (GRM6, Accession NM_000843). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRM6. HCS (Accession NM_018947) is another VGAM1965 host target gene. HCS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCS BINDING SITE, designated SEQ ID:21017, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68444] Another function of VGAM1965 is therefore inhibition of HCS (Accession NM_018947). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with HCS. Huntingtin Interacting Protein 1 (HIP1, Accession NM_005338) is another VGAM1965 host target gene. HIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIP1 BINDING SITE, designated SEQ ID:11811, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68445] Another function of VGAM1965 is therefore inhibition of Huntingtin Interacting Protein 1 (HIP1, Accession NM_005338), a gene which is a membrane protein and interacts with huntingtin. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIP1. The function of HIP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM474.Heterogeneous Nuclear Ribonucleoprotein D-like (HNRPDL, Accession NM_005463) is another VGAM1965 host target gene. HNRPDL BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HNRPDL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNRPDL BINDING SITE, designated SEQ ID:11955, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68446] Another function of VGAM1965 is therefore inhibition of Heterogeneous Nuclear Ribonucleoprotein D-like (HNRPDL, Accession NM_005463), a gene which binds to rna molecules that contain au-rich elements. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNRPDL. The function of HNRPDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM144.Homeo Box B9 (HOXB9, Accession NM_024017) is another VGAM1965 host target gene. HOXB9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HOXB9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of HOXB9 BINDING SITE, designated SEQ ID:23448, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68447] Another function of VGAM1965 is therefore inhibition of Homeo Box B9 (HOXB9, Accession NM_024017). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXB9. Histamine Receptor H1 (HRH1, Accession NM_000861) is another VGAM1965 host target gene. HRH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HRH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRH1 BINDING SITE, designated SEQ ID:6527, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68448] Another function of VGAM1965 is therefore inhibition of Histamine Receptor H1 (HRH1, Accession NM_000861), a gene which stimulates the synthesis of inositol phosphate. Accordingly, utilities of VGAM1965 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with HRH1. The function of HRH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM766.Heat Shock 70kDa Protein 5 (glucose-regulated protein, 78kDa) (HSPA5, Accession NM_005347) is another VGAM1965 host target gene. HSPA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSPA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPA5 BINDING SITE, designated SEQ ID:11822, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68449] Another function of VGAM1965 is therefore inhibition of Heat Shock 70kDa Protein 5 (glucose-regulated protein, 78kDa) (HSPA5, Accession NM_005347), a gene which is involved in the folding and assembly of proteins in the endoplasmic reticulum (ER). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPA5.

The function of HSPA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1782.Inducible T-cell Co-stimulator (ICOS, Accession NM_012092) is another VGAM1965 host target gene. ICOS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICOS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ICOS BINDING SITE, designated SEQ ID:14392, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68450] Another function of VGAM1965 is therefore inhibition of Inducible T-cell Co-stimulator (ICOS, Accession NM_012092), a gene which forms homodimers and functions as an inducible T-cell co-stimulator. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICOS. The function of ICOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM18.Inhibitor of DNA Binding 3, Domi-

nant Negative Helix-loop-helix Protein (ID3, Accession XM_086357) is another VGAM1965 host target gene. ID3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ID3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ID3 BINDING SITE, designated SEQ ID:38612, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68451] Another function of VGAM1965 is therefore inhibition of Inhibitor of DNA Binding 3, Dominant Negative Helix-loop-helix Protein (ID3, Accession XM_086357), a gene which inhibits DNA-binding of E2A-containing complexes. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ID3. The function of ID3 has been established by previous studies. Members of the ID family of helix-loop-helix (HLH) proteins lack a basic DNA-binding domain and inhibit transcription through formation of nonfunctional dimers that are incapable of binding to DNA. Ellmeier et al. (1992) isolated a novel human gene encoding a helix-loop-helix protein by molecu-

lar cloning of chromosome 1p36-specific CpG islands. Initially termed HEIR1, the ID3 gene was localized to the neuroblastoma consensus deletion region, 1p36.2-p36.12. Its predicted protein was 95.8% identical to the mouse HLH462 protein and had clear homology to the mouse Id and Drosophila emc proteins. The gene was expressed at high abundance in adult lung, kidney, and adrenal medulla, but not in adult brain. Despite prominent HEIR1 expression in adrenal medulla, which is a prime target for neuroblastomas, 10 of 12 neuroblastoma-derived cell lines showed very low levels of HEIR1 mRNA. Low HEIR1 expression was generally found in tumor cell lines with NMYC (OMIM Ref. No. 164840) overexpression, whereas the 2 cell lines displaying high HEIR1 levels did not overexpress NMYC. Mutually exclusive expression of the 2 genes was also found by in situ hybridization in developing mouse tissues, particularly in the forebrain neuroectoderm. Ellmeier et al. (1992) concluded that HEIR1 expression is reduced specifically in the majority of neuroblastomas and suggested an inverse correlation between HEIR1 and NMYC expression in these tumors and in embryonic development. ID3 is an inhibitor of E proteins, such as E2A (OMIM Ref. No. 147141). By Northern and

Western blot analysis, Kee et al. (2001) showed that transforming growth factor-beta (OMIM Ref. No. 190180) in mouse rapidly induced transient Id3 expression in B-lymphocyte precursors. This induction involved activation of the SMAD (see OMIM Ref. No. 602932) transcription factor pathway. Deed et al. (1994) reported a comparison of the ID3 gene with ID1 (OMIM Ref. No. 600349) and ID2 (OMIM Ref. No. 600386) that showed a highly conserved protein-coding gene organization consistent with evolution from a common ancestral gene. Animal model experiments lend further support to the function of ID3. Id proteins may control cell differentiation by interfering with DNA binding of transcription factors. Lyden et al. (1999) demonstrated that the targeted disruption of Id1 and Id3 in mice results in premature withdrawal of neuroblasts in the cell cycle and expression of neural-specific differentiation markers. Lyden et al. (1999) crossed Id1 +/- and Id3 +/- mice. Offspring lacking 1 to 3 Id alleles in any combination were indistinguishable from wildtype, but no animals lacking all 4 Id alleles were born. The Id1-Id3 double knockout mice displayed vascular malformations in forebrain and absence of branching and sprouting of blood vessels in the neuroectoderm. As angiogenesis both

in the brain and in tumors requires invasion of avascular tissue by endothelial cells, Lyden et al. (1999) examined Id knockout mice for their ability to support the growth of tumor xenografts. Three different tumors failed to grow and/or metastasize in Id1+/-Id3-/- mice, and any tumor growth present showed poor vascularization and extensive necrosis. Lyden et al. (1999) concluded that Id genes are required to maintain the timing of neuronal differentiation in the embryo and invasiveness of the vasculature. Because the Id genes are expressed at very low levels in adults, they make attractive targets for antiangiogenic drug design. Lyden et al. (1999) also concluded that the premature neuronal differentiation in Id1-Id3 double knockout mice indicates that ID1 or ID3 is required to block the precisely timed expression and activation of positively acting bHLH proteins during murine development. Pan et al. (1999) found that Id3-deficient mice had no overt abnormalities but had compromised humoral immunity. After immunization with T cell-dependent or T cell-independent antigens, the responses of Id3-deficient mice were attenuated and severely impaired, respectively. T-cell proliferative responses appeared to be intact, but IFNG expression may have been impaired. The defect in B-

cell proliferation could be rescued by ectopic expression of Id1.

[68452] It is appreciated that the abovementioned animal model for ID3 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[68453] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68454] Kee, B. L.; Rivera, R. R.; Murre, C. : Id3 inhibits B lymphocyte progenitor growth and survival in response to TGF-beta. Nature Immun. 2: 242-247, 2001. ; and

[68455] Lyden, D.; Young, A. Z.; Zagzag, D.; Yan, W.; Gerald, W.; O'Reilly, R.; Bader, B. L.; Hynes, R. O.; Zhuang, Y.; Manova, K.; Benezra, R. : Id1 and Id3 are required for neurogenesis, angi.

[68456] Further studies establishing the function and utilities of ID3 are found in John Hopkins OMIM database record ID 600277, and in sited publications numbered 8421-842 and 10357 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Inositol Hexaphosphate Kinase 1 (IHPK1, Accession XM_171045) is another VGAM1965 host target gene. IHPK1 BINDING

SITE1 and IHPK1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by IHPK1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IHPK1 BINDING SITE1 and IHPK1 BINDING SITE2, designated SEQ ID:45824 and SEQ ID:45825 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68457] Another function of VGAM1965 is therefore inhibition of Inositol Hexaphosphate Kinase 1 (IHPK1, Accession XM_171045), a gene which is a messenger molecule that releases calcium from intracellular stores. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IHPK1. The function of IHPK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1061.Interleukin 18 (interferon-gamma-inducing factor) (IL18, Accession NM_001562) is another VGAM1965 host target gene. IL18 BINDING SITE is HOST TARGET binding site found in the

5` untranslated region of mRNA encoded by IL18, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL18 BINDING SITE, designated SEQ ID:7292, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68458] Another function of VGAM1965 is therefore inhibition of Interleukin 18 (interferon-gamma-inducing factor) (IL18, Accession NM_001562), a gene which augments natural killer cell activity in spleen cells and stimulates interferon gamma production in t helper type i cells. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL18. The function of IL18 has been established by previous studies. Okamura et al. (1995) cloned an interferon-gamma (IFNG; 147570)-inducing factor that augments natural killer (NK) cell activity in spleen cells. The gene encodes a precursor protein of 192 amino acids and a mature protein of 157 amino acids. Messenger RNAs for the gene, designated IGIF by them, and for interleukin-12 (IL12; OMIM Ref. No. 161560) were readily detected in Kupffer cells and activated macrophages. Recombinant

IGIF induced IFNG more potently than did IL12, which is also a NK-cell stimulatory factor. Administration of anti-IGIF antibodies prevented liver damage in mice inoculated with Propionibacterium acnes and challenged with lipopolysaccharide that induces toxic shock. Okamura et al. (1995) speculated that IGIF may be involved in the development of Th1 cells and also in mechanisms of tissue injury in inflammatory reactions. The mechanism underlying the differentiation of CD4+ T cells into functionally distinct Th1 and Th2 subsets had been incompletely understood. The interferon-gamma-inducing factor is also known as interleukin-18 (Sarvetnick, 1997). Rothe et al. (1997) concluded that IGIF expression is normally regulated in autoimmune NOD mice and is closely associated with diabetes development. They showed that the Igif gene maps to mouse chromosome 9 within the Idd2 interval and is therefore a candidate for the Idd2 diabetes susceptibility gene, a non-MHC gene associated with the acceleration of diabetes development Animal model experiments lend further support to the function of IL18. In transgenic mice, Konishi et al. (2002) showed that IL18 contributes to the spontaneous development of atopic dermatitis-like inflammatory skin lesions independently of

IgE/Stat6 (OMIM Ref. No. 601512) under specific pathogen-free conditions. Overrelease of IL18 initiated atopic dermatitis-like inflammation, which was accelerated by interleukin 1-alpha (IL1A; 147760).

[68459] It is appreciated that the abovementioned animal model for IL18 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[68460] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68461] Okamura, H.; Tsutsui, H.; Komatsu, T.; Yutsudo, M.; Hakura, A.; Tanimoto, T.; Torigoe, K.; Okura, T.; Nukada, Y.; Hattori, K.; Akita, K.; Namba, M.; Tanabe, F.; Konishi, K.; Fukuda, S.; Kurimoto, M. : Cloning of a new cytokine that induces IFN-gamma production by T cells. Nature 378: 88-91, 1995. ; and

[68462] Konishi, H.; Tsutsui, H.; Murakami, T.; Yumikura-Futatsugi, S.; Yamanaka, K.; Tanaka, M.; Iwakura, Y.; Suzuki, N.; Takeda, K.; Akira, S.; Nakanishi, K.; Mizutani, H. : IL-18 contributes.

[68463] Further studies establishing the function and utilities of IL18 are found in John Hopkins OMIM database record ID

600953, and in sited publications numbered 8950-1320, 11688-1324, 1162, 943 and 11190 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Interleukin 1 Receptor, Type I (IL1R1, Accession NM_000877) is another VGAM1965 host target gene. IL1R1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL1R1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1R1 BINDING SITE, designated SEQ ID:6567, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68464] Another function of VGAM1965 is therefore inhibition of Interleukin 1 Receptor, Type I (IL1R1, Accession NM_000877), a gene which is a receptor for interleukin-1 alpha (il-1a), beta (il-1b), and interleukin-1 receptor antagonist protein (il-1ra). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1R1. The function of IL1R1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM704.Interleukin 1 Receptor Accessory Protein-like 2 (IL1RAPL2, Accession NM_017416) is another VGAM1965 host target gene. IL1RAPL2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IL1RAPL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1RAPL2 BINDING SITE, designated SEQ ID:18874, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68465] Another function of VGAM1965 is therefore inhibition of Interleukin 1 Receptor Accessory Protein-like 2 (IL1RAPL2, Accession NM_017416), a gene which may act in the development or function of the central nervous system. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1RAPL2. The function of IL1RAPL2 has been established by previous studies. The IL1 receptor family is composed of bona fide receptors (e.g., IL1R (OMIM Ref. No. 147810) and IL18R (OMIM Ref. No. 604494)), decoy receptors (e.g., IL1R2; 147811), signaling accessory receptors (e.g., IL1RAP (OMIM Ref. No. 602626)

and IL18RAP (OMIM Ref. No. 604509)), and structurally homologous orphan receptors. During searches of genomic databases with the IL1RAPL1 (OMIM Ref. No. 300206) cDNA sequence, Jin et al. (2000) identified a close homolog, which they designated IL1RAPL2, located on Xq22. They obtained a partial IL1RAPL2 cDNA by screening a human brain cDNA library. The cDNA encodes a deduced 658-amino acid protein that shares 65% identity with the IL1RAPL1 protein. Both proteins have novel C-terminal sequences not present in other members of the IL1 receptor family. The IL1RAPL2 gene is transcribed in a centromere-to-telomere direction. By searching genomic databases for sequences homologous to the Toll homology domain (THD), Sana et al. (2000) identified a cDNA encoding IL1RAPL2, which they termed IL1R9. Sequence analysis predicted that the 307-amino acid cytoplasmic tail of the 686-amino acid IL1RAPL2 protein contains an additional 120 to 130 residues beyond the THD, like IL1R8 (IL1RAPL1) but unlike other IL1Rs. Northern blot analysis revealed expression of a 5.5-kb transcript in fetal brain. Functional analysis determined that neither IL1RAPL1 nor IL1RAPL2 activate nuclear factor kappa-B (NFKB; OMIM Ref. No. 164011) except in the presence of

bona fide receptors but not orphan receptors. Evolutionary sequence analysis suggested that these orphan receptors probably form a functionally distinct subset of the IL1R superfamily. Jin et al. (2000) and Sana et al. (2000) suggested that, like IL1RAPL1, IL1RAPL2 may be the site of mutations causing nonspecific mental retardation.

[68466] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68467] Jin, H.; Gardner, R. J.; Viswesvaraiah, R.; Muntoni, F.; Roberts, R. G. : Two novel members of the interleukin-1 receptor gene family, one deleted in Xp22.1-Xp21.3 mental retardation. Europ. J. Hum. Genet. 8: 87-94, 2000. ; and

[68468] Sana, T. R.; Debets, R.; Timans, J. C.; Bazan, J. F.; Kastelein, R. A. : Computational identification, cloning, and characterization of IL1R9, a novel interleukin-1 receptor-like gene e.

[68469] Further studies establishing the function and utilities of IL1RAPL2 are found in John Hopkins OMIM database record ID 300277, and in sited publications numbered 899 and 10993 listed in the bibliography section hereinbelow, which are also hereby incorporated by refer-

ence.Interleukin 21 Receptor (IL21R, Accession NM_021798) is another VGAM1965 host target gene. IL21R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL21R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL21R BINDING SITE, designated SEQ ID:22355, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68470] Another function of VGAM1965 is therefore inhibition of Interleukin 21 Receptor (IL21R, Accession NM_021798), a gene which is involved in receptor mediated endocytosis and transduces the mitogenic signals of il-2. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL21R. The function of IL21R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1940.Interleukin Enhancer Binding Factor 1 (ILF1, Accession NM_004514) is another VGAM1965 host target gene. ILF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by ILF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ILF1 BINDING SITE, designated SEQ ID:10844, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68471] Another function of VGAM1965 is therefore inhibition of Interleukin Enhancer Binding Factor 1 (ILF1, Accession NM_004514), a gene which binds to nfat-like motifs (purine-rich) in the hiv-1 long terminal repeat and in the il-2 promoter. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ILF1. The function of ILF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1446.Insulin Receptor Substrate 1 (IRS1, Accession NM_005544) is another VGAM1965 host target gene. IRS1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IRS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of IRS1 BINDING SITE, designated SEQ ID:12070, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68472] Another function of VGAM1965 is therefore inhibition of Insulin Receptor Substrate 1 (IRS1, Accession NM_005544), a gene which may mediate the control of various cellular processes by insulin. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRS1. The function of IRS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM281.Insulin Receptor Substrate 2 (IRS2, Accession XM_007095) is another VGAM1965 host target gene. IRS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IRS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRS2 BINDING SITE, designated SEQ ID:30034, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68473] Another function of VGAM1965 is therefore inhibition of Insulin Receptor Substrate 2 (IRS2, Accession XM_007095), a gene which may mediate the control of various cellular processes by insulin. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRS2. The function of IRS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1217.ISL1 Transcription Factor, LIM/homeodomain, (islet-1) (ISL1, Accession NM_002202) is another VGAM1965 host target gene. ISL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ISL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ISL1 BINDING SITE, designated SEQ ID:7958, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68474] Another function of VGAM1965 is therefore inhibition of ISL1 Transcription Factor, LIM/homeodomain, (islet-1) (ISL1, Accession NM_002202), a gene which binds to one

of the cis-acting domain of the insulin gene enhancer. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ISL1. The function of ISL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM464.Integrin, Alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5, Accession XM_028642) is another VGAM1965 host target gene. ITGA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA5 BINDING SITE, designated SEQ ID:30722, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68475] Another function of VGAM1965 is therefore inhibition of Integrin, Alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5, Accession XM_028642), a gene which is receptor for fibronectin and fibrinogen and recognizes the sequence r-g-d in its ligands. Accordingly, utilities of

VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA5. The function of ITGA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1220.Inositol 1,4,5-triphosphate Receptor, Type 1 (ITPR1, Accession NM_002222) is another VGAM1965 host target gene. ITPR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITPR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITPR1 BINDING SITE, designated SEQ ID:7987, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68476] Another function of VGAM1965 is therefore inhibition of Inositol 1,4,5-triphosphate Receptor, Type 1 (ITPR1, Accession NM_002222), a gene which couples cell membrane receptors to Ca2+ signal transduction pathways. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPR1. The function of ITPR1 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM106.Jagged 1 (Alagille syndrome) (JAG1, Accession NM_000214) is another VGAM1965 host target gene. JAG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by JAG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JAG1 BINDING SITE, designated SEQ ID:5711, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68477] Another function of VGAM1965 is therefore inhibition of Jagged 1 (Alagille syndrome) (JAG1, Accession NM_000214). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAG1. Janus Kinase 2 (a protein tyrosine kinase) (JAK2, Accession NM_004972) is another VGAM1965 host target gene. JAK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by JAK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JAK2 BINDING SITE, designated SEQ ID:11417, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68478] Another function of VGAM1965 is therefore inhibition of Janus Kinase 2 (a protein tyrosine kinase) (JAK2, Accession NM_004972), a gene which tyrosine kinase of the non-receptor type, involved in interleukin 3 signal transduction. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAK2. The function of JAK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM445.JJAZ1 (Accession NM_015355) is another VGAM1965 host target gene. JJAZ1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by JJAZ1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JJAZ1 BINDING SITE, designated SEQ ID:17652, to the nucleotide sequence of VGAM1965 RNA, herein

designated VGAM RNA, also designated SEQ ID:4676.

[68479] Another function of VGAM1965 is therefore inhibition of JJAZ1 (Accession NM_015355), a gene which is a zinc finger protein. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JJAZ1. The function of JJAZ1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM231.Potassium Voltage-gated Channel, Shaker-related Subfamily, Member 5 (KCNA5, Accession XM_006988) is another VGAM1965 host target gene. KCNA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNA5 BINDING SITE, designated SEQ ID:30027, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68480] Another function of VGAM1965 is therefore inhibition of Potassium Voltage-gated Channel, Shaker-related Sub-

family, Member 5 (KCNA5, Accession XM_006988), a gene which mediates the voltage-dependent potassium ion permeability of excitable membranes. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNA5. The function of KCNA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM413.Potassium Channel, Subfamily K, Member 6 (KCNK6, Accession NM_004823) is another VGAM1965 host target gene. KCNK6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNK6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNK6 BINDING SITE, designated SEQ ID:11240, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68481] Another function of VGAM1965 is therefore inhibition of Potassium Channel, Subfamily K, Member 6 (KCNK6, Accession NM_004823), a gene which is an inward rectifying potassium channel protein. Accordingly, utilities of

VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK6. The function of KCNK6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1190.Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 2 (KCNS2, Accession XM_043106) is another VGAM1965 host target gene. KCNS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNS2 BINDING SITE, designated SEQ ID:33895, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68482] Another function of VGAM1965 is therefore inhibition of Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 2 (KCNS2, Accession XM_043106), a gene which mediates the voltage-dependent potassium ion permeability of excitable membranes. Accordingly, utilities of VGAM1965 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with KCNS2. The function of KCNS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM419.Kinase Insert Domain Receptor (a type III receptor tyrosine kinase) (KDR, Accession NM_002253) is another VGAM1965 host target gene. KDR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KDR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KDR BINDING SITE, designated SEQ ID:8051, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68483] Another function of VGAM1965 is therefore inhibition of Kinase Insert Domain Receptor (a type III receptor tyrosine kinase) (KDR, Accession NM_002253). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KDR. KIAA0857 (Accession XM_039552) is another VGAM1965 host target gene. KIAA0857 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA0857, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0857 BINDING SITE, designated SEQ ID:33122, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68484] Another function of VGAM1965 is therefore inhibition of KIAA0857 (Accession XM_039552), a gene which is involved in cytoskeletal organization and cellular growth. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0857. The function of KIAA0857 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM548.Kinesin Family Member 3B (KIF3B, Accession NM_004798) is another VGAM1965 host target gene. KIF3B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIF3B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of KIF3B BINDING SITE, designated SEQ ID:11219, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68485] Another function of VGAM1965 is therefore inhibition of Kinesin Family Member 3B (KIF3B, Accession NM_004798), a gene which is a microtubule-based anterograde translocator for membranous organelles. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF3B. The function of KIF3B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1017.Killer Cell Lectin-like Receptor Subfamily G, Member 1 (KLRG1, Accession NM_005810) is another VGAM1965 host target gene. KLRG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLRG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLRG1 BINDING SITE, designated SEQ ID:12393, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68486] Another function of VGAM1965 is therefore inhibition of Killer Cell Lectin-like Receptor Subfamily G, Member 1 (KLRG1, Accession NM_005810), a gene which plays a role in host defense;. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLRG1. The function of KLRG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM648.Lysosomal-associated Membrane Protein 2 (LAMP2, Accession NM_013995) is another VGAM1965 host target gene. LAMP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LAMP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAMP2 BINDING SITE, designated SEQ ID:15187, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68487] Another function of VGAM1965 is therefore inhibition of Lysosomal-associated Membrane Protein 2 (LAMP2, Accession NM_013995). Accordingly, utilities of VGAM1965

include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMP2. Leptin (obesity homolog, mouse) (LEP, Accession NM_000230) is another VGAM1965 host target gene. LEP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LEP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LEP BINDING SITE, designated SEQ ID:5741, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68488] Another function of VGAM1965 is therefore inhibition of Leptin (obesity homolog, mouse) (LEP, Accession NM_000230). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LEP. LIM Homeobox Protein 5 (LHX5, Accession NM_022363) is another VGAM1965 host target gene. LHX5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LHX5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the

nucleotide sequences of LHX5 BINDING SITE, designated SEQ ID:22751, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68489] Another function of VGAM1965 is therefore inhibition of LIM Homeobox Protein 5 (LHX5, Accession NM_022363). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHX5. Loss of Heterozygosity, 11, Chromosomal Region 2, Gene A (LOH11CR2A, Accession NM_014622) is another VGAM1965 host target gene. LOH11CR2A BINDING SITE1 and LOH11CR2A BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOH11CR2A, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOH11CR2A BINDING SITE1 and LOH11CR2A BINDING SITE2, designated SEQ ID:15987 and SEQ ID:15991 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68490] Another function of VGAM1965 is therefore inhibition of

Loss of Heterozygosity, 11, Chromosomal Region 2, Gene A (LOH11CR2A, Accession NM_014622). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOH11CR2A. Low Density Lipoprotein-related Protein 1 (alpha-2-macroglobulin receptor) (LRP1, Accession NM_002332) is another VGAM1965 host target gene. LRP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LRP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRP1 BINDING SITE, designated SEQ ID:8139, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68491] Another function of VGAM1965 is therefore inhibition of Low Density Lipoprotein-related Protein 1 (alpha-2-macroglobulin receptor) (LRP1, Accession NM_002332), a gene which is a recycling lipoprotein receptor with possible growth-modulating effects. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRP1. The function of LRP1 and its association

with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM885.Low Density Lipoprotein Receptor-related Protein 8, Apolipoprotein E Receptor (LRP8, Accession NM_033300) is another VGAM1965 host target gene. LRP8 BINDING SITE1 and LRP8 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LRP8, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRP8 BINDING SITE1 and LRP8 BINDING SITE2, designated SEQ ID:27133 and SEQ ID:11009 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68492] Another function of VGAM1965 is therefore inhibition of Low Density Lipoprotein Receptor-related Protein 8, Apolipoprotein E Receptor (LRP8, Accession NM_033300), a gene which binds vldl and transports it into cells by endocytosis. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRP8. The function of LRP8 and its association with various diseases and clinical condi-

tions, has been established by previous studies, as described hereinabove with reference to VGAM191.Mitogen-activated Protein Kinase Kinase 1 (MAP2K1, Accession NM_002755) is another VGAM1965 host target gene. MAP2K1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP2K1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP2K1 BINDING SITE, designated SEQ ID:8633, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68493] Another function of VGAM1965 is therefore inhibition of Mitogen-activated Protein Kinase Kinase 1 (MAP2K1, Accession NM_002755), a gene which is a signaling intermediate, may take part in cell transformation. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP2K1. The function of MAP2K1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM528.Mitogen-activated Protein Ki-

nase Kinase Kinase 7 Interacting Protein 2 (MAP3K7IP2, Accession NM_015093) is another VGAM1965 host target gene. MAP3K7IP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K7IP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K7IP2 BINDING SITE, designated SEQ ID:17488, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68494] Another function of VGAM1965 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 7 Interacting Protein 2 (MAP3K7IP2, Accession NM_015093). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K7IP2. Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_139125) is another VGAM1965 host target gene. MASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MASP1 BINDING SITE, designated SEQ ID:29160, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68495] Another function of VGAM1965 is therefore inhibition of Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_139125), a gene which a complement-dependent bactericidal factor . Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MASP1. The function of MASP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM566.Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog 2 (mouse) (MEIS2, Accession NM_020149) is another VGAM1965 host target gene. MEIS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEIS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEIS2 BIND-

ING SITE, designated SEQ ID:21348, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68496] Another function of VGAM1965 is therefore inhibition of Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog 2 (mouse) (MEIS2, Accession NM_020149), a gene which may regulate gene expression and control cell differentiation. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEIS2. The function of MEIS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1244.Multiple Endocrine Neoplasia I (MEN1, Accession XM_167804) is another VGAM1965 host target gene. MEN1 BINDING SITE1 and MEN1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MEN1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEN1 BINDING SITE1 and MEN1 BINDING SITE2, designated SEQ ID:44846 and SEQ ID:44847 respectively, to the nucleotide sequence of VGAM1965 RNA,

herein designated VGAM RNA, also designated SEQ ID:4676.

[68497] Another function of VGAM1965 is therefore inhibition of Multiple Endocrine Neoplasia I (MEN1, Accession XM_167804). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEN1. Mesenchyme Homeo Box 1 (MEOX1, Accession NM_004527) is another VGAM1965 host target gene. MEOX1 BINDING SITE1 and MEOX1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MEOX1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEOX1 BINDING SITE1 and MEOX1 BINDING SITE2, designated SEQ ID:10865 and SEQ ID:23309 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68498] Another function of VGAM1965 is therefore inhibition of Mesenchyme Homeo Box 1 (MEOX1, Accession NM_004527), a gene which plays a role in mesoderm induction and isomitogenesis, and sclerotomal differentia-

tion . Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEOX1. The function of MEOX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Maltase-glucoamylase (alpha-glucosidase) (MGAM, Accession XM_051351) is another VGAM1965 host target gene. MGAM BINDING SITE1 and MGAM BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MGAM, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGAM BINDING SITE1 and MGAM BINDING SITE2, designated SEQ ID:35825 and SEQ ID:35828 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68499] Another function of VGAM1965 is therefore inhibition of Maltase-glucoamylase (alpha-glucosidase) (MGAM, Accession XM_051351), a gene which plays a role in the final steps of digestion of starch. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MGAM. The function of MGAM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM791.Matrix Metalloproteinase 11 (stromelysin 3) (MMP11, Accession NM_005940) is another VGAM1965 host target gene. MMP11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MMP11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MMP11 BINDING SITE, designated SEQ ID:12579, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68500] Another function of VGAM1965 is therefore inhibition of Matrix Metalloproteinase 11 (stromelysin 3) (MMP11, Accession NM_005940). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMP11. MAX Binding Protein (MNT, Accession NM_020310) is another VGAM1965 host target gene. MNT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by MNT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MNT BINDING SITE, designated SEQ ID:21568, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68501] Another function of VGAM1965 is therefore inhibition of MAX Binding Protein (MNT, Accession NM_020310). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MNT. Mucin 4, Tracheobronchial (MUC4, Accession NM_138298) is another VGAM1965 host target gene. MUC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MUC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MUC4 BINDING SITE, designated SEQ ID:28712, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68502] Another function of VGAM1965 is therefore inhibition of Mucin 4, Tracheobronchial (MUC4, Accession

NM_138298), a gene which may act as a ligand for ErbB2 mediated cell signalling. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MUC4. The function of MUC4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1290.C-myc Binding Protein (MYCBP, Accession NM_012333) is another VGAM1965 host target gene. MYCBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYCBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYCBP BINDING SITE, designated SEQ ID:14725, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68503] Another function of VGAM1965 is therefore inhibition of C-myc Binding Protein (MYCBP, Accession NM_012333), a gene which binds c-Myc stimulating the activation of E-box-dependent transcription. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MYCBP. The function of MYCBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM435.N-ethylmaleimide-sensitive Factor Attachment Protein, Beta (NAPB, Accession XM_046652) is another VGAM1965 host target gene. NAPB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NAPB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAPB BINDING SITE, designated SEQ ID:34768, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68504] Another function of VGAM1965 is therefore inhibition of N-ethylmaleimide-sensitive Factor Attachment Protein, Beta (NAPB, Accession XM_046652). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAPB. Neurocalcin Delta (NCALD, Accession NM_032041) is another VGAM1965 host target gene. NCALD BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by NCALD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCALD BINDING SITE, designated SEQ ID:25743, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68505] Another function of VGAM1965 is therefore inhibition of Neurocalcin Delta (NCALD, Accession NM_032041). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCALD. NADH Dehydrogenase (ubiquinone) 1 Alpha Subcomplex, 6, 14kDa (NDUFA6, Accession NM_002490) is another VGAM1965 host target gene. NDUFA6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NDUFA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDUFA6 BINDING SITE, designated SEQ ID:8313, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68506] Another function of VGAM1965 is therefore inhibition of NADH Dehydrogenase (ubiquinone) 1 Alpha Subcomplex, 6, 14kDa (NDUFA6, Accession NM_002490), a gene which transfers electrons from nadh to the respiratory chain. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDUFA6. The function of NDUFA6 has been established by previous studies. See NDUFA2 (OMIM Ref. No. 602137). Dunbar et al. (1997) mapped the NDUFA6 gene to 21q22 by fluorescence in situ hybridization (FISH). However, by intron-based radiation hybrid mapping, Emahazion and Brookes (1998) assigned the NDUFA6 gene to 22q13.1. They stated that subsequent mapping studies with subfragments of the FISH-mapped recombinants of Dunbar et al. (1997) suggested chimerism and confirmed that the earlier FISH data were flawed. Ton et al. (1997) isolated human heart cDNAs encoding CI-B14 (OMIM Ref. No. NDUFA6) and 4 other complex I subunits.

[68507] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68508] Dunbar, D. R.; Shibasaki, Y.; Dobbie, L.; Andersson, B.; Brookes, A. J. : In situ hybridisation mapping of genomic

clones for five human respiratory chain complex I genes. Cytogenet. Cell Genet. 78: 21-24, 1997. ; and

[68509] Emahazion, T.; Brookes, A. J. : Mapping of the NDUFA2, NDUFA6, NDUFA7, NDUFB8, and NDUFS8 electron transport chain genes by intron based radiation hybrid mapping. Cytogenet. Cell Genet.

[68510] Further studies establishing the function and utilities of NDUFA6 are found in John Hopkins OMIM database record ID 602138, and in sited publications numbered 6283-6285 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.NEBL (Accession NM_006393) is another VGAM1965 host target gene. NEBL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NEBL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NEBL BINDING SITE, designated SEQ ID:13097, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68511] Another function of VGAM1965 is therefore inhibition of NEBL (Accession NM_006393). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with NEBL. Nuclear Factor I/A (NFIA, Accession XM_046827) is another VGAM1965 host target gene. NFIA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NFIA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFIA BINDING SITE, designated SEQ ID:34843, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68512] Another function of VGAM1965 is therefore inhibition of Nuclear Factor I/A (NFIA, Accession XM_046827). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFIA. Neuro-oncological Ventral Antigen 1 (NOVA1, Accession NM_006489) is another VGAM1965 host target gene. NOVA1 BINDING SITE1 and NOVA1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NOVA1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

NOVA1 BINDING SITE1 and NOVA1 BINDING SITE2, designated SEQ ID:13219 and SEQ ID:8350 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68513] Another function of VGAM1965 is therefore inhibition of Neuro-oncological Ventral Antigen 1 (NOVA1, Accession NM_006489), a gene which may regulate rna splicing or metabolism in a specific subset of developing neurons. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOVA1. The function of NOVA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM521.Neuropeptide Y Receptor Y1 (NPY1R, Accession NM_000909) is another VGAM1965 host target gene. NPY1R BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NPY1R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPY1R BINDING SITE, designated SEQ ID:6608, to the nucleotide sequence of VGAM1965 RNA, herein

designated VGAM RNA, also designated SEQ ID:4676.

[68514] Another function of VGAM1965 is therefore inhibition of Neuropeptide Y Receptor Y1 (NPY1R, Accession NM_000909), a gene which stimulates intracellular calcium flux and signals through an inhibitory G-protein. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPY1R. The function of NPY1R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1588.Neuronal Cell Adhesion Molecule (NRCAM, Accession NM_005010) is another VGAM1965 host target gene. NRCAM BINDING SITE1 and NRCAM BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NRCAM, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NRCAM BINDING SITE1 and NRCAM BINDING SITE2, designated SEQ ID:11453 and SEQ ID:11454 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68515] Another function of VGAM1965 is therefore inhibition of Neuronal Cell Adhesion Molecule (NRCAM, Accession NM_005010), a gene which functions as a cell surface protein and belongs to the immunoglobulin superfamily. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRCAM. The function of NRCAM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM268.Nuclear Respiratory Factor 1 (NRF1, Accession XM_011548) is another VGAM1965 host target gene. NRF1 BINDING SITE1 and NRF1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NRF1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NRF1 BINDING SITE1 and NRF1 BINDING SITE2, designated SEQ ID:30190 and SEQ ID:8378 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68516] Another function of VGAM1965 is therefore inhibition of Nuclear Respiratory Factor 1 (NRF1, Accession

XM_011548), a gene which is a basic leucine zipper (bZIP) transcriptional activator and involved in the regulation of genes for EIF2A and respiratory subunits. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRF1. The function of NRF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1314.Oxidative-stress Responsive 1 (OSR1, Accession NM_005109) is another VGAM1965 host target gene. OSR1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by OSR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSR1 BINDING SITE, designated SEQ ID:11592, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68517] Another function of VGAM1965 is therefore inhibition of Oxidative-stress Responsive 1 (OSR1, Accession NM_005109), a gene which mediats stress-activated signals. Accordingly, utilities of VGAM1965 include diagno-

sis, prevention and treatment of diseases and clinical conditions associated with OSR1. The function of OSR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM538.Platelet-activating Factor Acetylhydrolase, Isoform Ib, Alpha Subunit 45kDa (PAFAH1B1, Accession NM_000430) is another VGAM1965 host target gene. PAFAH1B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAFAH1B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAFAH1B1 BINDING SITE, designated SEQ ID:6014, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68518] Another function of VGAM1965 is therefore inhibition of Platelet-activating Factor Acetylhydrolase, Isoform Ib, Alpha Subunit 45kDa (PAFAH1B1, Accession NM_000430). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAFAH1B1. Paired Box Gene 5 (B-cell

lineage specific activator protein) (PAX5, Accession NM_016734) is another VGAM1965 host target gene. PAX5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAX5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAX5 BINDING SITE, designated SEQ ID:18791, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68519] Another function of VGAM1965 is therefore inhibition of Paired Box Gene 5 (B-cell lineage specific activator protein) (PAX5, Accession NM_016734), a gene which plays a role in B-cell differentiation, neural development and spermatogenesis. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAX5. The function of PAX5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1151.Protocadherin 11 X-linked (PCDH11X, Accession NM_032967) is another VGAM1965 host target gene. PCDH11X BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by PCDH11X, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11X BINDING SITE, designated SEQ ID:26782, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68520] Another function of VGAM1965 is therefore inhibition of Protocadherin 11 X-linked (PCDH11X, Accession NM_032967), a gene which is thought to play a fundamental role in cell-cell recognition essential for the segmental development and function of the central nervous system. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11X. The function of PCDH11X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Phosphatidylcholine Transfer Protein (PCTP, Accession NM_021213) is another VGAM1965 host target gene. PCTP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

PCTP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCTP BINDING SITE, designated SEQ ID:22194, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68521] Another function of VGAM1965 is therefore inhibition of Phosphatidylcholine Transfer Protein (PCTP, Accession NM_021213), a gene which catalyzes the transfer of phosphatidylcholine between membranes (by similarity). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCTP. The function of PCTP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1396.Phosphodiesterase 4C, CAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila) (PDE4C, Accession NM_000923) is another VGAM1965 host target gene. PDE4C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE4C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of PDE4C BINDING SITE, designated SEQ ID:6635, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68522] Another function of VGAM1965 is therefore inhibition of Phosphodiesterase 4C, CAMP-specific (phosphodiesterase E1 dunce homolog, Drosophila) (PDE4C, Accession NM_000923), a gene which is a cAMP-specific phosphodiesterase and may be a protein involved in learning and memory. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4C. The function of PDE4C has been established by previous studies. Milatovich et al. (1994) applied Southern analyses of somatic cell hybrid lines and of recombinant inbred mouse strains, as well as fluorescence chromosomal in situ hybridization (FISH), to map 4 'dunce-like' cAMP-specific nucleotide phosphodiesterase genes in human and mouse. DPDE1 (also symbolized PDE4C) was assigned to human chromosome 19 and mouse chromosome 8. DPDE2 (also symbolized PDE4A; 600126) was also assigned to human chromosome 19 but to mouse chromosome 9. DPDE3 (also symbolized PDE4D; 600129) was assigned to human 5q12

and mouse chromosome 13. DPDE4 (also symbolized PDE4B; 600127) was assigned to human 1p31 and mouse chromosome 4. By fluorescence in situ hybridization, Sullivan et al. (1999) localized the PDE4C gene to 19p13.1. They found that the PDE4C gene spans at least 38 kb, consists of at least 18 exons, and contains the marker D19S212 within an intron. Comparison of the published human PDE4C cDNA sequences with those of the genomic DNA identified 4 alternatively spliced exons and the possibility that the PDE4C locus contains at least 3 alternative promoters. The cosmids containing PDE4C also contained the genes for the growth regulatory transcription factor JUND (OMIM Ref. No. 165162), and the mini guanine nucleotide regulatory protein RAB3A (OMIM Ref. No. 179490). RAB3A was shown to consist of 5 exons spanning 7.9 kb, while the JUND gene was found to contain no introns. Analysis of cosmids containing PDE4C, JUND, and RAB3A showed that 27 kb separate JUND and PDE4C, while only 3.7 kb separate PDE4C and RAB3A. The 3 genes share the same orientation of transcription and are arranged in the 5-prime/3-prime order as follows: JUND--PDE4C--RAB3A--tel.

[68523] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[68524] Milatovich, A.; Bolger, G.; Michaeli, T.; Francke, U. : Chromosome localizations of genes for five cAMP-specific phosphodiesterases in man and mouse. Somat. Cell Molec. Genet. 20: 75-86, 1994. ; and

[68525] Sullivan, M.; Olsen, A. S.; Houslay, M. D. : Genomic organisation of the human cyclic AMP-specific phosphodiesterase PDE4C gene and its chromosomal localisation to 19p13.1, between RAB3A.

[68526] Further studies establishing the function and utilities of PDE4C are found in John Hopkins OMIM database record ID 600128, and in sited publications numbered 488 and 12445 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Platelet-derived Growth Factor Receptor, Beta Polypeptide (PDGFRB, Accession XM_038350) is another VGAM1965 host target gene. PDGFRB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDGFRB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDGFRB

BINDING SITE, designated SEQ ID:32817, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68527] Another function of VGAM1965 is therefore inhibition of Platelet-derived Growth Factor Receptor, Beta Polypeptide (PDGFRB, Accession XM_038350), a gene which Platelet-derived growth factor receptor beta chain; tyrosine kinase receptor. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFRB. The function of PDGFRB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM125.Phospholipase A2, Group IID (PLA2G2D, Accession NM_012400) is another VGAM1965 host target gene. PLA2G2D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLA2G2D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLA2G2D BINDING SITE, designated SEQ ID:14774, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ

ID:4676.

[68528] Another function of VGAM1965 is therefore inhibition of Phospholipase A2, Group IID (PLA2G2D, Accession NM_012400), a gene which is involved in phospholipid digestion, remodeling of cell membranes, and host defense, as well as pathophysiologic processes. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLA2G2D. The function of PLA2G2D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.PPAR Binding Protein (PPARBP, Accession NM_004774) is another VGAM1965 host target gene. PPARBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPARBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPARBP BINDING SITE, designated SEQ ID:11164, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68529] Another function of VGAM1965 is therefore inhibition of

PPAR Binding Protein (PPARBP, Accession NM_004774), a gene which interacts with thyroid hormone receptors to regulate nuclear receptor-mediated transcription; binds dna and p53 protein. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPARBP. The function of PPARBP has been established by previous studies. By immunoscreening a human B-lymphoma cell cDNA expression library with the anti-p53 (see OMIM Ref. No. TP53; 191170) monoclonal antibody PAb1801, Drane et al. (1997) identified PPARBP, which they called RB18A for 'recognized by PAb1801 monoclonal antibody.' The predicted 1,566-amino acid RB18A protein contains several potential nuclear localization signals, 13 potential N-glycosylation sites, and a high number of potential phosphorylation sites. Despite sharing common antigenic determinants with p53, RB18A does not show significant nucleotide or amino acid sequence similarity with p53. Whereas the calculated molecular mass of RB18A is 166 kD, the apparent mass of recombinant RB18A was 205 kD by SDS-PAGE analysis. Drane et al. (1997) demonstrated that RB18A shares functional properties with p53, including DNA binding, p53 binding, and self-oligomerization.

Furthermore, RB18A was able to activate the sequence-specific binding of p53 to DNA, which was induced through an unstable interaction between both proteins. Northern blot analysis of human tissues detected an 8.5-kb RB18A transcript in all tissues examined except kidney, with highest expression in heart. Animal model experiments lend further support to the function of PPARBP. Ito et al. (2000) generated mouse mutants with targeted disruption of the Trap220 gene. The null mutants died during an early gestational stage with heart failure and exhibited impaired neuronal development with extensive apoptosis. Primary embryonic fibroblasts derived from null mutants showed impaired cell cycle regulation and a prominent decrease of thyroid hormone receptor (see OMIM Ref. No. 190160) function that was restored by ectopic Trap220; no defect in activation by Gal4-RARA, Gal4-RXRA, p53, or Gal4-VP16 (see OMIM Ref. No. 300019) was detected. Haploinsufficient mice showed growth retardation, pituitary hypothyroidism, and widely impaired transcription in certain organs. The results indicated that TRAP220 is essential for a wide range of physiologic processes and that it also has gene- and activator-selective functions.

[68530] It is appreciated that the abovementioned animal model

for PPARBP is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[68531] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68532] Drane, P.; Barel, M.; Balbo, M.; Frade, R. : Identification of RB18A, a 205 kDa new p53 regulatory protein which shares antigenic and functional properties with p53. Oncogene 15: 3013-3024, 1997. ; and

[68533] Ito, M.; Yuan, C.-X.; Okano, H. J.; Darnell, R. B.; Roeder, R. G. : Involvement of the TRAP220 component of the TRAP/SMCC coactivator complex in embryonic development and thyroid hormone.

[68534] Further studies establishing the function and utilities of PPARBP are found in John Hopkins OMIM database record ID 604311, and in sited publications numbered 7006, 635 and 6199-4761 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Protein Phosphatase 2A, Regulatory Subunit B' (PR 53) (PPP2R4, Accession XM_026944) is another VGAM1965 host target gene. PPP2R4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by PPP2R4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP2R4 BINDING SITE, designated SEQ ID:30377, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68535] Another function of VGAM1965 is therefore inhibition of Protein Phosphatase 2A, Regulatory Subunit B' (PR 53) (PPP2R4, Accession XM_026944), a gene which is a regulatory subunit of protein phosphatase 2A. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP2R4. The function of PPP2R4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM435.Protein Phosphatase 2, Regulatory Subunit B (B56), Alpha Isoform (PPP2R5A, Accession NM_006243) is another VGAM1965 host target gene. PPP2R5A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP2R5A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of PPP2R5A BINDING SITE, designated SEQ ID:12912, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68536] Another function of VGAM1965 is therefore inhibition of Protein Phosphatase 2, Regulatory Subunit B (B56), Alpha Isoform (PPP2R5A, Accession NM_006243), a gene which is a regulatory subunit of protein phosphatase 2A. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP2R5A. The function of PPP2R5A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM675.Protein Phosphatase 2, Regulatory Subunit B (B56), Epsilon Isoform (PPP2R5E, Accession NM_006246) is another VGAM1965 host target gene. PPP2R5E BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP2R5E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP2R5E BINDING SITE,

designated SEQ ID:12923, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68537] Another function of VGAM1965 is therefore inhibition of Protein Phosphatase 2, Regulatory Subunit B (B56), Epsilon Isoform (PPP2R5E, Accession NM_006246), a gene which is a regulatory subunit of protein phosphatase 2A. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP2R5E. The function of PPP2R5E and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM302.PR Domain Containing 2, with ZNF Domain (PRDM2, Accession NM_015866) is another VGAM1965 host target gene. PRDM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRDM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRDM2 BINDING SITE, designated SEQ ID:18004, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ

ID:4676.

[68538] Another function of VGAM1965 is therefore inhibition of PR Domain Containing 2, with ZNF Domain (PRDM2, Accession NM_015866), a gene which plays a role in transcriptional regulation during neuronal differentiation and pathogenesis of retinoblastoma. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDM2. The function of PRDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM120.Protein Kinase, AMP-activated, Beta 1 Non-catalytic Subunit (PRKAB1, Accession NM_006253) is another VGAM1965 host target gene. PRKAB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKAB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKAB1 BINDING SITE, designated SEQ ID:12931, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68539] Another function of VGAM1965 is therefore inhibition of

Protein Kinase, AMP-activated, Beta 1 Non-catalytic Subunit (PRKAB1, Accession NM_006253), a gene which is responsible for the regulation of fatty acid synthesis by phosphorylation of acetyl-coa carboxylase. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKAB1. The function of PRKAB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1384.Protein S (alpha) (PROS1, Accession XM_113400) is another VGAM1965 host target gene. PROS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PROS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PROS1 BINDING SITE, designated SEQ ID:42256, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68540] Another function of VGAM1965 is therefore inhibition of Protein S (alpha) (PROS1, Accession XM_113400). Accordingly, utilities of VGAM1965 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with PROS1. Periaxin (PRX, Accession NM_020956) is another VGAM1965 host target gene. PRX BINDING SITE1 and PRX BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PRX, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRX BINDING SITE1 and PRX BINDING SITE2, designated SEQ ID:21932 and SEQ ID:21938 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68541] Another function of VGAM1965 is therefore inhibition of Periaxin (PRX, Accession NM_020956), a gene which seems to be required for maintenance of peripheral nerve myelin sheath. may have a role in axon-glial interactions, possibly by interacting with the cytoplasmic domains of integral membrane proteins such as myelin-associated glycoprotein in the periaxonal regions of the schwann cell plasma membrane. may have a role in the early phases of myelin deposition. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRX. The function of

PRX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM476.Pituitary Tumor-transforming 1 Interacting Protein (PTTG1IP, Accession NM_004339) is another VGAM1965 host target gene. PTTG1IP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTTG1IP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTTG1IP BINDING SITE, designated SEQ ID:10538, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68542] Another function of VGAM1965 is therefore inhibition of Pituitary Tumor-transforming 1 Interacting Protein (PTTG1IP, Accession NM_004339), a gene which facilitates the translocation of PTTG to the nucleus. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTTG1IP. The function of PTTG1IP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to VGAM131.Pumilio Homolog 2 (Drosophila) (PUM2, Accession NM_015317) is another VGAM1965 host target gene. PUM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PUM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PUM2 BINDING SITE, designated SEQ ID:17635, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68543] Another function of VGAM1965 is therefore inhibition of Pumilio Homolog 2 (Drosophila) (PUM2, Accession NM_015317). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PUM2. RAB5B, Member RAS Oncogene Family (RAB5B, Accession NM_002868) is another VGAM1965 host target gene. RAB5B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB5B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB5B BIND-

ING SITE, designated SEQ ID:8774, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68544] Another function of VGAM1965 is therefore inhibition of RAB5B, Member RAS Oncogene Family (RAB5B, Accession NM_002868), a gene which is presumably involved in vesicular trafficking at the plasma membrane. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB5B. The function of RAB5B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1237.RAD54B (Accession NM_134434) is another VGAM1965 host target gene. RAD54B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAD54B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD54B BINDING SITE, designated SEQ ID:28679, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68545] Another function of VGAM1965 is therefore inhibition of RAD54B (Accession NM_134434), a gene which is involved in dna repair and mitotic recombination. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD54B. The function of RAD54B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM595.RalA Binding Protein 1 (RALBP1, Accession NM_006788) is another VGAM1965 host target gene. RALBP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RALBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RALBP1 BINDING SITE, designated SEQ ID:13667, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68546] Another function of VGAM1965 is therefore inhibition of RalA Binding Protein 1 (RALBP1, Accession NM_006788), a gene which plays a role in signal transduction and catalyzes the transport of glutathione conjugates and xeno-

biotics. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RALBP1. The function of RALBP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM345.RAN Binding Protein 2-like 1 (RANBP2L1, Accession NM_005054) is another VGAM1965 host target gene. RANBP2L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RANBP2L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RANBP2L1 BINDING SITE, designated SEQ ID:11483, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68547] Another function of VGAM1965 is therefore inhibition of RAN Binding Protein 2-like 1 (RANBP2L1, Accession NM_005054). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RANBP2L1. RGL (Accession NM_015149) is another VGAM1965 host target gene. RGL

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RGL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RGL BINDING SITE, designated SEQ ID:17509, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68548] Another function of VGAM1965 is therefore inhibition of RGL (Accession NM_015149), a gene which is involved in nucleotide exchange factor. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGL. The function of RGL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM861.Arginyl Aminopeptidase (aminopeptidase B)-like 1 (RNPEPL1, Accession NM_018226) is another VGAM1965 host target gene. RNPEPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNPEPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of RNPEPL1 BINDING SITE, designated SEQ ID:20162, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68549] Another function of VGAM1965 is therefore inhibition of Arginyl Aminopeptidase (aminopeptidase B)-like 1 (RNPEPL1, Accession NM_018226). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNPEPL1. Ribonucleotide Reductase M2 B (TP53 inducible) (RRM2B, Accession XM_042096) is another VGAM1965 host target gene. RRM2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RRM2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RRM2B BINDING SITE, designated SEQ ID:33688, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68550] Another function of VGAM1965 is therefore inhibition of Ribonucleotide Reductase M2 B (TP53 inducible) (RRM2B, Accession XM_042096). Accordingly, utilities of

VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RRM2B. Retinoid X Receptor, Alpha (RXRA, Accession NM_002957) is another VGAM1965 host target gene. RXRA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RXRA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RXRA BINDING SITE, designated SEQ ID:8872, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68551] Another function of VGAM1965 is therefore inhibition of Retinoid X Receptor, Alpha (RXRA, Accession NM_002957), a gene which activates genes required for vitamin A metabolism, binds 9-cis retinoic acid. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RXRA. The function of RXRA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM349.Spastic Ataxia of Charlevoix-Saguenay (sacsin) (SACS, Accession XM_170738) is another

VGAM1965 host target gene. SACS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SACS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SACS BINDING SITE, designated SEQ ID:45496, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68552] Another function of VGAM1965 is therefore inhibition of Spastic Ataxia of Charlevoix-Saguenay (sacsin) (SACS, Accession XM_170738). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SACS. Src Family Associated Phosphoprotein 2 (SCAP2, Accession NM_003930) is another VGAM1965 host target gene. SCAP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCAP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAP2 BINDING SITE, designated SEQ ID:10027, to the nucleotide sequence of VGAM1965 RNA,

herein designated VGAM RNA, also designated SEQ ID:4676.

[68553] Another function of VGAM1965 is therefore inhibition of Src Family Associated Phosphoprotein 2 (SCAP2, Accession NM_003930), a gene which interacts with Src family protein tyrosine kinases and SLAP/FYB (SLA). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAP2. The function of SCAP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM134.Sodium Channel, Voltage-gated, Type I, Alpha Polypeptide (SCN1A, Accession XM_114281) is another VGAM1965 host target gene. SCN1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCN1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCN1A BINDING SITE, designated SEQ ID:42836, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68554] Another function of VGAM1965 is therefore inhibition of Sodium Channel, Voltage-gated, Type I, Alpha Polypeptide (SCN1A, Accession XM_114281). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN1A. Succinate Dehydrogenase Complex, Subunit D, Integral Membrane Protein (SDHD, Accession NM_003002) is another VGAM1965 host target gene. SDHD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SDHD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDHD BINDING SITE, designated SEQ ID:8897, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68555] Another function of VGAM1965 is therefore inhibition of Succinate Dehydrogenase Complex, Subunit D, Integral Membrane Protein (SDHD, Accession NM_003002). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDHD. Spondyloepiphyseal Dysplasia, Late (SEDL, Accession NM_014563) is another VGAM1965 host

target gene. SEDL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEDL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEDL BINDING SITE, designated SEQ ID:15917, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68556] Another function of VGAM1965 is therefore inhibition of Spondyloepiphyseal Dysplasia, Late (SEDL, Accession NM_014563), a gene which may play role in vesicular transport from endoplasmic reticulum to golgi. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEDL. The function of SEDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Surfactant, Pulmonary-associated Protein A2 (SFTPA2, Accession NM_006926) is another VGAM1965 host target gene. SFTPA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFTPA2, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFTPA2 BINDING SITE, designated SEQ ID:13811, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68557] Another function of VGAM1965 is therefore inhibition of Surfactant, Pulmonary-associated Protein A2 (SFTPA2, Accession NM_006926), a gene which plays a role in innate host defense in the lung. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFTPA2. The function of SFTPA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM148.Serine Hydroxymethyltransferase 2 (mitochondrial) (SHMT2, Accession NM_005412) is another VGAM1965 host target gene. SHMT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SHMT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SHMT2 BIND-

ING SITE, designated SEQ ID:11881, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68558] Another function of VGAM1965 is therefore inhibition of Serine Hydroxymethyltransferase 2 (mitochondrial) (SHMT2, Accession NM_005412), a gene which interconverts serine and glycine. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHMT2. The function of SHMT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.Single-minded Homolog 2 (Drosophila) (SIM2, Accession NM_009586) is another VGAM1965 host target gene. SIM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIM2 BINDING SITE, designated SEQ ID:14313, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68559] Another function of VGAM1965 is therefore inhibition of Single-minded Homolog 2 (Drosophila) (SIM2, Accession NM_009586), a gene which may be a master gene of cns development. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIM2. The function of SIM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM369.Src-like-adaptor (SLA, Accession NM_006748) is another VGAM1965 host target gene. SLA BINDING SITE1 and SLA BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SLA, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLA BINDING SITE1 and SLA BINDING SITE2, designated SEQ ID:13598 and SEQ ID:13597 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68560] Another function of VGAM1965 is therefore inhibition of Src-like-adaptor (SLA, Accession NM_006748), a gene which is a negative regulator of T-cell receptor signaling.

Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLA. The function of SLA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM383.Solute Carrier Family 13 (sodium/sulfate symporters), Member 4 (SLC13A4, Accession NM_012450) is another VGAM1965 host target gene. SLC13A4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC13A4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC13A4 BINDING SITE, designated SEQ ID:14820, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68561] Another function of VGAM1965 is therefore inhibition of Solute Carrier Family 13 (sodium/sulfate symporters), Member 4 (SLC13A4, Accession NM_012450). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC13A4. Solute Carrier Family 14 (urea transporter),

Member 1 (Kidd blood group) (SLC14A1, Accession NM_015865) is another VGAM1965 host target gene. SLC14A1 BINDING SITE1 through SLC14A1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SLC14A1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC14A1 BINDING SITE1 through SLC14A1 BINDING SITE3, designated SEQ ID:17998, SEQ ID:17999 and SEQ ID:17997 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68562] Another function of VGAM1965 is therefore inhibition of Solute Carrier Family 14 (urea transporter), Member 1 (Kidd blood group) (SLC14A1, Accession NM_015865), a gene which is a urea transporters in spermatogenesis. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC14A1. The function of SLC14A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM586.Solute Carrier

Family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), Member 1 (SLC1A1, Accession NM_004170) is another VGAM1965 host target gene. SLC1A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC1A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC1A1 BINDING SITE, designated SEQ ID:10381, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68563] Another function of VGAM1965 is therefore inhibition of Solute Carrier Family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), Member 1 (SLC1A1, Accession NM_004170), a gene which is a glutamate transporter, essential for terminating the postsynaptic action of glutamate by rapidly removing it from the synaptic cleft. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC1A1. The function of SLC1A1 and its association with various diseases and clinical conditions, has been established by previous studies, as de-

scribed hereinabove with reference to VGAM206.Solute Carrier Family 21 (organic anion transporter), Member 3 (SLC21A3, Accession NM_134431) is another VGAM1965 host target gene. SLC21A3 BINDING SITE1 and SLC21A3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SLC21A3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC21A3 BINDING SITE1 and SLC21A3 BINDING SITE2, designated SEQ ID:28672 and SEQ ID:22075 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68564] Another function of VGAM1965 is therefore inhibition of Solute Carrier Family 21 (organic anion transporter), Member 3 (SLC21A3, Accession NM_134431), a gene which mediates the na(+)-independent transport of organic anions such as bsp and conjugated (taurocholate) and unconjugated (cholate) bile acids. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC21A3. The function of SLC21A3 has been established by previous studies. The organic anion transporter

(OATP) of liver mediates the basolateral hepatocellular uptake of numerous cholephilic anions and steroidal compounds from sinusoidal blood. By screening a human liver cDNA library with a rat Oatp cDNA, Kullak-Ublick et al. (1995) cloned a cDNA encoding OATP. The deduced 670-amino acid OATP protein has 12 putative transmembrane domains and 8 potential N-linked glycosylation sites. The human and rat OATP proteins are 67% identical. In vitro translation produced unglycosylated and glycosylated human OATP proteins that migrated as 59-kD and 71-kD polypeptides, respectively, in SDS-polyacrylamide gels. Functional studies in Xenopus oocytes showed that OATP mediates sodium-independent transport of the xenobiotic bromosulfophthalein and of endogenous conjugated and unconjugated bile acids. Northern blot analysis detected an approximately 2.7-kb OATP transcript in human liver, brain, lung, kidney, and testis; additional transcripts were also observed. The authors stated that the extrahepatic expression of OATP suggests a general role for OATP in transepithelial organic anion transport

[68565] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68566] Kullak-Ublick, G. A.; Hagenbuch, B.; Stieger, B.; Schteingart, C. D.; Hofmann, A. F.; Wolkoff, A. W.; Meier, P. J. : Molecular and functional characterization of an organic anion transporting polypeptide cloned from human liver. :Gastroenterology 109: 1274-1282, 1995. ; and

[68567] By somatic cell hybrid analysis, Kullak-Ublick et al. (1995) mapped the SLC21A3 gene to chromosome 12. Kullak-Ublick et al. (1996) regionally localized the SLC21A3 gene to 12p12 using fluor.

[68568] Further studies establishing the function and utilities of SLC21A3 are found in John Hopkins OMIM database record ID 602883, and in sited publications numbered 5325-5326 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 7 (SLC4A7, Accession NM_003615) is another VGAM1965 host target gene. SLC4A7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC4A7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC4A7 BINDING SITE, designated SEQ ID:9672, to the nucleotide

sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68569] Another function of VGAM1965 is therefore inhibition of Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 7 (SLC4A7, Accession NM_003615), a gene which mediates the coupled movement of sodium and bicarbonate ions across the plasma membrane. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC4A7. The function of SLC4A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM66.Solute Carrier Family 8 (sodium-calcium exchanger), Member 2 (SLC8A2, Accession XM_038970) is another VGAM1965 host target gene. SLC8A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC8A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC8A2 BINDING SITE, designated SEQ ID:32969, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ

ID:4676.

[68570] Another function of VGAM1965 is therefore inhibition of Solute Carrier Family 8 (sodium-calcium exchanger), Member 2 (SLC8A2, Accession XM_038970). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC8A2. SWI/SNF Related, Matrix Associated, Actin Dependent Regulator of Chromatin, Subfamily A, Member 3 (SMARCA3, Accession NM_139048) is another VGAM1965 host target gene. SMARCA3 BINDING SITE1 and SMARCA3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SMARCA3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMARCA3 BINDING SITE1 and SMARCA3 BINDING SITE2, designated SEQ ID:29133 and SEQ ID:9038 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68571] Another function of VGAM1965 is therefore inhibition of SWI/SNF Related, Matrix Associated, Actin Dependent Regulator of Chromatin, Subfamily A, Member 3

(SMARCA3, Accession NM_139048), a gene which is involved in chromatin assembly and remodeling. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMARCA3. The function of SMARCA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1330.Small Nuclear Ribonucleoprotein Polypeptide N (SNRPN, Accession NM_022807) is another VGAM1965 host target gene. SNRPN BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SNRPN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNRPN BINDING SITE, designated SEQ ID:23084, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68572] Another function of VGAM1965 is therefore inhibition of Small Nuclear Ribonucleoprotein Polypeptide N (SNRPN, Accession NM_022807), a gene which may be involved in tissue-specific alternative RNA processing events. Accord-

ingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNRPN. The function of SNRPN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1924.Sorting Nexin 9 (SNX9, Accession NM_016224) is another VGAM1965 host target gene. SNX9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNX9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNX9 BINDING SITE, designated SEQ ID:18332, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68573] Another function of VGAM1965 is therefore inhibition of Sorting Nexin 9 (SNX9, Accession NM_016224). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX9. Sorbitol Dehydrogenase (SORD, Accession NM_003104) is another VGAM1965 host target gene. SORD BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by SORD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SORD BINDING SITE, designated SEQ ID:9070, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68574] Another function of VGAM1965 is therefore inhibition of Sorbitol Dehydrogenase (SORD, Accession NM_003104). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SORD. SRP46 (Accession NM_032102) is another VGAM1965 host target gene. SRP46 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SRP46, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SRP46 BINDING SITE, designated SEQ ID:25793, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68575] Another function of VGAM1965 is therefore inhibition of

SRP46 (Accession NM_032102). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRP46. Suppressor of Fused Homolog (Drosophila) (SUFU, Accession NM_016169) is another VGAM1965 host target gene. SUFU BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SUFU, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SUFU BINDING SITE, designated SEQ ID:18260, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68576] Another function of VGAM1965 is therefore inhibition of Suppressor of Fused Homolog (Drosophila) (SUFU, Accession NM_016169). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUFU. Synaptotagmin I (SYT1, Accession NM_005639) is another VGAM1965 host target gene. SYT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of SYT1 BINDING SITE, designated SEQ ID:12172, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68577] Another function of VGAM1965 is therefore inhibition of Synaptotagmin I (SYT1, Accession NM_005639), a gene which may have a regulatory role in the membrane interactions during trafficking of synaptic vesicles at the active zone of the synapse. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT1. The function of SYT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM739.Synaptotagmin V (SYT5, Accession NM_003180) is another VGAM1965 host target gene. SYT5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SYT5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYT5 BINDING SITE, designated SEQ ID:9152, to the nucleotide

sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68578] Another function of VGAM1965 is therefore inhibition of Synaptotagmin V (SYT5, Accession NM_003180), a gene which is a member of a family of calcium sensors regulating neurotransmitter release. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT5. The function of SYT5 has been established by previous studies. The synaptotagmins are a family of type III membrane proteins characterized by cytoplasmic repeats related to the protein kinase C regulatory (C2) domains which are thought to bind calcium. The synaptotagmins may act both as negative regulators of vesicle fusion, allowing fusion in the presence of calcium, and as calcium receptors or sensor molecules. Hudson and Birnbaum (1995) cloned a synaptotagmin cDNA from a rat adipose tissue cDNA library. The sequence predicts a 386-amino acid protein with 49% identity to synaptotagmins 1 (OMIM Ref. No. 185605) and 2 (OMIM Ref. No. 600104). The 1.7-kb synaptotagmin-5 mRNA is expressed in rat kidney, adipose tissue, lung and heart, and at higher levels in brain. An antibody to the SYT5 gene product detected an

approximately 50-kD protein. Kwon et al. (1995) mapped the SYT5 gene to mouse chromosome 7 and predicted that the human gene is located on 11p.

[68579] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68580] Hudson, A. W.; Birnbaum, M. J. : Identification of a non-neuronal isoform of synaptotagmin. Proc. Nat. Acad. Sci. 92: 5895-5899, 1995. ; and

[68581] Kwon, O.-J.; Adamson, M. C.; Chin, H.; Kozak, C. A. : Genetic mapping of five mouse genes encoding synaptotagmins. Mammalian Genome 6: 880-881, 1995.

[68582] Further studies establishing the function and utilities of SYT5 are found in John Hopkins OMIM database record ID 600782, and in sited publications numbered 9943 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Transforming, Acidic Coiled-coil Containing Protein 1 (TACC1, Accession NM_006283) is another VGAM1965 host target gene. TACC1 BINDING SITE1 and TACC1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TACC1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING

SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TACC1 BINDING SITE1 and TACC1 BINDING SITE2, designated SEQ ID:12961 and SEQ ID:12968 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68583] Another function of VGAM1965 is therefore inhibition of Transforming, Acidic Coiled-coil Containing Protein 1 (TACC1, Accession NM_006283). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TACC1. T-cell Acute Lymphocytic Leukemia 1 (TAL1, Accession NM_003189) is another VGAM1965 host target gene. TAL1 BINDING SITE1 and TAL1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TAL1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAL1 BINDING SITE1 and TAL1 BINDING SITE2, designated SEQ ID:9172 and SEQ ID:9186 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68584] Another function of VGAM1965 is therefore inhibition of T-cell Acute Lymphocytic Leukemia 1 (TAL1, Accession NM_003189), a gene which may help control cell growth and differentiation. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAL1. The function of TAL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM172.Transmembrane Protein 1 (TMEM1, Accession NM_003274) is another VGAM1965 host target gene. TMEM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TMEM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMEM1 BINDING SITE, designated SEQ ID:9288, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68585] Another function of VGAM1965 is therefore inhibition of Transmembrane Protein 1 (TMEM1, Accession NM_003274). Accordingly, utilities of VGAM1965 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with TMEM1. Transmembrane Protease, Serine 2 (TMPRSS2, Accession NM_005656) is another VGAM1965 host target gene. TMPRSS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TMPRSS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMPRSS2 BINDING SITE, designated SEQ ID:12195, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68586] Another function of VGAM1965 is therefore inhibition of Transmembrane Protease, Serine 2 (TMPRSS2, Accession NM_005656). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS2. Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession XM_165823) is another VGAM1965 host target gene. TNF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of TNF BINDING SITE, designated SEQ ID:43772, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68587] Another function of VGAM1965 is therefore inhibition of Tumor Necrosis Factor (TNF superfamily, member 2) (TNF, Accession XM_165823), a gene which mediates proinflammatory responses and apoptosis. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNF. The function of TNF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM175.TOX (Accession NM_014729) is another VGAM1965 host target gene. TOX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOX BINDING SITE, designated SEQ ID:16329, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68588] Another function of VGAM1965 is therefore inhibition of TOX (Accession NM_014729). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOX. Tumor Protein P53 (Li-Fraumeni syndrome) (TP53, Accession NM_000546) is another VGAM1965 host target gene. TP53 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TP53, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TP53 BINDING SITE, designated SEQ ID:6153, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68589] Another function of VGAM1965 is therefore inhibition of Tumor Protein P53 (Li-Fraumeni syndrome) (TP53, Accession NM_000546). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53. Tripartite Motif-containing 14 (TRIM14, Accession NM_014788) is another VGAM1965 host target gene. TRIM14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM14, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM14 BINDING SITE, designated SEQ ID:16671, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68590] Another function of VGAM1965 is therefore inhibition of Tripartite Motif-containing 14 (TRIM14, Accession NM_014788), a gene which is composed of 3 zinc-binding domains and is involved in development and cell growth. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM14. The function of TRIM14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM180.Transient Receptor Potential Cation Channel, Subfamily C, Member 6 (TRPC6, Accession NM_004621) is another VGAM1965 host target gene. TRPC6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRPC6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of TRPC6 BINDING SITE, designated SEQ ID:10980, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68591] Another function of VGAM1965 is therefore inhibition of Transient Receptor Potential Cation Channel, Subfamily C, Member 6 (TRPC6, Accession NM_004621), a gene which has calcium channel activity. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPC6. The function of TRPC6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM25.TSLP (Accession NM_033035) is another VGAM1965 host target gene. TSLP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TSLP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TSLP BINDING SITE, designated SEQ ID:26929, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68592] Another function of VGAM1965 is therefore inhibition of TSLP (Accession NM_033035), a gene which may contribute directly to the activation of Langerhans cells and inhibit apoptosis. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSLP. The function of TSLP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM558.Translin-associated Factor X (TSNAX, Accession NM_005999) is another VGAM1965 host target gene. TSNAX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TSNAX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TSNAX BINDING SITE, designated SEQ ID:12616, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68593] Another function of VGAM1965 is therefore inhibition of Translin-associated Factor X (TSNAX, Accession NM_005999), a gene which Interacts with translin (TSN).

Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSNAX. The function of TSNAX has been established by previous studies. Translin (TSN; 600575) is a DNA-binding protein that specifically binds to consensus sequences at breakpoint junctions of chromosomal translocations in many cases of lymphoid malignancies. Aoki et al. (1997) used a yeast 2-hybrid system to screen a human spleen cDNA library for potential interactions of TSN with other proteins. They isolated a TSNAX cDNA, termed TRAX (translin-associated factor X) by the authors, whose product specifically interacted with TSN in cotransformation and in vitro interaction assays. The cDNA encodes a putative 290-amino acid protein with a predicted molecular mass of 33 kD. The protein contains a heptad repeat of hydrophobic amino acids consistent with the hypothetical leucine zipper structure. The authors found 28% amino acid sequence identity between TSNAX and TSN, with 38% identity in the C-terminal regions. Northern blot analysis revealed a single TSNAX transcript of 2.7 kb, with a tissue distribution similar to that of the TSN transcript. Meng et al. (2000) determined that the genomic structure of TSNAX is similar to that of TSN, con-

sisting of 6 exons encompassing approximately 27 kb of genomic DNA. By fluorescence in situ hybridization, Meng et al. (2000) mapped the TSNAX gene to chromosome 1q41.

[68594] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68595] Aoki, K.; Ishida, R.; Kasai, M. : Isolation and characterization of a cDNA encoding a translin-like protein, TRAX. FEBS Lett. 401: 109-112, 1997. ; and

[68596] Meng, G.; Aoki, K.; Tokura, K.; Nakahara, K.; Inazawa, J.; Kasai, M. : Genomic structure and chromosomal localization of the gene encoding TRAX, a translin-associated factor X. J. Hum. G.

[68597] Further studies establishing the function and utilities of TSNAX are found in John Hopkins OMIM database record ID 602964, and in sited publications numbered 8476-8477 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Ubiquitin-like 1 (sentrin) (UBL1, Accession NM_003352) is another VGAM1965 host target gene. UBL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UBL1,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBL1 BINDING SITE, designated SEQ ID:9379, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68598] Another function of VGAM1965 is therefore inhibition of Ubiquitin-like 1 (sentrin) (UBL1, Accession NM_003352), a gene which generates proteins resistant to degradation through its modification. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBL1. The function of UBL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.UC28 (Accession NM_021635) is another VGAM1965 host target gene. UC28 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UC28, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UC28 BINDING SITE, designated SEQ ID:22281, to the nucleotide sequence of

VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68599] Another function of VGAM1965 is therefore inhibition of UC28 (Accession NM_021635). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UC28. Vang-like 2 (van gogh, Drosophila) (VANGL2, Accession XM_049695) is another VGAM1965 host target gene. VANGL2 BINDING SITE1 and VANGL2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by VANGL2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VANGL2 BINDING SITE1 and VANGL2 BINDING SITE2, designated SEQ ID:35476 and SEQ ID:35487 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68600] Another function of VGAM1965 is therefore inhibition of Vang-like 2 (van gogh, Drosophila) (VANGL2, Accession XM_049695), a gene which may take part in defining the lateral boundary of floorplate differentiation. Accordingly, utilities of VGAM1965 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with VANGL2. The function of VANGL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM111.WD Repeat Domain 3 (WDR3, Accession NM_006784) is another VGAM1965 host target gene. WDR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WDR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WDR3 BINDING SITE, designated SEQ ID:13654, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68601] Another function of VGAM1965 is therefore inhibition of WD Repeat Domain 3 (WDR3, Accession NM_006784), a gene which contains a WD repeat domain with unknown function. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WDR3. The function of WDR3 has been established by previous studies. A conserved core of 4 or more modular repeat units defines a group of functionally diverse regulatory proteins in eukaryotes

known as the WD repeat family. WD repeats are minimally conserved regions of approximately 40 amino acids typically bracketed by gly-his and trp-asp (GH-WD), which may facilitate formation of heterotrimeric or multiprotein complexes. Proteins belonging to the WD repeat family are involved in a variety of cellular processes, including cell cycle progression, signal transduction, apoptosis, and gene regulation. Claudio et al. (1998) identified a human CD34+ hematopoietic progenitor line (KG-1a) EST with significant sequence similarity to a portion of the yeast TUP1 gene, which encodes a WD repeat-containing transcriptional regulator. Using the EST, they isolated the complete coding sequence of the human WDR3 protein. Claudio et al. (1999) found that the predicted 943-amino acid WDR3 protein contains 10 WD repeat modules. The first 4 WD repeats are separated from the remaining 6 WD repeats by a nuclear localization signal (NLS); a second NLS is located near the C-terminal end of the protein. WDR3 also contains a potential tyrosine kinase phosphorylation site and a cAMP- and cGMP-dependent protein kinase phosphorylation site. WDR3 shares 37% amino acid sequence identity with the S. cerevisiae WD repeat-containing protein DIP2. Northern blot analysis detected

an approximately 4-kb WDR3 transcript in the majority of tissues examined, including brain, pancreas, skeletal muscle, and placenta. WDR3 expression was also found in all of the cell lines tested. By FISH, Claudio et al. (1999) mapped the WDR3 gene to 1p13-p12.

[68602] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[68603] Claudio, J. O.; Liew, C.-C.; Dempsey, A. A.; Cukerman, E.; Stewart, A. K.; Na, E.; Atkins, H. L.; Iscove, N. N.; Hawley, R. G. : Identification of sequence-tagged transcripts differentially expressed within the human hematopoietic hierarchy. Genomics 50: 44-52, 1998. ; and

[68604] Claudio, J. O.; Liew, C.-C.; Ma, J.; Heng, H. H. Q.; Stewart, A. K.; Hawley, R. G. : Cloning and expression analysis of a novel WD repeat gene, WDR3, mapping to 1p12-p13. Genomics 59: 8.

[68605] Further studies establishing the function and utilities of WDR3 are found in John Hopkins OMIM database record ID 604737, and in sited publications numbered 6742-6743 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_007331) is

another VGAM1965 host target gene. WHSC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WHSC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE, designated SEQ ID:14253, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68606] Another function of VGAM1965 is therefore inhibition of Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_007331), a gene which binds covalently to and repairs g/t mismatches. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WHSC1. The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Wingless-type MMTV Integration Site Family, Member 10B (WNT10B, Accession NM_003394) is another VGAM1965 host target gene. WNT10B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WNT10B, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT10B BINDING SITE, designated SEQ ID:9431, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68607] Another function of VGAM1965 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 10B (WNT10B, Accession NM_003394), a gene which is a ligand for members of the frizzled family of seven transmembrane receptors and may be a signaling molecule. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WNT10B. The function of WNT10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM594.Wingless-type MMTV Integration Site Family, Member 5B (WNT5B, Accession NM_030775) is another VGAM1965 host target gene. WNT5B BINDING SITE1 and WNT5B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WNT5B, corresponding to HOST TARGET binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT5B BINDING SITE1 and WNT5B BINDING SITE2, designated SEQ ID:25059 and SEQ ID:26361 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68608] Another function of VGAM1965 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 5B (WNT5B, Accession NM_030775), a gene which is the ligand for members of the frizzled family of seven transmembrane receptors and may be a signaling molecule . Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WNT5B. The function of WNT5B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1928.X-ray Repair Complementing Defective Repair In Chinese Hamster Cells 3 (XRCC3, Accession NM_005432) is another VGAM1965 host target gene. XRCC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XRCC3, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XRCC3 BINDING SITE, designated SEQ ID:11910, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68609] Another function of VGAM1965 is therefore inhibition of X-ray Repair Complementing Defective Repair In Chinese Hamster Cells 3 (XRCC3, Accession NM_005432), a gene which is required for meiotic recombination, synaptonemal complex formation and cell cycle progression. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XRCC3. The function of XRCC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1290.XT3 (Accession NM_020208) is another VGAM1965 host target gene. XT3 BINDING SITE1 and XT3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by XT3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of XT3 BINDING SITE1 and XT3 BINDING SITE2, designated SEQ ID:21448 and SEQ ID:21449 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68610] Another function of VGAM1965 is therefore inhibition of XT3 (Accession NM_020208), a gene which is a Kidney-specific orphan transporter. Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XT3. The function of XT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM21.Zinc Finger Protein 124 (HZF-16) (ZNF124, Accession NM_003431) is another VGAM1965 host target gene. ZNF124 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF124, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF124 BINDING SITE, designated SEQ ID:9483, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ

ID:4676.

[68611] Another function of VGAM1965 is therefore inhibition of Zinc Finger Protein 124 (HZF-16) (ZNF124, Accession NM_003431). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF124. Zinc Finger Protein 137 (clone pHZ-30) (ZNF137, Accession NM_003438) is another VGAM1965 host target gene. ZNF137 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF137, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF137 BINDING SITE, designated SEQ ID:9493, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68612] Another function of VGAM1965 is therefore inhibition of Zinc Finger Protein 137 (clone pHZ-30) (ZNF137, Accession NM_003438). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF137. Zinc Finger Protein 202 (ZNF202, Accession NM_003455) is another VGAM1965 host target gene. ZNF202 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF202, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF202 BINDING SITE, designated SEQ ID:9510, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68613] Another function of VGAM1965 is therefore inhibition of Zinc Finger Protein 202 (ZNF202, Accession NM_003455). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF202. Zinc Finger Protein 74 (Cos52) (ZNF74, Accession NM_003426) is another VGAM1965 host target gene. ZNF74 BINDING SITE1 and ZNF74 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ZNF74, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF74 BINDING SITE1 and ZNF74 BINDING SITE2, designated SEQ ID:9474 and SEQ ID:9476 respectively, to the nucleotide sequence of VGAM1965 RNA,

herein designated VGAM RNA, also designated SEQ ID:4676.

[68614] Another function of VGAM1965 is therefore inhibition of Zinc Finger Protein 74 (Cos52) (ZNF74, Accession NM_003426). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF74. A Kinase (PRKA) Anchor Protein 8 (AKAP8, Accession NM_005858) is another VGAM1965 host target gene. AKAP8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKAP8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP8 BINDING SITE, designated SEQ ID:12466, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68615] Another function of VGAM1965 is therefore inhibition of A Kinase (PRKA) Anchor Protein 8 (AKAP8, Accession NM_005858). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP8. Adaptor-related Protein Complex 4, Epsilon 1 Subunit (AP4E1, Accession

NM_007347) is another VGAM1965 host target gene. AP4E1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP4E1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP4E1 BINDING SITE, designated SEQ ID:14277, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68616] Another function of VGAM1965 is therefore inhibition of Adaptor-related Protein Complex 4, Epsilon 1 Subunit (AP4E1, Accession NM_007347). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP4E1. Apolipoprotein L, 4 (APOL4, Accession NM_030643) is another VGAM1965 host target gene. APOL4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by APOL4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APOL4 BINDING SITE, designated SEQ ID:24978, to the nucleotide se-

quence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68617] Another function of VGAM1965 is therefore inhibition of Apolipoprotein L, 4 (APOL4, Accession NM_030643). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL4. Apolipoprotein L, 6 (APOL6, Accession NM_030641) is another VGAM1965 host target gene. APOL6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APOL6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APOL6 BINDING SITE, designated SEQ ID:24972, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68618] Another function of VGAM1965 is therefore inhibition of Apolipoprotein L, 6 (APOL6, Accession NM_030641). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL6. ARHGAP10 (Accession NM_020824) is another VGAM1965 host target gene.

ARHGAP10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHGAP10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGAP10 BINDING SITE, designated SEQ ID:21886, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68619] Another function of VGAM1965 is therefore inhibition of ARHGAP10 (Accession NM_020824). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP10. ATPase, H+ Transporting, Lysosomal V0 Subunit A Isoform 1 (ATP6V0A1, Accession NM_005177) is another VGAM1965 host target gene. ATP6V0A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP6V0A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP6V0A1 BINDING SITE, designated SEQ ID:11677, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[68620] Another function of VGAM1965 is therefore inhibition of ATPase, H+ Transporting, Lysosomal V0 Subunit A Isoform 1 (ATP6V0A1, Accession NM_005177). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V0A1. UDP-GlcNAc:betaGal Beta-1,3-N-acetylglucosaminyltransferase 5 (B3GNT5, Accession NM_032047) is another VGAM1965 host target gene. B3GNT5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by B3GNT5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B3GNT5 BINDING SITE, designated SEQ ID:25765, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68621] Another function of VGAM1965 is therefore inhibition of UDP-GlcNAc:betaGal Beta-1,3-N-acetylglucosaminyltransferase 5 (B3GNT5, Accession NM_032047). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with B3GNT5. BDG-29 (Accession XM_051343) is another VGAM1965 host target gene. BDG-29 BINDING SITE1 and BDG-29 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by BDG-29, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BDG-29 BINDING SITE1 and BDG-29 BINDING SITE2, designated SEQ ID:35817 and SEQ ID:35812 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68622] Another function of VGAM1965 is therefore inhibition of BDG-29 (Accession XM_051343). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDG-29. Burkitt Lymphoma Receptor 1, GTP Binding Protein (chemokine (C-X-C motif) Receptor 5) (BLR1, Accession NM_032966) is another VGAM1965 host target gene. BLR1 BINDING SITE1 and BLR1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by BLR1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BLR1 BINDING SITE1 and BLR1 BINDING SITE2, designated SEQ ID:26779 and SEQ ID:7449 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68623] Another function of VGAM1965 is therefore inhibition of Burkitt Lymphoma Receptor 1, GTP Binding Protein (chemokine (C-X-C motif) Receptor 5) (BLR1, Accession NM_032966). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BLR1. BTB (POZ) Domain Containing 1 (BTBD1, Accession NM_025238) is another VGAM1965 host target gene. BTBD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTBD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTBD1 BINDING SITE, designated SEQ ID:24920, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68624] Another function of VGAM1965 is therefore inhibition of

BTB (POZ) Domain Containing 1 (BTBD1, Accession NM_025238). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTBD1. Butyrophilin, Subfamily 1, Member A1 (BTN1A1, Accession NM_001732) is another VGAM1965 host target gene. BTN1A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTN1A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTN1A1 BINDING SITE, designated SEQ ID:7470, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68625] Another function of VGAM1965 is therefore inhibition of Butyrophilin, Subfamily 1, Member A1 (BTN1A1, Accession NM_001732). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN1A1. Chromosome 14 Open Reading Frame 4 (C14orf4, Accession XM_041104) is another VGAM1965 host target gene. C14orf4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C14orf4, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C14orf4 BINDING SITE, designated SEQ ID:33446, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68626] Another function of VGAM1965 is therefore inhibition of Chromosome 14 Open Reading Frame 4 (C14orf4, Accession XM_041104). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf4. Chromosome 16 Open Reading Frame 7 (C16orf7, Accession NM_004913) is another VGAM1965 host target gene. C16orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C16orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C16orf7 BINDING SITE, designated SEQ ID:11346, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68627] Another function of VGAM1965 is therefore inhibition of

Chromosome 16 Open Reading Frame 7 (C16orf7, Accession NM_004913). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C16orf7. Chromosome 17 Open Reading Frame 26 (C17orf26, Accession NM_139177) is another VGAM1965 host target gene. C17orf26 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C17orf26, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C17orf26 BINDING SITE, designated SEQ ID:29188, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68628] Another function of VGAM1965 is therefore inhibition of Chromosome 17 Open Reading Frame 26 (C17orf26, Accession NM_139177). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C17orf26. Chromosome 1 Open Reading Frame 16 (C1orf16, Accession NM_014837) is another VGAM1965 host target gene. C1orf16 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by C1orf16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf16 BINDING SITE, designated SEQ ID:16860, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68629] Another function of VGAM1965 is therefore inhibition of Chromosome 1 Open Reading Frame 16 (C1orf16, Accession NM_014837). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf16. Chromosome 1 Open Reading Frame 24 (C1orf24, Accession NM_052966) is another VGAM1965 host target gene. C1orf24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:27535, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ

ID:4676.

[68630] Another function of VGAM1965 is therefore inhibition of Chromosome 1 Open Reading Frame 24 (C1orf24, Accession NM_052966). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24. Chromosome 1 Open Reading Frame 25 (C1orf25, Accession XM_051868) is another VGAM1965 host target gene. C1orf25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf25 BINDING SITE, designated SEQ ID:35911, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68631] Another function of VGAM1965 is therefore inhibition of Chromosome 1 Open Reading Frame 25 (C1orf25, Accession XM_051868). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf25. Chromosome 1 Open Reading Frame 34 (C1orf34, Accession

XM_027172) is another VGAM1965 host target gene. C1orf34 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf34, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf34 BINDING SITE, designated SEQ ID:30440, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68632] Another function of VGAM1965 is therefore inhibition of Chromosome 1 Open Reading Frame 34 (C1orf34, Accession XM_027172). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf34. Chromosome 20 Open Reading Frame 12 (C20orf12, Accession NM_018152) is another VGAM1965 host target gene. C20orf12 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C20orf12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf12 BINDING SITE, designated SEQ

ID:19961, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68633] Another function of VGAM1965 is therefore inhibition of Chromosome 20 Open Reading Frame 12 (C20orf12, Accession NM_018152). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf12. Chromosome 20 Open Reading Frame 121 (C20orf121, Accession NM_024331) is another VGAM1965 host target gene. C20orf121 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf121 BINDING SITE, designated SEQ ID:23631, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68634] Another function of VGAM1965 is therefore inhibition of Chromosome 20 Open Reading Frame 121 (C20orf121, Accession NM_024331). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with C20orf121. Chromosome 20 Open Reading Frame 124 (C20orf124, Accession NM_024777) is another VGAM1965 host target gene. C20orf124 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C20orf124, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf124 BINDING SITE, designated SEQ ID:24145, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68635] Another function of VGAM1965 is therefore inhibition of Chromosome 20 Open Reading Frame 124 (C20orf124, Accession NM_024777). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf124. Chromosome 20 Open Reading Frame 126 (C20orf126, Accession NM_030815) is another VGAM1965 host target gene. C20orf126 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf126, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf126 BINDING SITE, designated SEQ ID:25136, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68636] Another function of VGAM1965 is therefore inhibition of Chromosome 20 Open Reading Frame 126 (C20orf126, Accession NM_030815). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf126. Chromosome 20 Open Reading Frame 162 (C20orf162, Accession NM_080603) is another VGAM1965 host target gene. C20orf162 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C20orf162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf162 BINDING SITE, designated SEQ ID:27920, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68637] Another function of VGAM1965 is therefore inhibition of Chromosome 20 Open Reading Frame 162 (C20orf162,

Accession NM_080603). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf162. Chromosome 20 Open Reading Frame 39 (C20orf39, Accession NM_024893) is another VGAM1965 host target gene. C20orf39 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf39, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf39 BINDING SITE, designated SEQ ID:24370, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68638] Another function of VGAM1965 is therefore inhibition of Chromosome 20 Open Reading Frame 39 (C20orf39, Accession NM_024893). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf39. Chromosome 20 Open Reading Frame 43 (C20orf43, Accession XM_009549) is another VGAM1965 host target gene. C20orf43 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

C20orf43, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf43 BINDING SITE, designated SEQ ID:30114, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68639] Another function of VGAM1965 is therefore inhibition of Chromosome 20 Open Reading Frame 43 (C20orf43, Accession XM_009549). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf43. Chromosome 20 Open Reading Frame 60 (C20orf60, Accession NM_052970) is another VGAM1965 host target gene. C20orf60 BINDING SITE1 and C20orf60 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by C20orf60, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf60 BINDING SITE1 and C20orf60 BINDING SITE2, designated SEQ ID:27541 and SEQ ID:27542 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated

VGAM RNA, also designated SEQ ID:4676.

[68640] Another function of VGAM1965 is therefore inhibition of Chromosome 20 Open Reading Frame 60 (C20orf60, Accession NM_052970). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf60. Chromosome 21 Open Reading Frame 100 (C21orf100, Accession NM_145033) is another VGAM1965 host target gene. C21orf100 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C21orf100, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C21orf100 BINDING SITE, designated SEQ ID:29649, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68641] Another function of VGAM1965 is therefore inhibition of Chromosome 21 Open Reading Frame 100 (C21orf100, Accession NM_145033). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf100. Chromosome 21 Open Reading Frame 41

(C21orf41, Accession NM_138332) is another VGAM1965 host target gene. C21orf41 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C21orf41, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C21orf41 BINDING SITE, designated SEQ ID:28731, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68642] Another function of VGAM1965 is therefore inhibition of Chromosome 21 Open Reading Frame 41 (C21orf41, Accession NM_138332). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf41. Chromosome 21 Open Reading Frame 7 (C21orf7, Accession NM_020152) is another VGAM1965 host target gene. C21orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C21orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C21orf7 BINDING SITE, designated SEQ

ID:21363, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68643] Another function of VGAM1965 is therefore inhibition of Chromosome 21 Open Reading Frame 7 (C21orf7, Accession NM_020152). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf7. Chromosome 5 Open Reading Frame 7 (C5orf7, Accession XM_033576) is another VGAM1965 host target gene. C5orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C5orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5orf7 BINDING SITE, designated SEQ ID:31943, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68644] Another function of VGAM1965 is therefore inhibition of Chromosome 5 Open Reading Frame 7 (C5orf7, Accession XM_033576). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf7. Chromosome 6

Open Reading Frame 9 (C6orf9, Accession NM_022107) is another VGAM1965 host target gene. C6orf9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C6orf9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C6orf9 BINDING SITE, designated SEQ ID:22655, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68645] Another function of VGAM1965 is therefore inhibition of Chromosome 6 Open Reading Frame 9 (C6orf9, Accession NM_022107). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf9. Chromosome 8 Open Reading Frame 14 (C8orf14, Accession NM_054029) is another VGAM1965 host target gene. C8orf14 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C8orf14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C8orf14 BINDING SITE, designated SEQ ID:27641, to the

nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68646] Another function of VGAM1965 is therefore inhibition of Chromosome 8 Open Reading Frame 14 (C8orf14, Accession NM_054029). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf14. Chromosome 8 Open Reading Frame 7 (C8orf7, Accession XM_088376) is another VGAM1965 host target gene. C8orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C8orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C8orf7 BINDING SITE, designated SEQ ID:39649, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68647] Another function of VGAM1965 is therefore inhibition of Chromosome 8 Open Reading Frame 7 (C8orf7, Accession XM_088376). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf7. Chromosome 9 Open Reading Frame 7 (C9orf7, Accession NM_017586) is

another VGAM1965 host target gene. C9orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C9orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C9orf7 BINDING SITE, designated SEQ ID:19037, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68648] Another function of VGAM1965 is therefore inhibition of Chromosome 9 Open Reading Frame 7 (C9orf7, Accession NM_017586). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf7. CAPN13 (Accession NM_144575) is another VGAM1965 host target gene. CAPN13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAPN13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAPN13 BINDING SITE, designated SEQ ID:29381, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ

ID:4676.

[68649] Another function of VGAM1965 is therefore inhibition of CAPN13 (Accession NM_144575). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPN13. Chromobox Homolog 6 (CBX6, Accession NM_014292) is another VGAM1965 host target gene. CBX6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CBX6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBX6 BINDING SITE, designated SEQ ID:15578, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68650] Another function of VGAM1965 is therefore inhibition of Chromobox Homolog 6 (CBX6, Accession NM_014292). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBX6. Chemokine (C-C motif) Receptor 6 (CCR6, Accession NM_004367) is another VGAM1965 host target gene. CCR6 BINDING SITE1 through CCR6 BINDING SITE4 are HOST TARGET binding

sites found in untranslated regions of mRNA encoded by CCR6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCR6 BINDING SITE1 through CCR6 BINDING SITE4, designated SEQ ID:10581, SEQ ID:10582, SEQ ID:25376 and SEQ ID:25377 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68651] Another function of VGAM1965 is therefore inhibition of Chemokine (C-C motif) Receptor 6 (CCR6, Accession NM_004367). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCR6. CDV-1 (Accession NM_031473) is another VGAM1965 host target gene. CDV-1 BINDING SITE1 and CDV-1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CDV-1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDV-1 BINDING SITE1 and CDV-1 BINDING SITE2, designated SEQ ID:25542 and SEQ ID:40487 respectively, to the nu-

cleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68652] Another function of VGAM1965 is therefore inhibition of CDV-1 (Accession NM_031473). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDV-1. CHRNA7 (cholinergic receptor, nicotinic, alpha polypeptide 7, exons 5-10) and FAM7A (family with sequence similarity 7A, exons A-E) Fusion (CHRFAM7A, Accession XM_170784) is another VGAM1965 host target gene. CHRFAM7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHRFAM7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHRFAM7A BINDING SITE, designated SEQ ID:45551, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68653] Another function of VGAM1965 is therefore inhibition of CHRNA7 (cholinergic receptor, nicotinic, alpha polypeptide 7, exons 5-10) and FAM7A (family with sequence similarity 7A, exons A-E) Fusion (CHRFAM7A, Accession

XM_170784). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRFAM7A. Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273) is another VGAM1965 host target gene. CHST3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHST3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHST3 BINDING SITE, designated SEQ ID:10483, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68654] Another function of VGAM1965 is therefore inhibition of Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHST3. Claudin 15 (CLDN15, Accession NM_138429) is another VGAM1965 host target gene. CLDN15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLDN15, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLDN15 BINDING SITE, designated SEQ ID:28794, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68655] Another function of VGAM1965 is therefore inhibition of Claudin 15 (CLDN15, Accession NM_138429). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLDN15. C-type (calcium dependent, carbohydrate-recognition domain) Lectin, Superfamily Member 9 (CLECSF9, Accession NM_014358) is another VGAM1965 host target gene. CLECSF9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLECSF9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLECSF9 BINDING SITE, designated SEQ ID:15689, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68656] Another function of VGAM1965 is therefore inhibition of

C-type (calcium dependent, carbohydrate-recognition domain) Lectin, Superfamily Member 9 (CLECSF9, Accession NM_014358). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLECSF9. Chloride Intracellular Channel 5 (CLIC5, Accession NM_016929) is another VGAM1965 host target gene. CLIC5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLIC5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLIC5 BINDING SITE, designated SEQ ID:18848, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68657] Another function of VGAM1965 is therefore inhibition of Chloride Intracellular Channel 5 (CLIC5, Accession NM_016929). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLIC5. Cyclin M4 (CNNM4, Accession NM_020184) is another VGAM1965 host target gene. CNNM4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

CNNM4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNNM4 BINDING SITE, designated SEQ ID:21429, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68658] Another function of VGAM1965 is therefore inhibition of Cyclin M4 (CNNM4, Accession NM_020184). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNNM4. CCR4-NOT Transcription Complex, Subunit 3 (CNOT3, Accession NM_014516) is another VGAM1965 host target gene. CNOT3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CNOT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNOT3 BINDING SITE, designated SEQ ID:15844, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68659] Another function of VGAM1965 is therefore inhibition of

CCR4-NOT Transcription Complex, Subunit 3 (CNOT3, Accession NM_014516). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNOT3. CUB and Sushi Multiple Domains 1 (CSMD1, Accession XM_054838) is another VGAM1965 host target gene. CSMD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSMD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSMD1 BINDING SITE, designated SEQ ID:36195, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68660] Another function of VGAM1965 is therefore inhibition of CUB and Sushi Multiple Domains 1 (CSMD1, Accession XM_054838). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSMD1. DAMS (Accession NM_022001) is another VGAM1965 host target gene. DAMS BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DAMS,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAMS BINDING SITE, designated SEQ ID:22544, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68661] Another function of VGAM1965 is therefore inhibition of DAMS (Accession NM_022001). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAMS. Doublecortin and CaM Kinase-like 1 (DCAMKL1, Accession NM_004734) is another VGAM1965 host target gene. DCAMKL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCAMKL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCAMKL1 BINDING SITE, designated SEQ ID:11118, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68662] Another function of VGAM1965 is therefore inhibition of Doublecortin and CaM Kinase-like 1 (DCAMKL1, Accession

NM_004734). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCAMKL1. Degenerative Spermatocyte Homolog, Lipid Desaturase (Drosophila) (DEGS, Accession NM_003676) is another VGAM1965 host target gene. DEGS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DEGS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DEGS BINDING SITE, designated SEQ ID:9770, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68663] Another function of VGAM1965 is therefore inhibition of Degenerative Spermatocyte Homolog, Lipid Desaturase (Drosophila) (DEGS, Accession NM_003676). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DEGS. DIM1 (Accession NM_006701) is another VGAM1965 host target gene. DIM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DIM1, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DIM1 BINDING SITE, designated SEQ ID:13527, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68664] Another function of VGAM1965 is therefore inhibition of DIM1 (Accession NM_006701). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIM1. DJ122O8.2 (Accession NM_020466) is another VGAM1965 host target gene. DJ122O8.2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DJ122O8.2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DJ122O8.2 BINDING SITE, designated SEQ ID:21703, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68665] Another function of VGAM1965 is therefore inhibition of DJ122O8.2 (Accession NM_020466). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with DJ122O8.2. DKFZP434A043 (Accession NM_015396) is another VGAM1965 host target gene. DKFZP434A043 BINDING SITE1 and DKFZP434A043 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DKFZP434A043, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434A043 BINDING SITE1 and DKFZP434A043 BINDING SITE2, designated SEQ ID:17698 and SEQ ID:17705 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68666] Another function of VGAM1965 is therefore inhibition of DKFZP434A043 (Accession NM_015396). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434A043. DKFZP434B1727 (Accession NM_032143) is another VGAM1965 host target gene. DKFZP434B1727 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434B1727, corresponding to a HOST TARGET bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434B1727 BINDING SITE, designated SEQ ID:25831, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68667] Another function of VGAM1965 is therefore inhibition of DKFZP434B1727 (Accession NM_032143). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434B1727. DKFZP434D193 (Accession XM_114297) is another VGAM1965 host target gene. DKFZP434D193 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434D193, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434D193 BINDING SITE, designated SEQ ID:42853, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68668] Another function of VGAM1965 is therefore inhibition of DKFZP434D193 (Accession XM_114297). Accordingly,

utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434D193. DKFZp434E0519 (Accession NM_032247) is another VGAM1965 host target gene. DKFZp434E0519 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434E0519, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434E0519 BINDING SITE, designated SEQ ID:25984, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68669] Another function of VGAM1965 is therefore inhibition of DKFZp434E0519 (Accession NM_032247). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E0519. DKFZP434F0318 (Accession NM_030817) is another VGAM1965 host target gene. DKFZP434F0318 BINDING SITE1 and DKFZP434F0318 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DKFZP434F0318, corresponding to HOST TARGET binding sites such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434F0318 BINDING SITE1 and DKFZP434F0318 BINDING SITE2, designated SEQ ID:25145 and SEQ ID:25138 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68670] Another function of VGAM1965 is therefore inhibition of DKFZP434F0318 (Accession NM_030817). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F0318. DKFZp434G171 (Accession XM_086583) is another VGAM1965 host target gene. DKFZp434G171 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434G171, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434G171 BINDING SITE, designated SEQ ID:38778, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68671] Another function of VGAM1965 is therefore inhibition of

DKFZp434G171 (Accession XM_086583). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434G171. DKFZP434H204 (Accession XM_039153) is another VGAM1965 host target gene. DKFZP434H204 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434H204, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434H204 BINDING SITE, designated SEQ ID:33017, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68672] Another function of VGAM1965 is therefore inhibition of DKFZP434H204 (Accession XM_039153). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434H204. DKFZP434I1735 (Accession XM_113763) is another VGAM1965 host target gene. DKFZP434I1735 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434I1735, corresponding to a HOST TARGET bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434I1735 BINDING SITE, designated SEQ ID:42422, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68673] Another function of VGAM1965 is therefore inhibition of DKFZP434I1735 (Accession XM_113763). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434I1735. DKFZp434K1210 (Accession NM_017606) is another VGAM1965 host target gene. DKFZp434K1210 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434K1210, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434K1210 BINDING SITE, designated SEQ ID:19102, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68674] Another function of VGAM1965 is therefore inhibition of DKFZp434K1210 (Accession NM_017606). Accordingly,

utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434K1210. DKFZP434L187 (Accession XM_044070) is another VGAM1965 host target gene. DKFZP434L187 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434L187, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434L187 BINDING SITE, designated SEQ ID:34125, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68675] Another function of VGAM1965 is therefore inhibition of DKFZP434L187 (Accession XM_044070). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434L187. DKFZP434O047 (Accession NM_015594) is another VGAM1965 host target gene. DKFZP434O047 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434O047, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434O047 BINDING SITE, designated SEQ ID:17870, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68676] Another function of VGAM1965 is therefore inhibition of DKFZP434O047 (Accession NM_015594). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434O047. DKFZP434P0111 (Accession XM_041116) is another VGAM1965 host target gene. DKFZP434P0111 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434P0111, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434P0111 BINDING SITE, designated SEQ ID:33451, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68677] Another function of VGAM1965 is therefore inhibition of DKFZP434P0111 (Accession XM_041116). Accordingly, utilities of VGAM1965 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZP434P0111. DKFZP547L112 (Accession XM_039353) is another VGAM1965 host target gene. DKFZP547L112 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP547L112, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP547L112 BINDING SITE, designated SEQ ID:33060, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68678] Another function of VGAM1965 is therefore inhibition of DKFZP547L112 (Accession XM_039353). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP547L112. DKFZP564B1162 (Accession NM_031305) is another VGAM1965 host target gene. DKFZP564B1162 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564B1162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the

nucleotide sequences of DKFZP564B1162 BINDING SITE, designated SEQ ID:25340, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68679] Another function of VGAM1965 is therefore inhibition of DKFZP564B1162 (Accession NM_031305). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564B1162. DKFZP564F013 (Accession XM_168479) is another VGAM1965 host target gene. DKFZP564F013 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564F013, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564F013 BINDING SITE, designated SEQ ID:45204, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68680] Another function of VGAM1965 is therefore inhibition of DKFZP564F013 (Accession XM_168479). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZP564F013. DKFZP564I052 (Accession XM_039660) is another VGAM1965 host target gene. DKFZP564I052 BINDING SITE1 and DKFZP564I052 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DKFZP564I052, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564I052 BINDING SITE1 and DKFZP564I052 BINDING SITE2, designated SEQ ID:33140 and SEQ ID:33141 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68681] Another function of VGAM1965 is therefore inhibition of DKFZP564I052 (Accession XM_039660). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564I052. DKFZP564M182 (Accession XM_085525) is another VGAM1965 host target gene. DKFZP564M182 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564M182, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564M182 BINDING SITE, designated SEQ ID:38221, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68682] Another function of VGAM1965 is therefore inhibition of DKFZP564M182 (Accession XM_085525). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564M182. DKFZP564O1863 (Accession XM_043922) is another VGAM1965 host target gene. DKFZP564O1863 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O1863, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564O1863 BINDING SITE, designated SEQ ID:34043, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68683] Another function of VGAM1965 is therefore inhibition of DKFZP564O1863 (Accession XM_043922). Accordingly, utilities of VGAM1965 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZP564O1863. DKFZP566F2124 (Accession NM_015630) is another VGAM1965 host target gene. DKFZP566F2124 BINDING SITE1 and DKFZP566F2124 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DKFZP566F2124, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566F2124 BINDING SITE1 and DKFZP566F2124 BINDING SITE2, designated SEQ ID:17888 and SEQ ID:17890 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68684] Another function of VGAM1965 is therefore inhibition of DKFZP566F2124 (Accession NM_015630). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566F2124. DKFZp586I021 (Accession NM_032271) is another VGAM1965 host target gene. DKFZp586I021 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp586I021, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp586I021 BINDING SITE, designated SEQ ID:26030, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68685] Another function of VGAM1965 is therefore inhibition of DKFZp586I021 (Accession NM_032271). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp586I021. DKFZP727M111 (Accession NM_015540) is another VGAM1965 host target gene. DKFZP727M111 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP727M111, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP727M111 BINDING SITE, designated SEQ ID:17801, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68686] Another function of VGAM1965 is therefore inhibition of DKFZP727M111 (Accession NM_015540). Accordingly,

utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP727M111. DKFZp761F2014 (Accession NM_020215) is another VGAM1965 host target gene. DKFZp761F2014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761F2014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761F2014 BINDING SITE, designated SEQ ID:21464, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68687] Another function of VGAM1965 is therefore inhibition of DKFZp761F2014 (Accession NM_020215). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761F2014. DKFZP761F241 (Accession NM_031455) is another VGAM1965 host target gene. DKFZP761F241 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP761F241, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP761F241 BINDING SITE, designated SEQ ID:25479, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68688] Another function of VGAM1965 is therefore inhibition of DKFZP761F241 (Accession NM_031455). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761F241. DKFZp761G0313 (Accession XM_038026) is another VGAM1965 host target gene. DKFZp761G0313 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761G0313, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761G0313 BINDING SITE, designated SEQ ID:32743, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68689] Another function of VGAM1965 is therefore inhibition of DKFZp761G0313 (Accession XM_038026). Accordingly, utilities of VGAM1965 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZp761G0313. DKFZP761G1913 (Accession NM_031474) is another VGAM1965 host target gene. DKFZP761G1913 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP761G1913, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP761G1913 BINDING SITE, designated SEQ ID:25547, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68690] Another function of VGAM1965 is therefore inhibition of DKFZP761G1913 (Accession NM_031474). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761G1913. DKFZp761G2113 (Accession XM_046017) is another VGAM1965 host target gene. DKFZp761G2113 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761G2113, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the

nucleotide sequences of DKFZp761G2113 BINDING SITE, designated SEQ ID:34645, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68691] Another function of VGAM1965 is therefore inhibition of DKFZp761G2113 (Accession XM_046017). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761G2113. DKFZp761O0113 (Accession NM_018409) is another VGAM1965 host target gene. DKFZp761O0113 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp761O0113, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761O0113 BINDING SITE, designated SEQ ID:20448, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68692] Another function of VGAM1965 is therefore inhibition of DKFZp761O0113 (Accession NM_018409). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with DKFZp761O0113. DKFZp761P1010 (Accession NM_018423) is another VGAM1965 host target gene. DKFZp761P1010 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761P1010, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761P1010 BINDING SITE, designated SEQ ID:20480, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68693] Another function of VGAM1965 is therefore inhibition of DKFZp761P1010 (Accession NM_018423). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761P1010. DKFZp762L0311 (Accession NM_018719) is another VGAM1965 host target gene. DKFZp762L0311 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp762L0311, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp762L0311 BINDING SITE,

designated SEQ ID:20801, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68694] Another function of VGAM1965 is therefore inhibition of DKFZp762L0311 (Accession NM_018719). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762L0311. DRF1 (Accession NM_025104) is another VGAM1965 host target gene. DRF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DRF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DRF1 BINDING SITE, designated SEQ ID:24750, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68695] Another function of VGAM1965 is therefore inhibition of DRF1 (Accession NM_025104). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRF1. Down Syndrome Critical Region Gene 1-like 1 (DSCR1L1, Accession NM_005822) is another VGAM1965 host target

gene. DSCR1L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DSCR1L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DSCR1L1 BINDING SITE, designated SEQ ID:12429, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68696] Another function of VGAM1965 is therefore inhibition of Down Syndrome Critical Region Gene 1-like 1 (DSCR1L1, Accession NM_005822). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSCR1L1. Ephrin-A5 (EFNA5, Accession NM_001962) is another VGAM1965 host target gene. EFNA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EFNA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFNA5 BINDING SITE, designated SEQ ID:7687, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA,

also designated SEQ ID:4676.

[68697] Another function of VGAM1965 is therefore inhibition of Ephrin-A5 (EFNA5, Accession NM_001962). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFNA5. Echinoderm Microtubule Associated Protein Like 4 (EML4, Accession NM_019063) is another VGAM1965 host target gene. EML4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EML4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EML4 BINDING SITE, designated SEQ ID:21146, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68698] Another function of VGAM1965 is therefore inhibition of Echinoderm Microtubule Associated Protein Like 4 (EML4, Accession NM_019063). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EML4. Enabled Homolog (Drosophila) (ENAH, Accession NM_018212) is another VGAM1965 host target gene.

ENAH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ENAH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ENAH BINDING SITE, designated SEQ ID:20128, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68699] Another function of VGAM1965 is therefore inhibition of Enabled Homolog (Drosophila) (ENAH, Accession NM_018212). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENAH. Ectonucleotide Pyrophosphatase/phosphodiesterase 4 (putative function) (ENPP4, Accession NM_014936) is another VGAM1965 host target gene. ENPP4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ENPP4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ENPP4 BINDING SITE, designated SEQ ID:17241, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4676.

[68700] Another function of VGAM1965 is therefore inhibition of Ectonucleotide Pyrophosphatase/phosphodiesterase 4 (putative function) (ENPP4, Accession NM_014936). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENPP4. EPLIN (Accession NM_016357) is another VGAM1965 host target gene. EPLIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPLIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPLIN BINDING SITE, designated SEQ ID:18495, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68701] Another function of VGAM1965 is therefore inhibition of EPLIN (Accession NM_016357). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPLIN. Erythroblast Membrane-associated Protein (ERMAP, Accession NM_018538) is another VGAM1965 host target gene. ERMAP BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by ERMAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERMAP BINDING SITE, designated SEQ ID:20604, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68702] Another function of VGAM1965 is therefore inhibition of Erythroblast Membrane-associated Protein (ERMAP, Accession NM_018538). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERMAP. ET (Accession NM_024311) is another VGAM1965 host target gene. ET BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ET, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ET BINDING SITE, designated SEQ ID:23605, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68703] Another function of VGAM1965 is therefore inhibition of

ET (Accession NM_024311). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ET. Fatty Acid Desaturase 2 (FADS2, Accession NM_004265) is another VGAM1965 host target gene. FADS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FADS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FADS2 BINDING SITE, designated SEQ ID:10468, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68704] Another function of VGAM1965 is therefore inhibition of Fatty Acid Desaturase 2 (FADS2, Accession NM_004265). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FADS2. FBX30 (Accession NM_033182) is another VGAM1965 host target gene. FBX30 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBX30, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of FBX30 BINDING SITE, designated SEQ ID:27043, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68705] Another function of VGAM1965 is therefore inhibition of FBX30 (Accession NM_033182). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBX30. F-box Only Protein 8 (FBXO8, Accession NM_012180) is another VGAM1965 host target gene. FBXO8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXO8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXO8 BINDING SITE, designated SEQ ID:14467, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68706] Another function of VGAM1965 is therefore inhibition of F-box Only Protein 8 (FBXO8, Accession NM_012180). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with FBXO8. FGD1 Family, Member 3 (FGD3, Accession XM_053487) is another VGAM1965 host target gene. FGD3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGD3 BINDING SITE, designated SEQ ID:36093, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68707] Another function of VGAM1965 is therefore inhibition of FGD1 Family, Member 3 (FGD3, Accession XM_053487). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGD3. FLJ00001 (Accession XM_088525) is another VGAM1965 host target gene. FLJ00001 BINDING SITE1 and FLJ00001 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ00001, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00001 BINDING SITE1 and FLJ00001 BINDING SITE2, designated SEQ

ID:39781 and SEQ ID:39784 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68708] Another function of VGAM1965 is therefore inhibition of FLJ00001 (Accession XM_088525). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00001. FLJ00007 (Accession XM_048928) is another VGAM1965 host target gene. FLJ00007 BINDING SITE1 and FLJ00007 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ00007, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00007 BINDING SITE1 and FLJ00007 BINDING SITE2, designated SEQ ID:35314 and SEQ ID:19799 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68709] Another function of VGAM1965 is therefore inhibition of FLJ00007 (Accession XM_048928). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ00007. FLJ10460 (Accession NM_018097) is another VGAM1965 host target gene. FLJ10460 BINDING SITE1 and FLJ10460 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ10460, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10460 BINDING SITE1 and FLJ10460 BINDING SITE2, designated SEQ ID:19868 and SEQ ID:19870 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68710] Another function of VGAM1965 is therefore inhibition of FLJ10460 (Accession NM_018097). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10460. FLJ10520 (Accession NM_018124) is another VGAM1965 host target gene. FLJ10520 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10520, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10520

BINDING SITE, designated SEQ ID:19907, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68711] Another function of VGAM1965 is therefore inhibition of FLJ10520 (Accession NM_018124). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10520. FLJ10535 (Accession NM_018129) is another VGAM1965 host target gene. FLJ10535 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10535, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10535 BINDING SITE, designated SEQ ID:19923, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68712] Another function of VGAM1965 is therefore inhibition of FLJ10535 (Accession NM_018129). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10535. FLJ10539 (Accession NM_018130) is another VGAM1965 host target gene. FLJ10539 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10539, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10539 BINDING SITE, designated SEQ ID:19925, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68713] Another function of VGAM1965 is therefore inhibition of FLJ10539 (Accession NM_018130). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10539. FLJ10547 (Accession NM_018134) is another VGAM1965 host target gene. FLJ10547 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10547, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10547 BINDING SITE, designated SEQ ID:19932, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68714] Another function of VGAM1965 is therefore inhibition of

FLJ10547 (Accession NM_018134). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10547. FLJ10579 (Accession NM_018145) is another VGAM1965 host target gene. FLJ10579 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10579, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10579 BINDING SITE, designated SEQ ID:19947, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68715] Another function of VGAM1965 is therefore inhibition of FLJ10579 (Accession NM_018145). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10579. FLJ10619 (Accession NM_018156) is another VGAM1965 host target gene. FLJ10619 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10619, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ10619 BINDING SITE, designated SEQ ID:19968, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68716] Another function of VGAM1965 is therefore inhibition of FLJ10619 (Accession NM_018156). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10619. FLJ10704 (Accession NM_018185) is another VGAM1965 host target gene. FLJ10704 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10704, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10704 BINDING SITE, designated SEQ ID:20036, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68717] Another function of VGAM1965 is therefore inhibition of FLJ10704 (Accession NM_018185). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10704. FLJ10895 (Accession NM_019084) is another

VGAM1965 host target gene. FLJ10895 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10895, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10895 BINDING SITE, designated SEQ ID:21159, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68718] Another function of VGAM1965 is therefore inhibition of FLJ10895 (Accession NM_019084). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10895. FLJ10904 (Accession NM_018268) is another VGAM1965 host target gene. FLJ10904 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10904, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10904 BINDING SITE, designated SEQ ID:20241, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68719] Another function of VGAM1965 is therefore inhibition of FLJ10904 (Accession NM_018268). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10904. FLJ10922 (Accession NM_018273) is another VGAM1965 host target gene. FLJ10922 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10922, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10922 BINDING SITE, designated SEQ ID:20258, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68720] Another function of VGAM1965 is therefore inhibition of FLJ10922 (Accession NM_018273). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10922. FLJ10936 (Accession NM_018279) is another VGAM1965 host target gene. FLJ10936 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10936, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10936 BINDING SITE, designated SEQ ID:20269, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68721] Another function of VGAM1965 is therefore inhibition of FLJ10936 (Accession NM_018279). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10936. FLJ11210 (Accession XM_005298) is another VGAM1965 host target gene. FLJ11210 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11210, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11210 BINDING SITE, designated SEQ ID:29976, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68722] Another function of VGAM1965 is therefore inhibition of FLJ11210 (Accession XM_005298). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ11210. FLJ11539 (Accession NM_024748) is another VGAM1965 host target gene. FLJ11539 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11539, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11539 BINDING SITE, designated SEQ ID:24089, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68723] Another function of VGAM1965 is therefore inhibition of FLJ11539 (Accession NM_024748). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11539. FLJ12057 (Accession NM_024768) is another VGAM1965 host target gene. FLJ12057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12057 BINDING SITE, designated SEQ ID:24128, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM

RNA, also designated SEQ ID:4676.

[68724] Another function of VGAM1965 is therefore inhibition of FLJ12057 (Accession NM_024768). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12057. FLJ12363 (Accession NM_032167) is another VGAM1965 host target gene. FLJ12363 BINDING SITE1 and FLJ12363 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ12363, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12363 BINDING SITE1 and FLJ12363 BINDING SITE2, designated SEQ ID:25869 and SEQ ID:25870 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68725] Another function of VGAM1965 is therefore inhibition of FLJ12363 (Accession NM_032167). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12363. FLJ12425 (Accession XM_098290) is another VGAM1965 host target gene. FLJ12425 BINDING SITE1 and

FLJ12425 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ12425, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12425 BINDING SITE1 and FLJ12425 BINDING SITE2, designated SEQ ID:41563 and SEQ ID:24550 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68726] Another function of VGAM1965 is therefore inhibition of FLJ12425 (Accession XM_098290). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12425. FLJ12587 (Accession NM_022480) is another VGAM1965 host target gene. FLJ12587 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12587, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12587 BINDING SITE, designated SEQ ID:22854, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM

RNA, also designated SEQ ID:4676.

[68727] Another function of VGAM1965 is therefore inhibition of FLJ12587 (Accession NM_022480). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12587. FLJ12592 (Accession NM_032169) is another VGAM1965 host target gene. FLJ12592 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12592, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12592 BINDING SITE, designated SEQ ID:25876, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68728] Another function of VGAM1965 is therefore inhibition of FLJ12592 (Accession NM_032169). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12592. FLJ12687 (Accession NM_024917) is another VGAM1965 host target gene. FLJ12687 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12687, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12687 BINDING SITE, designated SEQ ID:24448, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68729] Another function of VGAM1965 is therefore inhibition of FLJ12687 (Accession NM_024917). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12687. FLJ12747 (Accession NM_032173) is another VGAM1965 host target gene. FLJ12747 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12747, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12747 BINDING SITE, designated SEQ ID:25882, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68730] Another function of VGAM1965 is therefore inhibition of FLJ12747 (Accession NM_032173). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12747. FLJ12770 (Accession NM_032174) is another VGAM1965 host target gene. FLJ12770 BINDING SITE1 and FLJ12770 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ12770, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12770 BINDING SITE1 and FLJ12770 BINDING SITE2, designated SEQ ID:25886 and SEQ ID:25887 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68731] Another function of VGAM1965 is therefore inhibition of FLJ12770 (Accession NM_032174). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12770. FLJ12994 (Accession NM_022841) is another VGAM1965 host target gene. FLJ12994 BINDING SITE1 and FLJ12994 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ12994, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12994 BINDING SITE1 and FLJ12994 BINDING SITE2, designated SEQ ID:23133 and SEQ ID:37975 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68732] Another function of VGAM1965 is therefore inhibition of FLJ12994 (Accession NM_022841). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12994. FLJ13612 (Accession NM_025202) is another VGAM1965 host target gene. FLJ13612 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13612, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13612 BINDING SITE, designated SEQ ID:24865, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68733] Another function of VGAM1965 is therefore inhibition of FLJ13612 (Accession NM_025202). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ13612. FLJ13614 (Accession NM_139076) is another VGAM1965 host target gene. FLJ13614 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13614, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13614 BINDING SITE, designated SEQ ID:29150, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68734] Another function of VGAM1965 is therefore inhibition of FLJ13614 (Accession NM_139076). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13614. FLJ13646 (Accession NM_024584) is another VGAM1965 host target gene. FLJ13646 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13646, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13646 BINDING SITE, designated SEQ ID:23816, to the nucleotide

sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68735] Another function of VGAM1965 is therefore inhibition of FLJ13646 (Accession NM_024584). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13646. FLJ13693 (Accession NM_024807) is another VGAM1965 host target gene. FLJ13693 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13693, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13693 BINDING SITE, designated SEQ ID:24189, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68736] Another function of VGAM1965 is therefore inhibition of FLJ13693 (Accession NM_024807). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13693. FLJ13902 (Accession NM_024653) is another VGAM1965 host target gene. FLJ13902 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ13902, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13902 BINDING SITE, designated SEQ ID:23952, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68737] Another function of VGAM1965 is therefore inhibition of FLJ13902 (Accession NM_024653). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13902. FLJ13952 (Accession NM_024798) is another VGAM1965 host target gene. FLJ13952 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13952, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13952 BINDING SITE, designated SEQ ID:24176, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68738] Another function of VGAM1965 is therefore inhibition of FLJ13952 (Accession NM_024798). Accordingly, utilities of

VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13952. FLJ14054 (Accession NM_024563) is another VGAM1965 host target gene. FLJ14054 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14054 BINDING SITE, designated SEQ ID:23787, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68739] Another function of VGAM1965 is therefore inhibition of FLJ14054 (Accession NM_024563). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14054. FLJ14084 (Accession NM_021637) is another VGAM1965 host target gene. FLJ14084 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14084, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14084

BINDING SITE, designated SEQ ID:22287, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68740] Another function of VGAM1965 is therefore inhibition of FLJ14084 (Accession NM_021637). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14084. FLJ14356 (Accession NM_030824) is another VGAM1965 host target gene. FLJ14356 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ14356, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14356 BINDING SITE, designated SEQ ID:25154, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68741] Another function of VGAM1965 is therefore inhibition of FLJ14356 (Accession NM_030824). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14356. FLJ14431 (Accession NM_032783) is another VGAM1965 host target gene. FLJ14431 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14431, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14431 BINDING SITE, designated SEQ ID:26527, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68742] Another function of VGAM1965 is therefore inhibition of FLJ14431 (Accession NM_032783). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14431. FLJ14525 (Accession NM_032800) is another VGAM1965 host target gene. FLJ14525 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14525, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14525 BINDING SITE, designated SEQ ID:26550, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68743] Another function of VGAM1965 is therefore inhibition of

FLJ14525 (Accession NM_032800). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14525. FLJ14751 (Accession NM_032834) is another VGAM1965 host target gene. FLJ14751 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14751, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14751 BINDING SITE, designated SEQ ID:26611, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68744] Another function of VGAM1965 is therefore inhibition of FLJ14751 (Accession NM_032834). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14751. FLJ14871 (Accession NM_032854) is another VGAM1965 host target gene. FLJ14871 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ14871 BINDING SITE, designated SEQ ID:26653, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68745] Another function of VGAM1965 is therefore inhibition of FLJ14871 (Accession NM_032854). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14871. FLJ14888 (Accession NM_032856) is another VGAM1965 host target gene. FLJ14888 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14888, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14888 BINDING SITE, designated SEQ ID:26656, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68746] Another function of VGAM1965 is therefore inhibition of FLJ14888 (Accession NM_032856). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14888. FLJ20034 (Accession NM_017630) is another

VGAM1965 host target gene. FLJ20034 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20034 BINDING SITE, designated SEQ ID:19138, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68747] Another function of VGAM1965 is therefore inhibition of FLJ20034 (Accession NM_017630). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20034. FLJ20139 (Accession NM_017685) is another VGAM1965 host target gene. FLJ20139 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20139 BINDING SITE, designated SEQ ID:19235, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68748] Another function of VGAM1965 is therefore inhibition of FLJ20139 (Accession NM_017685). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20139. FLJ20150 (Accession NM_017688) is another VGAM1965 host target gene. FLJ20150 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20150, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20150 BINDING SITE, designated SEQ ID:19244, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68749] Another function of VGAM1965 is therefore inhibition of FLJ20150 (Accession NM_017688). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20150. FLJ20232 (Accession NM_019008) is another VGAM1965 host target gene. FLJ20232 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20232, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20232 BINDING SITE, designated SEQ ID:21089, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68750] Another function of VGAM1965 is therefore inhibition of FLJ20232 (Accession NM_019008). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20232. FLJ20308 (Accession XM_039852) is another VGAM1965 host target gene. FLJ20308 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20308 BINDING SITE, designated SEQ ID:33198, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68751] Another function of VGAM1965 is therefore inhibition of FLJ20308 (Accession XM_039852). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20308. FLJ20343 (Accession NM_017775) is another VGAM1965 host target gene. FLJ20343 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20343, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20343 BINDING SITE, designated SEQ ID:19400, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68752] Another function of VGAM1965 is therefore inhibition of FLJ20343 (Accession NM_017775). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20343. FLJ20413 (Accession NM_017808) is another VGAM1965 host target gene. FLJ20413 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20413, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20413 BINDING SITE, designated SEQ ID:19454, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM

RNA, also designated SEQ ID:4676.

[68753] Another function of VGAM1965 is therefore inhibition of FLJ20413 (Accession NM_017808). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20413. FLJ20511 (Accession NM_017853) is another VGAM1965 host target gene. FLJ20511 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20511, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20511 BINDING SITE, designated SEQ ID:19530, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68754] Another function of VGAM1965 is therefore inhibition of FLJ20511 (Accession NM_017853). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20511. FLJ20666 (Accession NM_017922) is another VGAM1965 host target gene. FLJ20666 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20666, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20666 BINDING SITE, designated SEQ ID:19584, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68755] Another function of VGAM1965 is therefore inhibition of FLJ20666 (Accession NM_017922). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20666. FLJ20686 (Accession NM_017925) is another VGAM1965 host target gene. FLJ20686 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20686, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20686 BINDING SITE, designated SEQ ID:19596, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68756] Another function of VGAM1965 is therefore inhibition of FLJ20686 (Accession NM_017925). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20686. FLJ20689 (Accession NM_017926) is another VGAM1965 host target gene. FLJ20689 BINDING SITE1 and FLJ20689 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ20689, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20689 BINDING SITE1 and FLJ20689 BINDING SITE2, designated SEQ ID:19600 and SEQ ID:19704 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68757] Another function of VGAM1965 is therefore inhibition of FLJ20689 (Accession NM_017926). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20689. FLJ22004 (Accession NM_025181) is another VGAM1965 host target gene. FLJ22004 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22004, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ22004 BINDING SITE, designated SEQ ID:24817, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68758] Another function of VGAM1965 is therefore inhibition of FLJ22004 (Accession NM_025181). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22004. FLJ22301 (Accession NM_024836) is another VGAM1965 host target gene. FLJ22301 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22301 BINDING SITE, designated SEQ ID:24242, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68759] Another function of VGAM1965 is therefore inhibition of FLJ22301 (Accession NM_024836). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22301. FLJ22761 (Accession NM_025130) is another

VGAM1965 host target gene. FLJ22761 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22761, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22761 BINDING SITE, designated SEQ ID:24772, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68760] Another function of VGAM1965 is therefore inhibition of FLJ22761 (Accession NM_025130). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22761. FLJ23040 (Accession NM_025174) is another VGAM1965 host target gene. FLJ23040 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23040 BINDING SITE, designated SEQ ID:24809, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68761] Another function of VGAM1965 is therefore inhibition of FLJ23040 (Accession NM_025174). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23040. FLJ23119 (Accession NM_024652) is another VGAM1965 host target gene. FLJ23119 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23119, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23119 BINDING SITE, designated SEQ ID:23949, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68762] Another function of VGAM1965 is therefore inhibition of FLJ23119 (Accession NM_024652). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23119. FLJ23311 (Accession NM_024680) is another VGAM1965 host target gene. FLJ23311 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23311, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23311 BINDING SITE, designated SEQ ID:23993, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68763] Another function of VGAM1965 is therefore inhibition of FLJ23311 (Accession NM_024680). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23311. FLJ23342 (Accession NM_024631) is another VGAM1965 host target gene. FLJ23342 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23342, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23342 BINDING SITE, designated SEQ ID:23899, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68764] Another function of VGAM1965 is therefore inhibition of FLJ23342 (Accession NM_024631). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ23342. FLJ23462 (Accession NM_024843) is another VGAM1965 host target gene. FLJ23462 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23462, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23462 BINDING SITE, designated SEQ ID:24268, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68765] Another function of VGAM1965 is therefore inhibition of FLJ23462 (Accession NM_024843). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23462. FLJ23499 (Accession NM_022761) is another VGAM1965 host target gene. FLJ23499 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23499, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23499 BINDING SITE, designated SEQ ID:23008, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM

RNA, also designated SEQ ID:4676.

[68766] Another function of VGAM1965 is therefore inhibition of FLJ23499 (Accession NM_022761). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23499. FLJ23556 (Accession NM_024880) is another VGAM1965 host target gene. FLJ23556 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23556, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23556 BINDING SITE, designated SEQ ID:24321, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68767] Another function of VGAM1965 is therefore inhibition of FLJ23556 (Accession NM_024880). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23556. FLJ23590 (Accession NM_024649) is another VGAM1965 host target gene. FLJ23590 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23590, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23590 BINDING SITE, designated SEQ ID:23942, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68768] Another function of VGAM1965 is therefore inhibition of FLJ23590 (Accession NM_024649). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23590. FLJ25415 (Accession NM_144708) is another VGAM1965 host target gene. FLJ25415 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ25415, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ25415 BINDING SITE, designated SEQ ID:29534, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68769] Another function of VGAM1965 is therefore inhibition of FLJ25415 (Accession NM_144708). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ25415. FLJ30294 (Accession NM_144632) is another VGAM1965 host target gene. FLJ30294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ30294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ30294 BINDING SITE, designated SEQ ID:29450, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68770] Another function of VGAM1965 is therefore inhibition of FLJ30294 (Accession NM_144632). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30294. FLJ30567 (Accession NM_145022) is another VGAM1965 host target gene. FLJ30567 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ30567, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ30567 BINDING SITE, designated SEQ ID:29634, to the nucleotide

sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68771] Another function of VGAM1965 is therefore inhibition of FLJ30567 (Accession NM_145022). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30567. FLJ31890 (Accession XM_166117) is another VGAM1965 host target gene. FLJ31890 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ31890, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ31890 BINDING SITE, designated SEQ ID:43893, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68772] Another function of VGAM1965 is therefore inhibition of FLJ31890 (Accession XM_166117). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31890. FLJ32865 (Accession NM_144613) is another VGAM1965 host target gene. FLJ32865 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ32865, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32865 BINDING SITE, designated SEQ ID:29428, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68773] Another function of VGAM1965 is therefore inhibition of FLJ32865 (Accession NM_144613). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32865. FLJ32894 (Accession NM_144667) is another VGAM1965 host target gene. FLJ32894 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ32894, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32894 BINDING SITE, designated SEQ ID:29486, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68774] Another function of VGAM1965 is therefore inhibition of FLJ32894 (Accession NM_144667). Accordingly, utilities of

VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32894. FLJ33069 (Accession NM_144649) is another VGAM1965 host target gene. FLJ33069 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ33069, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ33069 BINDING SITE, designated SEQ ID:29476, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68775] Another function of VGAM1965 is therefore inhibition of FLJ33069 (Accession NM_144649). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ33069. Forkhead Box H1 (FOXH1, Accession NM_003923) is another VGAM1965 host target gene. FOXH1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FOXH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of FOXH1 BINDING SITE, designated SEQ ID:10012, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68776] Another function of VGAM1965 is therefore inhibition of Forkhead Box H1 (FOXH1, Accession NM_003923). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXH1. FRSB (Accession NM_005687) is another VGAM1965 host target gene. FRSB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FRSB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FRSB BINDING SITE, designated SEQ ID:12247, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68777] Another function of VGAM1965 is therefore inhibition of FRSB (Accession NM_005687). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FRSB. GRB2-associated Binding Protein 3 (GAB3, Accession

NM_080612) is another VGAM1965 host target gene. GAB3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GAB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAB3 BINDING SITE, designated SEQ ID:27929, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68778] Another function of VGAM1965 is therefore inhibition of GRB2-associated Binding Protein 3 (GAB3, Accession NM_080612). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAB3. GAPCENA (Accession NM_012197) is another VGAM1965 host target gene. GAPCENA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GAPCENA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAPCENA BINDING SITE, designated SEQ ID:14496, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ

ID:4676.

[68779] Another function of VGAM1965 is therefore inhibition of GAPCENA (Accession NM_012197). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAPCENA. Ganglioside-induced Differentiation-associated Protein 1-like 1 (GDAP1L1, Accession NM_024034) is another VGAM1965 host target gene. GDAP1L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GDAP1L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GDAP1L1 BINDING SITE, designated SEQ ID:23466, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68780] Another function of VGAM1965 is therefore inhibition of Ganglioside-induced Differentiation-associated Protein 1-like 1 (GDAP1L1, Accession NM_024034). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GDAP1L1. GENX-3414 (Accession NM_003943) is another VGAM1965 host target gene. GENX-3414 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GENX-3414, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GENX-3414 BINDING SITE, designated SEQ ID:10060, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68781] Another function of VGAM1965 is therefore inhibition of GENX-3414 (Accession NM_003943). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GENX-3414. Golgi Associated, Gamma Adaptin Ear Containing, ARF Binding Protein 2 (GGA2, Accession NM_138640) is another VGAM1965 host target gene. GGA2 BINDING SITE1 and GGA2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GGA2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE1 and GGA2 BINDING SITE2, designated SEQ ID:28927 and SEQ ID:17405 respectively, to the nucleotide sequence of

VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68782] Another function of VGAM1965 is therefore inhibition of Golgi Associated, Gamma Adaptin Ear Containing, ARF Binding Protein 2 (GGA2, Accession NM_138640). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2. Golgi Autoantigen, Golgin Subfamily A, 2-like, Y-linked (GOLGA2LY, Accession XM_034789) is another VGAM1965 host target gene. GOLGA2LY BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GOLGA2LY, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GOLGA2LY BINDING SITE, designated SEQ ID:32145, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68783] Another function of VGAM1965 is therefore inhibition of Golgi Autoantigen, Golgin Subfamily A, 2-like, Y-linked (GOLGA2LY, Accession XM_034789). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

GOLGA2LY. Glycoprotein V (platelet) (GP5, Accession NM_004488) is another VGAM1965 host target gene. GP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GP5 BINDING SITE, designated SEQ ID:10820, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68784] Another function of VGAM1965 is therefore inhibition of Glycoprotein V (platelet) (GP5, Accession NM_004488). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GP5. G Protein Pathway Suppressor 2 (GPS2, Accession NM_004489) is another VGAM1965 host target gene. GPS2 BINDING SITE1 through GPS2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GPS2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPS2 BINDING SITE1 through GPS2 BINDING SITE3, designated

SEQ ID:10828, SEQ ID:42149 and SEQ ID:42150 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68785] Another function of VGAM1965 is therefore inhibition of G Protein Pathway Suppressor 2 (GPS2, Accession NM_004489). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPS2. GTP Binding Protein 2 (GTPBP2, Accession NM_019096) is another VGAM1965 host target gene. GTPBP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GTPBP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTPBP2 BINDING SITE, designated SEQ ID:21174, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68786] Another function of VGAM1965 is therefore inhibition of GTP Binding Protein 2 (GTPBP2, Accession NM_019096). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with GTPBP2. G-2 and S-phase Expressed 1 (GTSE1, Accession NM_016426) is another VGAM1965 host target gene. GTSE1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GTSE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTSE1 BINDING SITE, designated SEQ ID:18547, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68787] Another function of VGAM1965 is therefore inhibition of G-2 and S-phase Expressed 1 (GTSE1, Accession NM_016426). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTSE1. H326 (Accession NM_015726) is another VGAM1965 host target gene. H326 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by H326, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H326 BINDING SITE, designated SEQ ID:17940,

to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68788] Another function of VGAM1965 is therefore inhibition of H326 (Accession NM_015726). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H326. HCA127 (Accession NM_018684) is another VGAM1965 host target gene. HCA127 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCA127, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCA127 BINDING SITE, designated SEQ ID:20757, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68789] Another function of VGAM1965 is therefore inhibition of HCA127 (Accession NM_018684). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCA127. HIG2 (Accession NM_013332) is another VGAM1965 host target gene. HIG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by HIG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIG2 BINDING SITE, designated SEQ ID:14979, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68790] Another function of VGAM1965 is therefore inhibition of HIG2 (Accession NM_013332). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIG2. HSPC065 (Accession NM_014157) is another VGAM1965 host target gene. HSPC065 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSPC065, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPC065 BINDING SITE, designated SEQ ID:15456, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68791] Another function of VGAM1965 is therefore inhibition of HSPC065 (Accession NM_014157). Accordingly, utilities of

VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC065. HT002 (Accession NM_014066) is another VGAM1965 host target gene. HT002 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HT002, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HT002 BINDING SITE, designated SEQ ID:15280, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68792] Another function of VGAM1965 is therefore inhibition of HT002 (Accession NM_014066). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HT002. HT007 (Accession NM_018480) is another VGAM1965 host target gene. HT007 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HT007, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HT007 BINDING SITE, des-

ignated SEQ ID:20543, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68793] Another function of VGAM1965 is therefore inhibition of HT007 (Accession NM_018480). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HT007. HUMNPIIY20 (Accession XM_096782) is another VGAM1965 host target gene. HUMNPIIY20 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HUMNPIIY20, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HUMNPIIY20 BINDING SITE, designated SEQ ID:40538, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68794] Another function of VGAM1965 is therefore inhibition of HUMNPIIY20 (Accession XM_096782). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUMNPIIY20. HYA22 (Accession NM_005808) is another VGAM1965 host target gene. HYA22 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HYA22, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HYA22 BINDING SITE, designated SEQ ID:12390, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68795] Another function of VGAM1965 is therefore inhibition of HYA22 (Accession NM_005808). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HYA22. IDN3 (Accession NM_133433) is another VGAM1965 host target gene. IDN3 BINDING SITE1 and IDN3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by IDN3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IDN3 BINDING SITE1 and IDN3 BINDING SITE2, designated SEQ ID:28513 and SEQ ID:17685 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68796] Another function of VGAM1965 is therefore inhibition of IDN3 (Accession NM_133433). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IDN3. Interleukin 1 Receptor Accessory Protein-like 1 (IL1RAPL1, Accession NM_014271) is another VGAM1965 host target gene. IL1RAPL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IL1RAPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1RAPL1 BINDING SITE, designated SEQ ID:15555, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68797] Another function of VGAM1965 is therefore inhibition of Interleukin 1 Receptor Accessory Protein-like 1 (IL1RAPL1, Accession NM_014271). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1RAPL1. IMAGE:4907098 (Accession XM_166247) is another VGAM1965 host target gene. IMAGE:4907098 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by IMAGE:4907098, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IMAGE:4907098 BINDING SITE, designated SEQ ID:44059, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68798] Another function of VGAM1965 is therefore inhibition of IMAGE:4907098 (Accession XM_166247). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMAGE:4907098. IMPACT (Accession NM_018439) is another VGAM1965 host target gene. IMPACT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IMPACT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IMPACT BINDING SITE, designated SEQ ID:20504, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68799] Another function of VGAM1965 is therefore inhibition of

IMPACT (Accession NM_018439). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMPACT. jdp2 (Accession NM_130469) is another VGAM1965 host target gene. jdp2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by jdp2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of jdp2 BINDING SITE, designated SEQ ID:28231, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68800] Another function of VGAM1965 is therefore inhibition of jdp2 (Accession NM_130469). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with jdp2. Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 1 (KCNS1, Accession NM_002251) is another VGAM1965 host target gene. KCNS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNS1 BINDING SITE, designated SEQ ID:8043, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68801] Another function of VGAM1965 is therefore inhibition of Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 1 (KCNS1, Accession NM_002251). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNS1. KIAA0040 (Accession NM_014656) is another VGAM1965 host target gene. KIAA0040 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0040 BINDING SITE, designated SEQ ID:16097, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68802] Another function of VGAM1965 is therefore inhibition of KIAA0040 (Accession NM_014656). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0040. KIAA0061 (Accession XM_043094) is another VGAM1965 host target gene. KIAA0061 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0061, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0061 BINDING SITE, designated SEQ ID:33893, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68803] Another function of VGAM1965 is therefore inhibition of KIAA0061 (Accession XM_043094). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0061. KIAA0090 (Accession XM_114045) is another VGAM1965 host target gene. KIAA0090 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0090, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0090 BINDING SITE, designated SEQ ID:42654, to the

nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68804] Another function of VGAM1965 is therefore inhibition of KIAA0090 (Accession XM_114045). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0090. KIAA0092 (Accession NM_014679) is another VGAM1965 host target gene. KIAA0092 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0092 BINDING SITE, designated SEQ ID:16156, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68805] Another function of VGAM1965 is therefore inhibition of KIAA0092 (Accession NM_014679). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0092. KIAA0102 (Accession NM_014752) is another VGAM1965 host target gene. KIAA0102 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by KIAA0102, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0102 BINDING SITE, designated SEQ ID:16476, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68806] Another function of VGAM1965 is therefore inhibition of KIAA0102 (Accession NM_014752). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0102. KIAA0133 (Accession NM_014777) is another VGAM1965 host target gene. KIAA0133 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0133, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0133 BINDING SITE, designated SEQ ID:16608, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68807] Another function of VGAM1965 is therefore inhibition of KIAA0133 (Accession NM_014777). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0133. KIAA0161 (Accession NM_014746) is another VGAM1965 host target gene. KIAA0161 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0161, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0161 BINDING SITE, designated SEQ ID:16433, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68808] Another function of VGAM1965 is therefore inhibition of KIAA0161 (Accession NM_014746). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0161. KIAA0173 (Accession NM_014640) is another VGAM1965 host target gene. KIAA0173 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0173, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0173 BINDING SITE, designated SEQ ID:16043, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68809] Another function of VGAM1965 is therefore inhibition of KIAA0173 (Accession NM_014640). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0173. KIAA0186 (Accession NM_021067) is another VGAM1965 host target gene. KIAA0186 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0186, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0186 BINDING SITE, designated SEQ ID:22039, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68810] Another function of VGAM1965 is therefore inhibition of KIAA0186 (Accession NM_021067). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0186. KIAA0227 (Accession XM_027236) is another VGAM1965 host target gene. KIAA0227 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0227, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0227 BINDING SITE, designated SEQ ID:30453, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68811] Another function of VGAM1965 is therefore inhibition of KIAA0227 (Accession XM_027236). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0227. KIAA0232 (Accession XM_052627) is another VGAM1965 host target gene. KIAA0232 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0232, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0232 BINDING SITE, designated SEQ ID:36039, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68812] Another function of VGAM1965 is therefore inhibition of

KIAA0232 (Accession XM_052627). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0232. KIAA0247 (Accession NM_014734) is another VGAM1965 host target gene. KIAA0247 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0247, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0247 BINDING SITE, designated SEQ ID:16378, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68813] Another function of VGAM1965 is therefore inhibition of KIAA0247 (Accession NM_014734). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0247. KIAA0258 (Accession NM_014785) is another VGAM1965 host target gene. KIAA0258 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0258, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0258 BINDING SITE, designated SEQ ID:16646, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68814] Another function of VGAM1965 is therefore inhibition of KIAA0258 (Accession NM_014785). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0258. KIAA0265 (Accession XM_045954) is another VGAM1965 host target gene. KIAA0265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0265 BINDING SITE, designated SEQ ID:34631, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68815] Another function of VGAM1965 is therefore inhibition of KIAA0265 (Accession XM_045954). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0265. KIAA0326 (Accession XM_034819) is another

VGAM1965 host target gene. KIAA0326 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0326, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0326 BINDING SITE, designated SEQ ID:32161, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68816] Another function of VGAM1965 is therefore inhibition of KIAA0326 (Accession XM_034819). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0326. KIAA0336 (Accession NM_014635) is another VGAM1965 host target gene. KIAA0336 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0336, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0336 BINDING SITE, designated SEQ ID:16012, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68817] Another function of VGAM1965 is therefore inhibition of KIAA0336 (Accession NM_014635). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0336. KIAA0349 (Accession XM_166449) is another VGAM1965 host target gene. KIAA0349 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0349, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0349 BINDING SITE, designated SEQ ID:44342, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68818] Another function of VGAM1965 is therefore inhibition of KIAA0349 (Accession XM_166449). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0349. KIAA0352 (Accession NM_014830) is another VGAM1965 host target gene. KIAA0352 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0352, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0352 BINDING SITE, designated SEQ ID:16825, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68819] Another function of VGAM1965 is therefore inhibition of KIAA0352 (Accession NM_014830). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0352. KIAA0354 (Accession NM_014872) is another VGAM1965 host target gene. KIAA0354 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0354, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0354 BINDING SITE, designated SEQ ID:16999, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68820] Another function of VGAM1965 is therefore inhibition of KIAA0354 (Accession NM_014872). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0354. KIAA0365 (Accession XM_086055) is another VGAM1965 host target gene. KIAA0365 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0365, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0365 BINDING SITE, designated SEQ ID:38471, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68821] Another function of VGAM1965 is therefore inhibition of KIAA0365 (Accession XM_086055). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0365. KIAA0375 (Accession XM_048462) is another VGAM1965 host target gene. KIAA0375 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0375, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0375 BINDING SITE, designated SEQ ID:35177, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[68822] Another function of VGAM1965 is therefore inhibition of KIAA0375 (Accession XM_048462). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0375. KIAA0410 (Accession NM_014778) is another VGAM1965 host target gene. KIAA0410 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0410, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0410 BINDING SITE, designated SEQ ID:16612, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68823] Another function of VGAM1965 is therefore inhibition of KIAA0410 (Accession NM_014778). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0410. KIAA0419 (Accession NM_014711) is another VGAM1965 host target gene. KIAA0419 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0419, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0419 BINDING SITE, designated SEQ ID:16261, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68824] Another function of VGAM1965 is therefore inhibition of KIAA0419 (Accession NM_014711). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0419. KIAA0446 (Accession XM_044155) is another VGAM1965 host target gene. KIAA0446 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0446, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0446 BINDING SITE, designated SEQ ID:34153, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68825] Another function of VGAM1965 is therefore inhibition of KIAA0446 (Accession XM_044155). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0446. KIAA0449 (Accession NM_017596) is another VGAM1965 host target gene. KIAA0449 BINDING SITE1 and KIAA0449 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0449, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0449 BINDING SITE1 and KIAA0449 BINDING SITE2, designated SEQ ID:19056 and SEQ ID:19057 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68826] Another function of VGAM1965 is therefore inhibition of KIAA0449 (Accession NM_017596). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0449. KIAA0450 (Accession NM_014638) is another VGAM1965 host target gene. KIAA0450 BINDING SITE1 and KIAA0450 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0450, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0450 BINDING SITE1 and KIAA0450 BINDING SITE2, designated SEQ ID:16035 and SEQ ID:16989 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68827] Another function of VGAM1965 is therefore inhibition of KIAA0450 (Accession NM_014638). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0450. KIAA0527 (Accession XM_171054) is another VGAM1965 host target gene. KIAA0527 BINDING SITE1 and KIAA0527 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0527, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0527 BINDING SITE1 and KIAA0527 BINDING SITE2, designated SEQ ID:45842 and SEQ ID:45845 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68828] Another function of VGAM1965 is therefore inhibition of

KIAA0527 (Accession XM_171054). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0527. KIAA0563 (Accession NM_014834) is another VGAM1965 host target gene. KIAA0563 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0563, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0563 BINDING SITE, designated SEQ ID:16843, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68829] Another function of VGAM1965 is therefore inhibition of KIAA0563 (Accession NM_014834). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0563. KIAA0565 (Accession XM_039912) is another VGAM1965 host target gene. KIAA0565 BINDING SITE1 and KIAA0565 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0565, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0565 BINDING SITE1 and KIAA0565 BINDING SITE2, designated SEQ ID:33219 and SEQ ID:33221 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68830] Another function of VGAM1965 is therefore inhibition of KIAA0565 (Accession XM_039912). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0565. KIAA0574 (Accession XM_045076) is another VGAM1965 host target gene. KIAA0574 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0574, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0574 BINDING SITE, designated SEQ ID:34350, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68831] Another function of VGAM1965 is therefore inhibition of KIAA0574 (Accession XM_045076). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0574. KIAA0607 (Accession XM_051931) is another VGAM1965 host target gene. KIAA0607 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0607, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0607 BINDING SITE, designated SEQ ID:35927, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68832] Another function of VGAM1965 is therefore inhibition of KIAA0607 (Accession XM_051931). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0607. KIAA0685 (Accession NM_014678) is another VGAM1965 host target gene. KIAA0685 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0685, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0685 BINDING SITE, designated SEQ ID:16150, to the

nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68833] Another function of VGAM1965 is therefore inhibition of KIAA0685 (Accession NM_014678). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0685. KIAA0703 (Accession NM_014861) is another VGAM1965 host target gene. KIAA0703 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0703, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0703 BINDING SITE, designated SEQ ID:16928, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68834] Another function of VGAM1965 is therefore inhibition of KIAA0703 (Accession NM_014861). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0703. KIAA0712 (Accession NM_014715) is another VGAM1965 host target gene. KIAA0712 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by KIAA0712, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0712 BINDING SITE, designated SEQ ID:16268, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68835] Another function of VGAM1965 is therefore inhibition of KIAA0712 (Accession NM_014715). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0712. KIAA0792 (Accession NM_014698) is another VGAM1965 host target gene. KIAA0792 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0792, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0792 BINDING SITE, designated SEQ ID:16216, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68836] Another function of VGAM1965 is therefore inhibition of KIAA0792 (Accession NM_014698). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0792. KIAA0794 (Accession XM_087353) is another VGAM1965 host target gene. KIAA0794 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0794 BINDING SITE, designated SEQ ID:39187, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68837] Another function of VGAM1965 is therefore inhibition of KIAA0794 (Accession XM_087353). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0794. KIAA0798 (Accession NM_014650) is another VGAM1965 host target gene. KIAA0798 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0798, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0798 BINDING SITE, designated SEQ ID:16073, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68838] Another function of VGAM1965 is therefore inhibition of KIAA0798 (Accession NM_014650). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0798. KIAA0825 (Accession XM_027906) is another VGAM1965 host target gene. KIAA0825 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0825, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0825 BINDING SITE, designated SEQ ID:30593, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68839] Another function of VGAM1965 is therefore inhibition of KIAA0825 (Accession XM_027906). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0825. KIAA0847 (Accession XM_085298) is another VGAM1965 host target gene. KIAA0847 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0847, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0847 BINDING SITE, designated SEQ ID:38049, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68840] Another function of VGAM1965 is therefore inhibition of KIAA0847 (Accession XM_085298). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0847. KIAA0854 (Accession NM_014943) is another VGAM1965 host target gene. KIAA0854 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0854, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0854 BINDING SITE, designated SEQ ID:17253, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68841] Another function of VGAM1965 is therefore inhibition of

KIAA0854 (Accession NM_014943). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0854. KIAA0869 (Accession XM_047992) is another VGAM1965 host target gene. KIAA0869 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0869, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0869 BINDING SITE, designated SEQ ID:35094, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68842] Another function of VGAM1965 is therefore inhibition of KIAA0869 (Accession XM_047992). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0869. KIAA0870 (Accession XM_088315) is another VGAM1965 host target gene. KIAA0870 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0870, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0870 BINDING SITE, designated SEQ ID:39610, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68843] Another function of VGAM1965 is therefore inhibition of KIAA0870 (Accession XM_088315). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0870. KIAA0884 (Accession XM_046660) is another VGAM1965 host target gene. KIAA0884 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0884, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0884 BINDING SITE, designated SEQ ID:34778, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68844] Another function of VGAM1965 is therefore inhibition of KIAA0884 (Accession XM_046660). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0884. KIAA0889 (Accession NM_015377) is another

VGAM1965 host target gene. KIAA0889 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0889, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0889 BINDING SITE, designated SEQ ID:17681, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68845] Another function of VGAM1965 is therefore inhibition of KIAA0889 (Accession NM_015377). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0889. KIAA0930 (Accession XM_047214) is another VGAM1965 host target gene. KIAA0930 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0930, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0930 BINDING SITE, designated SEQ ID:34918, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68846] Another function of VGAM1965 is therefore inhibition of KIAA0930 (Accession XM_047214). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0930. KIAA0937 (Accession XM_166213) is another VGAM1965 host target gene. KIAA0937 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0937, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0937 BINDING SITE, designated SEQ ID:44020, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68847] Another function of VGAM1965 is therefore inhibition of KIAA0937 (Accession XM_166213). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0937. KIAA0939 (Accession XM_030524) is another VGAM1965 host target gene. KIAA0939 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0939, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0939 BINDING SITE, designated SEQ ID:31069, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68848] Another function of VGAM1965 is therefore inhibition of KIAA0939 (Accession XM_030524). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0939. KIAA0953 (Accession XM_039733) is another VGAM1965 host target gene. KIAA0953 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0953, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0953 BINDING SITE, designated SEQ ID:33170, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68849] Another function of VGAM1965 is therefore inhibition of KIAA0953 (Accession XM_039733). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0953. KIAA0971 (Accession NM_014929) is another VGAM1965 host target gene. KIAA0971 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0971, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0971 BINDING SITE, designated SEQ ID:17225, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68850] Another function of VGAM1965 is therefore inhibition of KIAA0971 (Accession NM_014929). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0971. KIAA1013 (Accession XM_114303) is another VGAM1965 host target gene. KIAA1013 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1013, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1013 BINDING SITE, designated SEQ ID:42861, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[68851] Another function of VGAM1965 is therefore inhibition of KIAA1013 (Accession XM_114303). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1013. KIAA1023 (Accession NM_017604) is another VGAM1965 host target gene. KIAA1023 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1023, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1023 BINDING SITE, designated SEQ ID:19098, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68852] Another function of VGAM1965 is therefore inhibition of KIAA1023 (Accession NM_017604). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1023. KIAA1029 (Accession NM_007286) is another VGAM1965 host target gene. KIAA1029 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1029, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1029 BINDING SITE, designated SEQ ID:14147, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68853] Another function of VGAM1965 is therefore inhibition of KIAA1029 (Accession NM_007286). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1029. KIAA1037 (Accession NM_015023) is another VGAM1965 host target gene. KIAA1037 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1037, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1037 BINDING SITE, designated SEQ ID:17385, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68854] Another function of VGAM1965 is therefore inhibition of KIAA1037 (Accession NM_015023). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1037. KIAA1040 (Accession XM_051091) is another VGAM1965 host target gene. KIAA1040 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1040 BINDING SITE, designated SEQ ID:35742, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68855] Another function of VGAM1965 is therefore inhibition of KIAA1040 (Accession XM_051091). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1040. KIAA1054 (Accession XM_043493) is another VGAM1965 host target gene. KIAA1054 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1054 BINDING SITE, designated SEQ ID:33951, to the

nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68856] Another function of VGAM1965 is therefore inhibition of KIAA1054 (Accession XM_043493). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1054. KIAA1055 (Accession XM_038509) is another VGAM1965 host target gene. KIAA1055 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1055, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1055 BINDING SITE, designated SEQ ID:32853, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68857] Another function of VGAM1965 is therefore inhibition of KIAA1055 (Accession XM_038509). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1055. KIAA1110 (Accession XM_029973) is another VGAM1965 host target gene. KIAA1110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1110 BINDING SITE, designated SEQ ID:30986, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68858] Another function of VGAM1965 is therefore inhibition of KIAA1110 (Accession XM_029973). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1110. KIAA1161 (Accession XM_088501) is another VGAM1965 host target gene. KIAA1161 BINDING SITE1 and KIAA1161 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1161, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1161 BINDING SITE1 and KIAA1161 BINDING SITE2, designated SEQ ID:39748 and SEQ ID:39755 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68859] Another function of VGAM1965 is therefore inhibition of KIAA1161 (Accession XM_088501). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1161. KIAA1189 (Accession XM_050508) is another VGAM1965 host target gene. KIAA1189 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1189, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1189 BINDING SITE, designated SEQ ID:35652, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68860] Another function of VGAM1965 is therefore inhibition of KIAA1189 (Accession XM_050508). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1189. KIAA1191 (Accession NM_020444) is another VGAM1965 host target gene. KIAA1191 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1191, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1191 BINDING SITE, designated SEQ ID:21684, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68861] Another function of VGAM1965 is therefore inhibition of KIAA1191 (Accession NM_020444). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1191. KIAA1198 (Accession XM_032674) is another VGAM1965 host target gene. KIAA1198 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1198, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE, designated SEQ ID:31712, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68862] Another function of VGAM1965 is therefore inhibition of KIAA1198 (Accession XM_032674). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1198. KIAA1254 (Accession XM_046132) is another VGAM1965 host target gene. KIAA1254 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1254, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1254 BINDING SITE, designated SEQ ID:34698, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68863] Another function of VGAM1965 is therefore inhibition of KIAA1254 (Accession XM_046132). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1254. KIAA1265 (Accession XM_047707) is another VGAM1965 host target gene. KIAA1265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1265 BINDING SITE, designated SEQ ID:35033, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[68864] Another function of VGAM1965 is therefore inhibition of KIAA1265 (Accession XM_047707). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1265. KIAA1266 (Accession XM_038567) is another VGAM1965 host target gene. KIAA1266 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1266 BINDING SITE, designated SEQ ID:32868, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68865] Another function of VGAM1965 is therefore inhibition of KIAA1266 (Accession XM_038567). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1266. KIAA1280 (Accession XM_045766) is another VGAM1965 host target gene. KIAA1280 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1280, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1280 BINDING SITE, designated SEQ ID:34555, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68866] Another function of VGAM1965 is therefore inhibition of KIAA1280 (Accession XM_045766). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1280. KIAA1322 (Accession XM_052626) is another VGAM1965 host target gene. KIAA1322 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1322, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1322 BINDING SITE, designated SEQ ID:36019, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68867] Another function of VGAM1965 is therefore inhibition of KIAA1322 (Accession XM_052626). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1322. KIAA1332 (Accession XM_048774) is another VGAM1965 host target gene. KIAA1332 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1332, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1332 BINDING SITE, designated SEQ ID:35262, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68868] Another function of VGAM1965 is therefore inhibition of KIAA1332 (Accession XM_048774). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1332. KIAA1337 (Accession XM_052561) is another VGAM1965 host target gene. KIAA1337 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1337, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1337 BINDING SITE, designated SEQ ID:35985, to the

nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68869] Another function of VGAM1965 is therefore inhibition of KIAA1337 (Accession XM_052561). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1337. KIAA1363 (Accession XM_045056) is another VGAM1965 host target gene. KIAA1363 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1363, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1363 BINDING SITE, designated SEQ ID:34332, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68870] Another function of VGAM1965 is therefore inhibition of KIAA1363 (Accession XM_045056). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1363. KIAA1389 (Accession XM_045839) is another VGAM1965 host target gene. KIAA1389 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1389, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1389 BINDING SITE, designated SEQ ID:34571, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68871] Another function of VGAM1965 is therefore inhibition of KIAA1389 (Accession XM_045839). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1389. KIAA1404 (Accession XM_030494) is another VGAM1965 host target gene. KIAA1404 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1404, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1404 BINDING SITE, designated SEQ ID:31050, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68872] Another function of VGAM1965 is therefore inhibition of KIAA1404 (Accession XM_030494). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1404. KIAA1463 (Accession XM_051160) is another VGAM1965 host target gene. KIAA1463 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1463, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1463 BINDING SITE, designated SEQ ID:35774, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68873] Another function of VGAM1965 is therefore inhibition of KIAA1463 (Accession XM_051160). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1463. KIAA1484 (Accession XM_046088) is another VGAM1965 host target gene. KIAA1484 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1484, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1484 BINDING SITE, designated SEQ ID:34679, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68874] Another function of VGAM1965 is therefore inhibition of KIAA1484 (Accession XM_046088). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1484. KIAA1559 (Accession XM_054472) is another VGAM1965 host target gene. KIAA1559 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1559, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1559 BINDING SITE, designated SEQ ID:36166, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68875] Another function of VGAM1965 is therefore inhibition of KIAA1559 (Accession XM_054472). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1559. KIAA1579 (Accession NM_018211) is another VGAM1965 host target gene. KIAA1579 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1579, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1579 BINDING SITE, designated SEQ ID:20120, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68876] Another function of VGAM1965 is therefore inhibition of KIAA1579 (Accession NM_018211). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1579. KIAA1622 (Accession NM_058237) is another VGAM1965 host target gene. KIAA1622 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1622, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1622 BINDING SITE, designated SEQ ID:27763, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68877] Another function of VGAM1965 is therefore inhibition of

KIAA1622 (Accession NM_058237). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1622. KIAA1649 (Accession NM_032311) is another VGAM1965 host target gene. KIAA1649 BINDING SITE1 and KIAA1649 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1649, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1649 BINDING SITE1 and KIAA1649 BINDING SITE2, designated SEQ ID:26112 and SEQ ID:26113 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68878] Another function of VGAM1965 is therefore inhibition of KIAA1649 (Accession NM_032311). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1649. KIAA1676 (Accession XM_167612) is another VGAM1965 host target gene. KIAA1676 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1676, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1676 BINDING SITE, designated SEQ ID:44729, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68879] Another function of VGAM1965 is therefore inhibition of KIAA1676 (Accession XM_167612). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1676. KIAA1679 (Accession XM_046570) is another VGAM1965 host target gene. KIAA1679 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1679, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1679 BINDING SITE, designated SEQ ID:34752, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68880] Another function of VGAM1965 is therefore inhibition of KIAA1679 (Accession XM_046570). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1679. KIAA1706 (Accession XM_166595) is another VGAM1965 host target gene. KIAA1706 BINDING SITE1 and KIAA1706 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1706, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1706 BINDING SITE1 and KIAA1706 BINDING SITE2, designated SEQ ID:44578 and SEQ ID:44579 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68881] Another function of VGAM1965 is therefore inhibition of KIAA1706 (Accession XM_166595). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1706. KIAA1727 (Accession XM_034262) is another VGAM1965 host target gene. KIAA1727 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1727, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1727 BINDING SITE, designated SEQ ID:32038, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68882] Another function of VGAM1965 is therefore inhibition of KIAA1727 (Accession XM_034262). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1727. KIAA1729 (Accession XM_114418) is another VGAM1965 host target gene. KIAA1729 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1729, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1729 BINDING SITE, designated SEQ ID:42949, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68883] Another function of VGAM1965 is therefore inhibition of KIAA1729 (Accession XM_114418). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1729. KIAA1754 (Accession XM_032587) is another

VGAM1965 host target gene. KIAA1754 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1754, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1754 BINDING SITE, designated SEQ ID:31681, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68884] Another function of VGAM1965 is therefore inhibition of KIAA1754 (Accession XM_032587). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1754. KIAA1765 (Accession XM_047355) is another VGAM1965 host target gene. KIAA1765 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1765, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1765 BINDING SITE, designated SEQ ID:34957, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68885] Another function of VGAM1965 is therefore inhibition of KIAA1765 (Accession XM_047355). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1765. KIAA1789 (Accession XM_040486) is another VGAM1965 host target gene. KIAA1789 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1789, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1789 BINDING SITE, designated SEQ ID:33312, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68886] Another function of VGAM1965 is therefore inhibition of KIAA1789 (Accession XM_040486). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1789. KIAA1804 (Accession XM_045864) is another VGAM1965 host target gene. KIAA1804 BINDING SITE1 and KIAA1804 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1804, corresponding to HOST TARGET binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1804 BINDING SITE1 and KIAA1804 BINDING SITE2, designated SEQ ID:34588 and SEQ ID:34591 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68887] Another function of VGAM1965 is therefore inhibition of KIAA1804 (Accession XM_045864). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1804. KIAA1813 (Accession XM_046743) is another VGAM1965 host target gene. KIAA1813 BINDING SITE1 and KIAA1813 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1813, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1813 BINDING SITE1 and KIAA1813 BINDING SITE2, designated SEQ ID:34809 and SEQ ID:31036 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68888] Another function of VGAM1965 is therefore inhibition of KIAA1813 (Accession XM_046743). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1813. KIAA1872 (Accession XM_031917) is another VGAM1965 host target gene. KIAA1872 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1872, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1872 BINDING SITE, designated SEQ ID:31522, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68889] Another function of VGAM1965 is therefore inhibition of KIAA1872 (Accession XM_031917). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1872. KIAA1887 (Accession XM_084801) is another VGAM1965 host target gene. KIAA1887 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1887, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1887 BINDING SITE, designated SEQ ID:37715, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68890] Another function of VGAM1965 is therefore inhibition of KIAA1887 (Accession XM_084801). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1887. KIAA1908 (Accession XM_055834) is another VGAM1965 host target gene. KIAA1908 BINDING SITE1 and KIAA1908 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1908, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1908 BINDING SITE1 and KIAA1908 BINDING SITE2, designated SEQ ID:36339 and SEQ ID:36326 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68891] Another function of VGAM1965 is therefore inhibition of KIAA1908 (Accession XM_055834). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1908. KIAA1987 (Accession XM_113870) is another VGAM1965 host target gene. KIAA1987 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1987, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1987 BINDING SITE, designated SEQ ID:42502, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68892] Another function of VGAM1965 is therefore inhibition of KIAA1987 (Accession XM_113870). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1987. Kelch-like 6 (Drosophila) (KLHL6, Accession NM_130446) is another VGAM1965 host target gene. KLHL6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLHL6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of KLHL6 BINDING SITE, designated SEQ ID:28212, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68893] Another function of VGAM1965 is therefore inhibition of Kelch-like 6 (Drosophila) (KLHL6, Accession NM_130446). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLHL6. Kelch-like 8 (Drosophila) (KLHL8, Accession XM_031735) is another VGAM1965 host target gene. KLHL8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLHL8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLHL8 BINDING SITE, designated SEQ ID:31478, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68894] Another function of VGAM1965 is therefore inhibition of Kelch-like 8 (Drosophila) (KLHL8, Accession XM_031735). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with KLHL8. Keratin, Hair, Basic, 2 (KRTHB2, Accession NM_033033) is another VGAM1965 host target gene. KRTHB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KRTHB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KRTHB2 BINDING SITE, designated SEQ ID:26924, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68895] Another function of VGAM1965 is therefore inhibition of Keratin, Hair, Basic, 2 (KRTHB2, Accession NM_033033). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KRTHB2. Kv6.3 (Accession NM_133490) is another VGAM1965 host target gene. Kv6.3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Kv6.3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Kv6.3 BINDING SITE, designated SEQ ID:28567,

to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68896] Another function of VGAM1965 is therefore inhibition of Kv6.3 (Accession NM_133490). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Kv6.3. LIM and SH3 Protein 1 (LASP1, Accession NM_006148) is another VGAM1965 host target gene. LASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LASP1 BINDING SITE, designated SEQ ID:12804, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68897] Another function of VGAM1965 is therefore inhibition of LIM and SH3 Protein 1 (LASP1, Accession NM_006148). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LASP1. LATS, Large Tumor Suppressor, Homolog 1 (Drosophila) (LATS1, Accession XM_015547) is another VGAM1965 host target gene.

LATS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LATS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LATS1 BINDING SITE, designated SEQ ID:30236, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68898] Another function of VGAM1965 is therefore inhibition of LATS, Large Tumor Suppressor, Homolog 1 (Drosophila) (LATS1, Accession XM_015547). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LATS1. LIN-7-C (Accession NM_018362) is another VGAM1965 host target gene. LIN-7-C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIN-7-C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIN-7-C BINDING SITE, designated SEQ ID:20369, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4676.

[68899] Another function of VGAM1965 is therefore inhibition of LIN-7-C (Accession NM_018362). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIN-7-C. Leucine-rich Repeat Protein, Neuronal 3 (LRRN3, Accession XM_045261) is another VGAM1965 host target gene. LRRN3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LRRN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRRN3 BINDING SITE, designated SEQ ID:34403, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68900] Another function of VGAM1965 is therefore inhibition of Leucine-rich Repeat Protein, Neuronal 3 (LRRN3, Accession XM_045261). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRRN3. MAD, Mothers Against Decapentaplegic Homolog (Drosophila) Interacting Protein, Receptor Activation Anchor (MADHIP, Accession

NM_007324) is another VGAM1965 host target gene. MADHIP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MADHIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MADHIP BINDING SITE, designated SEQ ID:14244, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68901] Another function of VGAM1965 is therefore inhibition of MAD, Mothers Against Decapentaplegic Homolog (Drosophila) Interacting Protein, Receptor Activation Anchor (MADHIP, Accession NM_007324). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADHIP. MAN1 (Accession NM_014319) is another VGAM1965 host target gene. MAN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAN1 BINDING SITE,

designated SEQ ID:15619, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68902] Another function of VGAM1965 is therefore inhibition of MAN1 (Accession NM_014319). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAN1. Mitogen-activated Protein Kinase Kinase Kinase 3 (MAP3K3, Accession NM_002401) is another VGAM1965 host target gene. MAP3K3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K3 BINDING SITE, designated SEQ ID:8223, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68903] Another function of VGAM1965 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 3 (MAP3K3, Accession NM_002401). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MAP3K3. MAWBP (Accession NM_022129) is another VGAM1965 host target gene. MAWBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAWBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAWBP BINDING SITE, designated SEQ ID:22682, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68904] Another function of VGAM1965 is therefore inhibition of MAWBP (Accession NM_022129). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAWBP. Methyl-CpG Binding Domain Protein 2 (MBD2, Accession NM_015832) is another VGAM1965 host target gene. MBD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MBD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MBD2 BINDING SITE, designated SEQ ID:17947, to the nucleotide sequence of VGAM1965 RNA, herein

designated VGAM RNA, also designated SEQ ID:4676.

[68905] Another function of VGAM1965 is therefore inhibition of Methyl-CpG Binding Domain Protein 2 (MBD2, Accession NM_015832). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBD2. Mesoderm Development Candidate 2 (MESDC2, Accession XM_051854) is another VGAM1965 host target gene. MESDC2 BINDING SITE1 and MESDC2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MESDC2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MESDC2 BINDING SITE1 and MESDC2 BINDING SITE2, designated SEQ ID:35896 and SEQ ID:35895 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68906] Another function of VGAM1965 is therefore inhibition of Mesoderm Development Candidate 2 (MESDC2, Accession XM_051854). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MESDC2. MGC10814

(Accession NM_032671) is another VGAM1965 host target gene. MGC10814 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC10814, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10814 BINDING SITE, designated SEQ ID:26396, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68907] Another function of VGAM1965 is therefore inhibition of MGC10814 (Accession NM_032671). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10814. MGC10960 (Accession NM_032653) is another VGAM1965 host target gene. MGC10960 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC10960, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10960 BINDING SITE, designated SEQ ID:26383, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[68908] Another function of VGAM1965 is therefore inhibition of MGC10960 (Accession NM_032653). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10960. MGC11034 (Accession NM_031453) is another VGAM1965 host target gene. MGC11034 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC11034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11034 BINDING SITE, designated SEQ ID:25471, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68909] Another function of VGAM1965 is therefore inhibition of MGC11034 (Accession NM_031453). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11034. MGC11115 (Accession NM_032310) is another VGAM1965 host target gene. MGC11115 BINDING SITE1 and MGC11115 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA en-

coded by MGC11115, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11115 BINDING SITE1 and MGC11115 BINDING SITE2, designated SEQ ID:26097 and SEQ ID:26098 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68910] Another function of VGAM1965 is therefore inhibition of MGC11115 (Accession NM_032310). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11115. MGC13114 (Accession NM_032366) is another VGAM1965 host target gene. MGC13114 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC13114, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13114 BINDING SITE, designated SEQ ID:26155, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68911] Another function of VGAM1965 is therefore inhibition of

MGC13114 (Accession NM_032366). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13114. MGC14407 (Accession NM_032908) is another VGAM1965 host target gene. MGC14407 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC14407, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC14407 BINDING SITE, designated SEQ ID:26730, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68912] Another function of VGAM1965 is therefore inhibition of MGC14407 (Accession NM_032908). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14407. MGC15873 (Accession NM_032920) is another VGAM1965 host target gene. MGC15873 BINDING SITE1 and MGC15873 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MGC15873, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15873 BINDING SITE1 and MGC15873 BINDING SITE2, designated SEQ ID:26744 and SEQ ID:26745 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68913] Another function of VGAM1965 is therefore inhibition of MGC15873 (Accession NM_032920). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15873. MGC2603 (Accession NM_024037) is another VGAM1965 host target gene. MGC2603 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2603, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2603 BINDING SITE, designated SEQ ID:23471, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68914] Another function of VGAM1965 is therefore inhibition of MGC2603 (Accession NM_024037). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC2603. MGC2668 (Accession XM_026968) is another VGAM1965 host target gene. MGC2668 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2668, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2668 BINDING SITE, designated SEQ ID:30380, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68915] Another function of VGAM1965 is therefore inhibition of MGC2668 (Accession XM_026968). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2668. MGC2848 (Accession NM_032917) is another VGAM1965 host target gene. MGC2848 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2848, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2848 BINDING SITE, designated SEQ ID:26735, to the nucleotide

sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68916] Another function of VGAM1965 is therefore inhibition of MGC2848 (Accession NM_032917). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2848. MGC5576 (Accession NM_024056) is another VGAM1965 host target gene. MGC5576 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC5576, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5576 BINDING SITE, designated SEQ ID:23493, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68917] Another function of VGAM1965 is therefore inhibition of MGC5576 (Accession NM_024056). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5576. MIDORI (Accession XM_057651) is another VGAM1965 host target gene. MIDORI BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by MIDORI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MIDORI BINDING SITE, designated SEQ ID:36526, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68918] Another function of VGAM1965 is therefore inhibition of MIDORI (Accession XM_057651). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIDORI. MKP-7 (Accession XM_039106) is another VGAM1965 host target gene. MKP-7 BINDING SITE1 and MKP-7 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MKP-7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MKP-7 BINDING SITE1 and MKP-7 BINDING SITE2, designated SEQ ID:33010 and SEQ ID:33011 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68919] Another function of VGAM1965 is therefore inhibition of MKP-7 (Accession XM_039106). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKP-7. MRPL56 (Accession NM_032857) is another VGAM1965 host target gene. MRPL56 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPL56, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPL56 BINDING SITE, designated SEQ ID:26660, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68920] Another function of VGAM1965 is therefore inhibition of MRPL56 (Accession NM_032857). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL56. MTCH1 (Accession NM_014341) is another VGAM1965 host target gene. MTCH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTCH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTCH1 BINDING SITE, designated SEQ ID:15662, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68921] Another function of VGAM1965 is therefore inhibition of MTCH1 (Accession NM_014341). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTCH1. MY014 (Accession NM_030918) is another VGAM1965 host target gene. MY014 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MY014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MY014 BINDING SITE, designated SEQ ID:25192, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68922] Another function of VGAM1965 is therefore inhibition of MY014 (Accession NM_030918). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MY014.

My015 (Accession XM_039512) is another VGAM1965 host target gene. My015 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by My015, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of My015 BINDING SITE, designated SEQ ID:33109, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68923] Another function of VGAM1965 is therefore inhibition of My015 (Accession XM_039512). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with My015. N4BP2 (Accession NM_018177) is another VGAM1965 host target gene. N4BP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by N4BP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of N4BP2 BINDING SITE, designated SEQ ID:20005, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ

ID:4676.

[68924] Another function of VGAM1965 is therefore inhibition of N4BP2 (Accession NM_018177). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with N4BP2. N4BP3 (Accession XM_038920) is another VGAM1965 host target gene. N4BP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by N4BP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of N4BP3 BINDING SITE, designated SEQ ID:32940, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68925] Another function of VGAM1965 is therefore inhibition of N4BP3 (Accession XM_038920). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with N4BP3. NIBAN (Accession NM_022083) is another VGAM1965 host target gene. NIBAN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NIBAN, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NIBAN BINDING SITE, designated SEQ ID:22631, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68926] Another function of VGAM1965 is therefore inhibition of NIBAN (Accession NM_022083). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NIBAN. N-myristoyltransferase 1 (NMT1, Accession NM_021079) is another VGAM1965 host target gene. NMT1 BINDING SITE1 and NMT1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NMT1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NMT1 BINDING SITE1 and NMT1 BINDING SITE2, designated SEQ ID:22050 and SEQ ID:22051 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68927] Another function of VGAM1965 is therefore inhibition of

N-myristoyltransferase 1 (NMT1, Accession NM_021079). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NMT1. NX-17 (Accession NM_020665) is another VGAM1965 host target gene. NX-17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NX-17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NX-17 BINDING SITE, designated SEQ ID:21835, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68928] Another function of VGAM1965 is therefore inhibition of NX-17 (Accession NM_020665). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NX-17. NXP-2 (Accession XM_048706) is another VGAM1965 host target gene. NXP-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NXP-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of NXP-2 BINDING SITE, designated SEQ ID:35230, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68929] Another function of VGAM1965 is therefore inhibition of NXP-2 (Accession XM_048706). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXP-2. Neurexophilin 3 (NXPH3, Accession XM_037847) is another VGAM1965 host target gene. NXPH3 BINDING SITE1 and NXPH3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NXPH3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NXPH3 BINDING SITE1 and NXPH3 BINDING SITE2, designated SEQ ID:32721 and SEQ ID:32723 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68930] Another function of VGAM1965 is therefore inhibition of Neurexophilin 3 (NXPH3, Accession XM_037847). Accord-

ingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXPH3. Oxysterol Binding Protein-like 10 (OSBPL10, Accession NM_017784) is another VGAM1965 host target gene. OSBPL10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL10 BINDING SITE, designated SEQ ID:19417, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68931] Another function of VGAM1965 is therefore inhibition of Oxysterol Binding Protein-like 10 (OSBPL10, Accession NM_017784). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL10. P11 (Accession NM_006025) is another VGAM1965 host target gene. P11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of P11 BINDING SITE, designated SEQ ID:12643, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68932] Another function of VGAM1965 is therefore inhibition of P11 (Accession NM_006025). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P11. Purinergic Receptor P2X, Ligand-gated Ion Channel, 1 (P2RX1, Accession XM_040635) is another VGAM1965 host target gene. P2RX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P2RX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P2RX1 BINDING SITE, designated SEQ ID:33359, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68933] Another function of VGAM1965 is therefore inhibition of Purinergic Receptor P2X, Ligand-gated Ion Channel, 1 (P2RX1, Accession XM_040635). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with P2RX1. P5-1 (Accession NM_006674) is another VGAM1965 host target gene. P5-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P5-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P5-1 BINDING SITE, designated SEQ ID:13500, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68934] Another function of VGAM1965 is therefore inhibition of P5-1 (Accession NM_006674). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P5-1. Peptidyl Arginine Deiminase, Type III (PADI3, Accession NM_016233) is another VGAM1965 host target gene. PADI3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PADI3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PADI3 BINDING SITE, designated SEQ

ID:18347, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68935] Another function of VGAM1965 is therefore inhibition of Peptidyl Arginine Deiminase, Type III (PADI3, Accession NM_016233). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PADI3. PANK (Accession NM_138316) is another VGAM1965 host target gene. PANK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PANK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PANK BINDING SITE, designated SEQ ID:28715, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68936] Another function of VGAM1965 is therefore inhibition of PANK (Accession NM_138316). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PANK. Phosphodiesterase 2A, CGMP-stimulated (PDE2A, Accession NM_002599) is another VGAM1965 host target gene.

PDE2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE2A BINDING SITE, designated SEQ ID:8462, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68937] Another function of VGAM1965 is therefore inhibition of Phosphodiesterase 2A, CGMP-stimulated (PDE2A, Accession NM_002599). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE2A. Platelet Derived Growth Factor C (PDGFC, Accession NM_016205) is another VGAM1965 host target gene. PDGFC BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PDGFC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDGFC BINDING SITE, designated SEQ ID:18303, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68938] Another function of VGAM1965 is therefore inhibition of Platelet Derived Growth Factor C (PDGFC, Accession NM_016205). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFC. Pyruvate Dehydrogenase Kinase, Isoenzyme 2 (PDK2, Accession NM_002611) is another VGAM1965 host target gene. PDK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDK2 BINDING SITE, designated SEQ ID:8474, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68939] Another function of VGAM1965 is therefore inhibition of Pyruvate Dehydrogenase Kinase, Isoenzyme 2 (PDK2, Accession NM_002611). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDK2. PDZ Domain Containing 2 (PDZD2, Accession XM_087705) is another VGAM1965 host target gene. PDZD2 BINDING SITE1 and PDZD2 BINDING SITE2 are HOST TARGET binding sites

found in untranslated regions of mRNA encoded by PDZD2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDZD2 BINDING SITE1 and PDZD2 BINDING SITE2, designated SEQ ID:39398 and SEQ ID:39394 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68940] Another function of VGAM1965 is therefore inhibition of PDZ Domain Containing 2 (PDZD2, Accession XM_087705). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDZD2. PGR1 (Accession NM_033296) is another VGAM1965 host target gene. PGR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PGR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PGR1 BINDING SITE, designated SEQ ID:27124, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68941] Another function of VGAM1965 is therefore inhibition of PGR1 (Accession NM_033296). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PGR1. Phytanoyl-CoA Hydroxylase Interacting Protein (PHYHIP, Accession NM_014759) is another VGAM1965 host target gene. PHYHIP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PHYHIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PHYHIP BINDING SITE, designated SEQ ID:16514, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68942] Another function of VGAM1965 is therefore inhibition of Phytanoyl-CoA Hydroxylase Interacting Protein (PHYHIP, Accession NM_014759). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHYHIP. Phosphatidylinositol-4-phosphate 5-kinase, Type II, Beta (PIP5K2B, Accession NM_003559) is another VGAM1965 host target gene. PIP5K2B BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by PIP5K2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIP5K2B BINDING SITE, designated SEQ ID:9616, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68943] Another function of VGAM1965 is therefore inhibition of Phosphatidylinositol-4-phosphate 5-kinase, Type II, Beta (PIP5K2B, Accession NM_003559). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIP5K2B. POF1B (Accession NM_024921) is another VGAM1965 host target gene. POF1B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POF1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POF1B BINDING SITE, designated SEQ ID:24455, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68944] Another function of VGAM1965 is therefore inhibition of POF1B (Accession NM_024921). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POF1B. Polymerase (DNA directed), Mu (POLM, Accession XM_165867) is another VGAM1965 host target gene. POLM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POLM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POLM BINDING SITE, designated SEQ ID:43785, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68945] Another function of VGAM1965 is therefore inhibition of Polymerase (DNA directed), Mu (POLM, Accession XM_165867). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLM. PP1057 (Accession NM_031285) is another VGAM1965 host target gene. PP1057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PP1057, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP1057 BINDING SITE, designated SEQ ID:25312, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68946] Another function of VGAM1965 is therefore inhibition of PP1057 (Accession NM_031285). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1057. Protein Tyrosine Phosphatase, Receptor Type, F Polypeptide (PTPRF), Interacting Protein (liprin), Alpha 4 (PPFIA4, Accession XM_046751) is another VGAM1965 host target gene. PPFIA4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPFIA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPFIA4 BINDING SITE, designated SEQ ID:34820, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68947] Another function of VGAM1965 is therefore inhibition of

Protein Tyrosine Phosphatase, Receptor Type, F Polypeptide (PTPRF), Interacting Protein (liprin), Alpha 4 (PPFIA4, Accession XM_046751). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPFIA4. PPI5PIV (Accession NM_019892) is another VGAM1965 host target gene. PPI5PIV BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPI5PIV, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPI5PIV BINDING SITE, designated SEQ ID:21279, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68948] Another function of VGAM1965 is therefore inhibition of PPI5PIV (Accession NM_019892). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPI5PIV. Protein Phosphatase 4, Regulatory Subunit 1-like (PPP4R1L, Accession XM_086650) is another VGAM1965 host target gene. PPP4R1L BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA

encoded by PPP4R1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP4R1L BINDING SITE, designated SEQ ID:38818, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68949] Another function of VGAM1965 is therefore inhibition of Protein Phosphatase 4, Regulatory Subunit 1-like (PPP4R1L, Accession XM_086650). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP4R1L. PRO0233 (Accession NM_014121) is another VGAM1965 host target gene. PRO0233 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0233, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0233 BINDING SITE, designated SEQ ID:15375, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68950] Another function of VGAM1965 is therefore inhibition of

PRO0233 (Accession NM_014121). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0233. PRO0245 (Accession NM_014122) is another VGAM1965 host target gene. PRO0245 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0245, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0245 BINDING SITE, designated SEQ ID:15378, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68951] Another function of VGAM1965 is therefore inhibition of PRO0245 (Accession NM_014122). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0245. PRO0246 (Accession NM_014123) is another VGAM1965 host target gene. PRO0246 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0246, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PRO0246 BINDING SITE, designated SEQ ID:15380, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68952] Another function of VGAM1965 is therefore inhibition of PRO0246 (Accession NM_014123). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0246. PRO0456 (Accession NM_014127) is another VGAM1965 host target gene. PRO0456 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO0456, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0456 BINDING SITE, designated SEQ ID:15395, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68953] Another function of VGAM1965 is therefore inhibition of PRO0456 (Accession NM_014127). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0456. PRO0899 (Accession NM_018565) is another

VGAM1965 host target gene. PRO0899 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0899, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0899 BINDING SITE, designated SEQ ID:20649, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68954] Another function of VGAM1965 is therefore inhibition of PRO0899 (Accession NM_018565). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0899. PRO1048 (Accession NM_018497) is another VGAM1965 host target gene. PRO1048 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO1048, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1048 BINDING SITE, designated SEQ ID:20558, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68955] Another function of VGAM1965 is therefore inhibition of PRO1048 (Accession NM_018497). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1048. PRO1866 (Accession NM_018510) is another VGAM1965 host target gene. PRO1866 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1866, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1866 BINDING SITE, designated SEQ ID:20581, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68956] Another function of VGAM1965 is therefore inhibition of PRO1866 (Accession NM_018510). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1866. PRO2198 (Accession NM_018621) is another VGAM1965 host target gene. PRO2198 BINDING SITE1 and PRO2198 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PRO2198, corresponding to HOST TARGET binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2198 BINDING SITE1 and PRO2198 BINDING SITE2, designated SEQ ID:20696 and SEQ ID:20697 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68957] Another function of VGAM1965 is therefore inhibition of PRO2198 (Accession NM_018621). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2198. PRO2859 (Accession NM_018543) is another VGAM1965 host target gene. PRO2859 BINDING SITE1 and PRO2859 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PRO2859, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2859 BINDING SITE1 and PRO2859 BINDING SITE2, designated SEQ ID:20614 and SEQ ID:20632 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68958] Another function of VGAM1965 is therefore inhibition of PRO2859 (Accession NM_018543). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2859. Proline-serine-threonine Phosphatase Interacting Protein 2 (PSTPIP2, Accession NM_024430) is another VGAM1965 host target gene. PSTPIP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSTPIP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSTPIP2 BINDING SITE, designated SEQ ID:23682, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68959] Another function of VGAM1965 is therefore inhibition of Proline-serine-threonine Phosphatase Interacting Protein 2 (PSTPIP2, Accession NM_024430). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSTPIP2. Quiescin Q6 (QSCN6, Accession NM_002826) is another VGAM1965 host target gene. QSCN6 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by QSCN6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of QSCN6 BINDING SITE, designated SEQ ID:8700, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68960] Another function of VGAM1965 is therefore inhibition of Quiescin Q6 (QSCN6, Accession NM_002826). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with QSCN6. RA-GEF-2 (Accession NM_016340) is another VGAM1965 host target gene. RA-GEF-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RA-GEF-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RA-GEF-2 BINDING SITE, designated SEQ ID:18468, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68961] Another function of VGAM1965 is therefore inhibition of RA-GEF-2 (Accession NM_016340). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RA-GEF-2. RAB17, Member RAS Oncogene Family (RAB17, Accession NM_022449) is another VGAM1965 host target gene. RAB17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB17 BINDING SITE, designated SEQ ID:22788, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68962] Another function of VGAM1965 is therefore inhibition of RAB17, Member RAS Oncogene Family (RAB17, Accession NM_022449). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB17. RAB33B, Member RAS Oncogene Family (RAB33B, Accession NM_031296) is another VGAM1965 host target gene. RAB33B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB33B, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB33B BINDING SITE, designated SEQ ID:25333, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68963] Another function of VGAM1965 is therefore inhibition of RAB33B, Member RAS Oncogene Family (RAB33B, Accession NM_031296). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB33B. RAB35, Member RAS Oncogene Family (RAB35, Accession NM_006861) is another VGAM1965 host target gene. RAB35 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB35, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB35 BINDING SITE, designated SEQ ID:13734, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68964] Another function of VGAM1965 is therefore inhibition of RAB35, Member RAS Oncogene Family (RAB35, Accession NM_006861). Accordingly, utilities of VGAM1965 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB35. Rabip4R (Accession NM_017987) is another VGAM1965 host target gene. Rabip4R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Rabip4R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rabip4R BINDING SITE, designated SEQ ID:19718, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68965] Another function of VGAM1965 is therefore inhibition of Rabip4R (Accession NM_017987). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Rabip4R. RAN, Member RAS Oncogene Family (RAN, Accession NM_006325) is another VGAM1965 host target gene. RAN BINDING SITE1 and RAN BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RAN, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of RAN BINDING SITE1 and RAN BINDING SITE2, designated SEQ ID:13019 and SEQ ID:13018 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68966] Another function of VGAM1965 is therefore inhibition of RAN, Member RAS Oncogene Family (RAN, Accession NM_006325). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAN. RAN Binding Protein 6 (RANBP6, Accession XM_029423) is another VGAM1965 host target gene. RANBP6 BINDING SITE1 and RANBP6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RANBP6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RANBP6 BINDING SITE1 and RANBP6 BINDING SITE2, designated SEQ ID:30886 and SEQ ID:16396 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68967] Another function of VGAM1965 is therefore inhibition of RAN Binding Protein 6 (RANBP6, Accession XM_029423).

Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RANBP6. Rpo1-2 (Accession NM_032212) is another VGAM1965 host target gene. Rpo1-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Rpo1-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rpo1-2 BINDING SITE, designated SEQ ID:25937, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68968] Another function of VGAM1965 is therefore inhibition of Rpo1-2 (Accession NM_032212). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Rpo1-2. RYK Receptor-like Tyrosine Kinase (RYK, Accession XM_093692) is another VGAM1965 host target gene. RYK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RYK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of RYK BINDING SITE, designated SEQ ID:40206, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68969] Another function of VGAM1965 is therefore inhibition of RYK Receptor-like Tyrosine Kinase (RYK, Accession XM_093692). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RYK. SBB103 (Accession NM_005785) is another VGAM1965 host target gene. SBB103 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SBB103, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SBB103 BINDING SITE, designated SEQ ID:12367, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68970] Another function of VGAM1965 is therefore inhibition of SBB103 (Accession NM_005785). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

SBB103. SC65 (Accession NM_006455) is another VGAM1965 host target gene. SC65 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SC65, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SC65 BINDING SITE, designated SEQ ID:13175, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68971] Another function of VGAM1965 is therefore inhibition of SC65 (Accession NM_006455). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SC65. SCAMP5 (Accession NM_138967) is another VGAM1965 host target gene. SCAMP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCAMP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAMP5 BINDING SITE, designated SEQ ID:29078, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4676.

[68972] Another function of VGAM1965 is therefore inhibition of SCAMP5 (Accession NM_138967). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP5. SCYA5 (Accession NM_002985) is another VGAM1965 host target gene. SCYA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCYA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCYA5 BINDING SITE, designated SEQ ID:8883, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68973] Another function of VGAM1965 is therefore inhibition of SCYA5 (Accession NM_002985). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCYA5. Serologically Defined Colon Cancer Antigen 3 (SDCCAG3, Accession NM_006643) is another VGAM1965 host target gene. SDCCAG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by SDCCAG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDCCAG3 BINDING SITE, designated SEQ ID:13437, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68974] Another function of VGAM1965 is therefore inhibition of Serologically Defined Colon Cancer Antigen 3 (SDCCAG3, Accession NM_006643). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDCCAG3. SE57-1 (Accession NM_025214) is another VGAM1965 host target gene. SE57-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SE57-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SE57-1 BINDING SITE, designated SEQ ID:24893, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68975] Another function of VGAM1965 is therefore inhibition of

SE57-1 (Accession NM_025214). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SE57-1. SEC24 Related Gene Family, Member A (S. cerevisiae) (SEC24A, Accession XM_094581) is another VGAM1965 host target gene. SEC24A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC24A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC24A BINDING SITE, designated SEQ ID:40231, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68976] Another function of VGAM1965 is therefore inhibition of SEC24 Related Gene Family, Member A (S. cerevisiae) (SEC24A, Accession XM_094581). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC24A. Sema Domain, Immunoglobulin Domain (Ig), Short Basic Domain, Secreted, (semaphorin) 3E (SEMA3E, Accession NM_012431) is another VGAM1965 host target gene. SEMA3E BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by SEMA3E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEMA3E BINDING SITE, designated SEQ ID:14810, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68977] Another function of VGAM1965 is therefore inhibition of Sema Domain, Immunoglobulin Domain (Ig), Short Basic Domain, Secreted, (semaphorin) 3E (SEMA3E, Accession NM_012431). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA3E. Sema Domain, Immunoglobulin Domain (Ig), Transmembrane Domain (TM) and Short Cytoplasmic Domain, (semaphorin) 4B (SEMA4B, Accession XM_044533) is another VGAM1965 host target gene. SEMA4B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEMA4B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEMA4B BINDING SITE, designated SEQ

ID:34224, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68978] Another function of VGAM1965 is therefore inhibition of Sema Domain, Immunoglobulin Domain (Ig), Transmembrane Domain (TM) and Short Cytoplasmic Domain, (semaphorin) 4B (SEMA4B, Accession XM_044533). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA4B. Sema Domain, Immunoglobulin Domain (Ig), Transmembrane Domain (TM) and Short Cytoplasmic Domain, (semaphorin) 4G (SEMA4G, Accession XM_170638) is another VGAM1965 host target gene. SEMA4G BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SEMA4G, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEMA4G BINDING SITE, designated SEQ ID:45415, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68979] Another function of VGAM1965 is therefore inhibition of

Sema Domain, Immunoglobulin Domain (Ig), Transmembrane Domain (TM) and Short Cytoplasmic Domain, (semaphorin) 4G (SEMA4G, Accession XM_170638). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA4G. Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 7 (SERPINB7, Accession NM_003784) is another VGAM1965 host target gene. SERPINB7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SERPINB7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERPINB7 BINDING SITE, designated SEQ ID:9874, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68980] Another function of VGAM1965 is therefore inhibition of Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 7 (SERPINB7, Accession NM_003784). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINB7. Sideroflexin 5

(SFXN5, Accession NM_144579) is another VGAM1965 host target gene. SFXN5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFXN5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFXN5 BINDING SITE, designated SEQ ID:29385, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68981] Another function of VGAM1965 is therefore inhibition of Sideroflexin 5 (SFXN5, Accession NM_144579). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN5. Sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9, Accession NM_003896) is another VGAM1965 host target gene. SIAT9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SIAT9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIAT9 BINDING SITE,

designated SEQ ID:9978, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68982] Another function of VGAM1965 is therefore inhibition of Sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9, Accession NM_003896). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIAT9. SIMRP7 (Accession XM_166462) is another VGAM1965 host target gene. SIMRP7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIMRP7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIMRP7 BINDING SITE, designated SEQ ID:44374, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68983] Another function of VGAM1965 is therefore inhibition of SIMRP7 (Accession XM_166462). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIMRP7.

Signal-regulatory Protein Beta 1 (SIRPB1, Accession NM_006065) is another VGAM1965 host target gene. SIRPB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIRPB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIRPB1 BINDING SITE, designated SEQ ID:12709, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68984] Another function of VGAM1965 is therefore inhibition of Signal-regulatory Protein Beta 1 (SIRPB1, Accession NM_006065). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIRPB1. Solute Carrier Family 7, (cationic amino acid transporter, y+ system) Member 11 (SLC7A11, Accession NM_014331) is another VGAM1965 host target gene. SLC7A11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC7A11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of SLC7A11 BINDING SITE, designated SEQ ID:15644, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68985] Another function of VGAM1965 is therefore inhibition of Solute Carrier Family 7, (cationic amino acid transporter, y+ system) Member 11 (SLC7A11, Accession NM_014331). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC7A11. SNF1 Sucrose Nonfermenting Like Kinase (yeast) (SLK, Accession NM_014720) is another VGAM1965 host target gene. SLK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLK BINDING SITE, designated SEQ ID:16280, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68986] Another function of VGAM1965 is therefore inhibition of SNF1 Sucrose Nonfermenting Like Kinase (yeast) (SLK, Accession NM_014720). Accordingly, utilities of VGAM1965

include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLK. Small Nuclear RNA Activating Complex, Polypeptide 1, 43kDa (SNAPC1, Accession NM_003082) is another VGAM1965 host target gene. SNAPC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNAPC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNAPC1 BINDING SITE, designated SEQ ID:9057, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68987] Another function of VGAM1965 is therefore inhibition of Small Nuclear RNA Activating Complex, Polypeptide 1, 43kDa (SNAPC1, Accession NM_003082). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAPC1. SP192 (Accession NM_021639) is another VGAM1965 host target gene. SP192 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SP192, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SP192 BINDING SITE, designated SEQ ID:22297, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68988] Another function of VGAM1965 is therefore inhibition of SP192 (Accession NM_021639). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SP192. SPEC1 (Accession NM_020239) is another VGAM1965 host target gene. SPEC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPEC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPEC1 BINDING SITE, designated SEQ ID:21515, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68989] Another function of VGAM1965 is therefore inhibition of SPEC1 (Accession NM_020239). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPEC1.

Serine Protease Inhibitor-like, with Kunitz and WAP Domains 1 (eppin) (SPINLW1, Accession NM_020398) is another VGAM1965 host target gene. SPINLW1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPINLW1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPINLW1 BINDING SITE, designated SEQ ID:21667, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68990] Another function of VGAM1965 is therefore inhibition of Serine Protease Inhibitor-like, with Kunitz and WAP Domains 1 (eppin) (SPINLW1, Accession NM_020398). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPINLW1. SSH2 (Accession XM_030846) is another VGAM1965 host target gene. SSH2 BINDING SITE1 and SSH2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SSH2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of SSH2 BINDING SITE1 and SSH2 BINDING SITE2, designated SEQ ID:31188 and SEQ ID:31186 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68991] Another function of VGAM1965 is therefore inhibition of SSH2 (Accession XM_030846). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSH2. Stathmin-like 3 (STMN3, Accession NM_015894) is another VGAM1965 host target gene. STMN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STMN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STMN3 BINDING SITE, designated SEQ ID:18041, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68992] Another function of VGAM1965 is therefore inhibition of Stathmin-like 3 (STMN3, Accession NM_015894). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STMN3. Stomatin (EPB72)-like 1 (STOML1, Ac-

cession NM_004809) is another VGAM1965 host target gene. STOML1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STOML1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STOML1 BINDING SITE, designated SEQ ID:11234, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68993] Another function of VGAM1965 is therefore inhibition of Stomatin (EPB72)-like 1 (STOML1, Accession NM_004809). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STOML1. Suppressor of Ty 4 Homolog 1 (S. cerevisiae) (SUPT4H1, Accession NM_003168) is another VGAM1965 host target gene. SUPT4H1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SUPT4H1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SUPT4H1 BINDING SITE, designated SEQ ID:9146, to the

nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68994] Another function of VGAM1965 is therefore inhibition of Suppressor of Ty 4 Homolog 1 (S. cerevisiae) (SUPT4H1, Accession NM_003168). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUPT4H1. SV2 (Accession NM_014849) is another VGAM1965 host target gene. SV2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SV2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SV2 BINDING SITE, designated SEQ ID:16886, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68995] Another function of VGAM1965 is therefore inhibition of SV2 (Accession NM_014849). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SV2. SYNCOILIN (Accession NM_030786) is another VGAM1965 host target gene. SYNCOILIN BINDING SITE is HOST TAR-

GET binding site found in the 3` untranslated region of mRNA encoded by SYNCOILIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYNCOILIN BINDING SITE, designated SEQ ID:25081, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68996] Another function of VGAM1965 is therefore inhibition of SYNCOILIN (Accession NM_030786). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYNCOILIN. TAO1 (Accession NM_004783) is another VGAM1965 host target gene. TAO1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAO1 BINDING SITE, designated SEQ ID:11189, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68997] Another function of VGAM1965 is therefore inhibition of

TAO1 (Accession NM_004783). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAO1. Transducin (beta)-like 1Y-linked (TBL1Y, Accession NM_033284) is another VGAM1965 host target gene. TBL1Y BINDING SITE1 and TBL1Y BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TBL1Y, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBL1Y BINDING SITE1 and TBL1Y BINDING SITE2, designated SEQ ID:27100 and SEQ ID:28611 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68998] Another function of VGAM1965 is therefore inhibition of Transducin (beta)-like 1Y-linked (TBL1Y, Accession NM_033284). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBL1Y. TERE1 (Accession NM_013319) is another VGAM1965 host target gene. TERE1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TERE1,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TERE1 BINDING SITE, designated SEQ ID:14966, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[68999] Another function of VGAM1965 is therefore inhibition of TERE1 (Accession NM_013319). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERE1. TIP47 (Accession NM_005817) is another VGAM1965 host target gene. TIP47 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIP47, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIP47 BINDING SITE, designated SEQ ID:12418, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69000] Another function of VGAM1965 is therefore inhibition of TIP47 (Accession NM_005817). Accordingly, utilities of

VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIP47. Translocase of Outer Mitochondrial Membrane 34 (TOMM34, Accession NM_006809) is another VGAM1965 host target gene. TOMM34 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOMM34, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOMM34 BINDING SITE, designated SEQ ID:13681, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69001] Another function of VGAM1965 is therefore inhibition of Translocase of Outer Mitochondrial Membrane 34 (TOMM34, Accession NM_006809). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOMM34. TOPK (Accession NM_018492) is another VGAM1965 host target gene. TOPK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOPK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOPK BINDING SITE, designated SEQ ID:20553, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69002] Another function of VGAM1965 is therefore inhibition of TOPK (Accession NM_018492). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOPK. Tripartite Motif-containing 2 (TRIM2, Accession NM_015271) is another VGAM1965 host target gene. TRIM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM2 BINDING SITE, designated SEQ ID:17599, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69003] Another function of VGAM1965 is therefore inhibition of Tripartite Motif-containing 2 (TRIM2, Accession NM_015271). Accordingly, utilities of VGAM1965 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM2. UBCE7IP5 (Accession NM_014948) is another VGAM1965 host target gene. UBCE7IP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UBCE7IP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBCE7IP5 BINDING SITE, designated SEQ ID:17274, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69004] Another function of VGAM1965 is therefore inhibition of UBCE7IP5 (Accession NM_014948). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBCE7IP5. UQCR (Accession NM_006830) is another VGAM1965 host target gene. UQCR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UQCR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UQCR BINDING SITE,

designated SEQ ID:13712, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69005] Another function of VGAM1965 is therefore inhibition of UQCR (Accession NM_006830). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UQCR. VIT1 (Accession NM_018693) is another VGAM1965 host target gene. VIT1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by VIT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VIT1 BINDING SITE, designated SEQ ID:20768, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69006] Another function of VGAM1965 is therefore inhibition of VIT1 (Accession NM_018693). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIT1. Vacuolar Protein Sorting 4B (yeast) (VPS4B, Accession NM_004869) is another VGAM1965 host target gene.

VPS4B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VPS4B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS4B BINDING SITE, designated SEQ ID:11295, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69007] Another function of VGAM1965 is therefore inhibition of Vacuolar Protein Sorting 4B (yeast) (VPS4B, Accession NM_004869). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS4B. Williams-Beuren Syndrome Chromosome Region 17 (WBSCR17, Accession XM_088168) is another VGAM1965 host target gene. WBSCR17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WBSCR17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WBSCR17 BINDING SITE, designated SEQ ID:39547, to the nucleotide sequence of VGAM1965 RNA,

herein designated VGAM RNA, also designated SEQ ID:4676.

[69008] Another function of VGAM1965 is therefore inhibition of Williams-Beuren Syndrome Chromosome Region 17 (WBSCR17, Accession XM_088168). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR17. WIT-1 (Accession NM_015855) is another VGAM1965 host target gene. WIT-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WIT-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WIT-1 BINDING SITE, designated SEQ ID:17993, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69009] Another function of VGAM1965 is therefore inhibition of WIT-1 (Accession NM_015855). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WIT-1. WSB1 (Accession NM_134264) is another VGAM1965 host target gene. WSB1 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by WSB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WSB1 BINDING SITE, designated SEQ ID:28618, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69010] Another function of VGAM1965 is therefore inhibition of WSB1 (Accession NM_134264). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WSB1. ZAK (Accession NM_016653) is another VGAM1965 host target gene. ZAK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZAK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZAK BINDING SITE, designated SEQ ID:18777, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69011] Another function of VGAM1965 is therefore inhibition of

ZAK (Accession NM_016653). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAK. Zinc Finger, DHHC Domain Containing 7 (ZDHHC7, Accession NM_017740) is another VGAM1965 host target gene. ZDHHC7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZDHHC7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZDHHC7 BINDING SITE, designated SEQ ID:19331, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69012] Another function of VGAM1965 is therefore inhibition of Zinc Finger, DHHC Domain Containing 7 (ZDHHC7, Accession NM_017740). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZDHHC7. ZER6 (Accession XM_032742) is another VGAM1965 host target gene. ZER6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZER6, corresponding to a HOST TARGET binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZER6 BINDING SITE, designated SEQ ID:31746, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69013] Another function of VGAM1965 is therefore inhibition of ZER6 (Accession XM_032742). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZER6. ZID (Accession NM_006626) is another VGAM1965 host target gene. ZID BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZID, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZID BINDING SITE, designated SEQ ID:13413, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69014] Another function of VGAM1965 is therefore inhibition of ZID (Accession NM_006626). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZID. Zinc Finger Protein 237 (ZNF237, Accession NM_014242)

is another VGAM1965 host target gene. ZNF237 BINDING SITE1 and ZNF237 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ZNF237, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF237 BINDING SITE1 and ZNF237 BINDING SITE2, designated SEQ ID:15506 and SEQ ID:15507 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69015] Another function of VGAM1965 is therefore inhibition of Zinc Finger Protein 237 (ZNF237, Accession NM_014242). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF237. Zinc Finger Protein 297B (ZNF297B, Accession NM_014007) is another VGAM1965 host target gene. ZNF297B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF297B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF297B BINDING SITE,

designated SEQ ID:15223, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69016] Another function of VGAM1965 is therefore inhibition of Zinc Finger Protein 297B (ZNF297B, Accession NM_014007). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF297B. Zinc Finger Protein 31 (KOX 29) (ZNF31, Accession XM_036305) is another VGAM1965 host target gene. ZNF31 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF31, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF31 BINDING SITE, designated SEQ ID:32423, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69017] Another function of VGAM1965 is therefore inhibition of Zinc Finger Protein 31 (KOX 29) (ZNF31, Accession XM_036305). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF31. Zinc Finger Protein

33a (KOX 31) (ZNF33A, Accession XM_166119) is another VGAM1965 host target gene. ZNF33A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF33A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF33A BINDING SITE, designated SEQ ID:43901, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69018] Another function of VGAM1965 is therefore inhibition of Zinc Finger Protein 33a (KOX 31) (ZNF33A, Accession XM_166119). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF33A. LOC113523 (Accession XM_054378) is another VGAM1965 host target gene. LOC113523 BINDING SITE1 and LOC113523 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC113523, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC113523 BINDING SITE1 and LOC113523 BINDING

SITE2, designated SEQ ID:36154 and SEQ ID:36155 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69019] Another function of VGAM1965 is therefore inhibition of LOC113523 (Accession XM_054378). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113523. LOC115297 (Accession XM_053313) is another VGAM1965 host target gene. LOC115297 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115297, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115297 BINDING SITE, designated SEQ ID:36071, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69020] Another function of VGAM1965 is therefore inhibition of LOC115297 (Accession XM_053313). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115297. LOC116166 (Accession XM_007651) is an-

other VGAM1965 host target gene. LOC116166 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC116166, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC116166 BINDING SITE, designated SEQ ID:30061, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69021] Another function of VGAM1965 is therefore inhibition of LOC116166 (Accession XM_007651). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116166. LOC120196 (Accession XM_061916) is another VGAM1965 host target gene. LOC120196 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120196 BINDING SITE, designated SEQ ID:37217, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69022] Another function of VGAM1965 is therefore inhibition of LOC120196 (Accession XM_061916). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120196. LOC120526 (Accession XM_058475) is another VGAM1965 host target gene. LOC120526 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120526, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120526 BINDING SITE, designated SEQ ID:36624, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69023] Another function of VGAM1965 is therefore inhibition of LOC120526 (Accession XM_058475). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120526. LOC121219 (Accession XM_058544) is another VGAM1965 host target gene. LOC121219 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC121219, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC121219 BINDING SITE, designated SEQ ID:36651, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69024] Another function of VGAM1965 is therefore inhibition of LOC121219 (Accession XM_058544). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121219. LOC121601 (Accession XM_058577) is another VGAM1965 host target gene. LOC121601 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC121601, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC121601 BINDING SITE, designated SEQ ID:36673, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69025] Another function of VGAM1965 is therefore inhibition of LOC121601 (Accession XM_058577). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC121601. LOC122786 (Accession XM_058660) is another VGAM1965 host target gene. LOC122786 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC122786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122786 BINDING SITE, designated SEQ ID:36700, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69026] Another function of VGAM1965 is therefore inhibition of LOC122786 (Accession XM_058660). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122786. LOC124145 (Accession XM_058775) is another VGAM1965 host target gene. LOC124145 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC124145, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124145 BINDING SITE, designated SEQ ID:36734, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[69027] Another function of VGAM1965 is therefore inhibition of LOC124145 (Accession XM_058775). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124145. LOC124446 (Accession XM_058805) is another VGAM1965 host target gene. LOC124446 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC124446, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124446 BINDING SITE, designated SEQ ID:36752, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69028] Another function of VGAM1965 is therefore inhibition of LOC124446 (Accession XM_058805). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124446. LOC124944 (Accession XM_058876) is another VGAM1965 host target gene. LOC124944 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC124944, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124944 BINDING SITE, designated SEQ ID:36778, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69029] Another function of VGAM1965 is therefore inhibition of LOC124944 (Accession XM_058876). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124944. LOC126167 (Accession XM_058997) is another VGAM1965 host target gene. LOC126167 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC126167, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126167 BINDING SITE, designated SEQ ID:36814, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69030] Another function of VGAM1965 is therefore inhibition of LOC126167 (Accession XM_058997). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC126167. LOC126917 (Accession XM_059091) is another VGAM1965 host target gene. LOC126917 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126917, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126917 BINDING SITE, designated SEQ ID:36876, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69031] Another function of VGAM1965 is therefore inhibition of LOC126917 (Accession XM_059091). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126917. LOC126964 (Accession XM_059100) is another VGAM1965 host target gene. LOC126964 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126964, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126964 BINDING SITE, designated SEQ ID:36885, to

the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69032] Another function of VGAM1965 is therefore inhibition of LOC126964 (Accession XM_059100). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126964. LOC127162 (Accession XM_059117) is another VGAM1965 host target gene. LOC127162 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC127162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127162 BINDING SITE, designated SEQ ID:36887, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69033] Another function of VGAM1965 is therefore inhibition of LOC127162 (Accession XM_059117). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127162. LOC127281 (Accession XM_059128) is another VGAM1965 host target gene. LOC127281 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC127281, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127281 BINDING SITE, designated SEQ ID:36889, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69034] Another function of VGAM1965 is therefore inhibition of LOC127281 (Accession XM_059128). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127281. LOC127534 (Accession XM_060532) is another VGAM1965 host target gene. LOC127534 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC127534, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127534 BINDING SITE, designated SEQ ID:37173, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69035] Another function of VGAM1965 is therefore inhibition of LOC127534 (Accession XM_060532). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127534. LOC127841 (Accession XM_059184) is another VGAM1965 host target gene. LOC127841 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC127841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127841 BINDING SITE, designated SEQ ID:36910, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69036] Another function of VGAM1965 is therefore inhibition of LOC127841 (Accession XM_059184). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127841. LOC128077 (Accession XM_059208) is another VGAM1965 host target gene. LOC128077 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC128077, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC128077 BINDING SITE, designated SEQ ID:36919, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69037] Another function of VGAM1965 is therefore inhibition of LOC128077 (Accession XM_059208). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128077. LOC129198 (Accession XM_072197) is another VGAM1965 host target gene. LOC129198 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC129198, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC129198 BINDING SITE, designated SEQ ID:37465, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69038] Another function of VGAM1965 is therefore inhibition of LOC129198 (Accession XM_072197). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129198. LOC133022 (Accession XM_068144) is another VGAM1965 host target gene. LOC133022 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC133022, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133022 BINDING SITE, designated SEQ ID:37376, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69039] Another function of VGAM1965 is therefore inhibition of LOC133022 (Accession XM_068144). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133022. LOC133088 (Accession XM_059624) is another VGAM1965 host target gene. LOC133088 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC133088, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133088 BINDING SITE, designated SEQ ID:37032, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69040] Another function of VGAM1965 is therefore inhibition of

LOC133088 (Accession XM_059624). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133088. LOC133584 (Accession XM_059661) is another VGAM1965 host target gene. LOC133584 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC133584, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133584 BINDING SITE, designated SEQ ID:37048, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69041] Another function of VGAM1965 is therefore inhibition of LOC133584 (Accession XM_059661). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133584. LOC134121 (Accession XM_059692) is another VGAM1965 host target gene. LOC134121 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC134121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC134121 BINDING SITE, designated SEQ ID:37065, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69042] Another function of VGAM1965 is therefore inhibition of LOC134121 (Accession XM_059692). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC134121. LOC134147 (Accession NM_138809) is another VGAM1965 host target gene. LOC134147 BINDING SITE1 and LOC134147 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC134147, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC134147 BINDING SITE1 and LOC134147 BINDING SITE2, designated SEQ ID:29033 and SEQ ID:29034 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69043] Another function of VGAM1965 is therefore inhibition of LOC134147 (Accession NM_138809). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC134147. LOC135818 (Accession XM_059804) is another VGAM1965 host target gene. LOC135818 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC135818, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC135818 BINDING SITE, designated SEQ ID:37096, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69044] Another function of VGAM1965 is therefore inhibition of LOC135818 (Accession XM_059804). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135818. LOC139221 (Accession XM_066558) is another VGAM1965 host target gene. LOC139221 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC139221, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC139221 BINDING SITE, designated SEQ ID:37333, to

the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69045] Another function of VGAM1965 is therefore inhibition of LOC139221 (Accession XM_066558). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139221. LOC139248 (Accession XM_066582) is another VGAM1965 host target gene. LOC139248 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC139248, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC139248 BINDING SITE, designated SEQ ID:37338, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69046] Another function of VGAM1965 is therefore inhibition of LOC139248 (Accession XM_066582). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139248. LOC139770 (Accession XM_060053) is another VGAM1965 host target gene. LOC139770 BINDING SITE1 through LOC139770 BINDING SITE3 are HOST TAR-

GET binding sites found in untranslated regions of mRNA encoded by LOC139770, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC139770 BINDING SITE1 through LOC139770 BINDING SITE3, designated SEQ ID:37146, SEQ ID:37148 and SEQ ID:37149 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69047] Another function of VGAM1965 is therefore inhibition of LOC139770 (Accession XM_060053). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139770. LOC143188 (Accession XM_096387) is another VGAM1965 host target gene. LOC143188 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143188, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143188 BINDING SITE, designated SEQ ID:40328, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69048] Another function of VGAM1965 is therefore inhibition of LOC143188 (Accession XM_096387). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143188. LOC143465 (Accession XM_096430) is another VGAM1965 host target gene. LOC143465 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143465, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143465 BINDING SITE, designated SEQ ID:40365, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69049] Another function of VGAM1965 is therefore inhibition of LOC143465 (Accession XM_096430). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143465. LOC144245 (Accession XM_047770) is another VGAM1965 host target gene. LOC144245 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144245, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144245 BINDING SITE, designated SEQ ID:35051, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69050] Another function of VGAM1965 is therefore inhibition of LOC144245 (Accession XM_047770). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144245. LOC144266 (Accession XM_084795) is another VGAM1965 host target gene. LOC144266 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144266 BINDING SITE, designated SEQ ID:37707, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69051] Another function of VGAM1965 is therefore inhibition of LOC144266 (Accession XM_084795). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC144266. LOC144512 (Accession XM_096623) is another VGAM1965 host target gene. LOC144512 BINDING SITE1 and LOC144512 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC144512, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144512 BINDING SITE1 and LOC144512 BINDING SITE2, designated SEQ ID:40430 and SEQ ID:40431 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69052] Another function of VGAM1965 is therefore inhibition of LOC144512 (Accession XM_096623). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144512. LOC144920 (Accession XM_096688) is another VGAM1965 host target gene. LOC144920 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144920, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC144920 BINDING SITE, designated SEQ ID:40464, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69053] Another function of VGAM1965 is therefore inhibition of LOC144920 (Accession XM_096688). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144920. LOC145082 (Accession XM_096719) is another VGAM1965 host target gene. LOC145082 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145082, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145082 BINDING SITE, designated SEQ ID:40495, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69054] Another function of VGAM1965 is therefore inhibition of LOC145082 (Accession XM_096719). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145082. LOC145231 (Accession XM_096740) is another VGAM1965 host target gene. LOC145231 BINDING

SITE1 and LOC145231 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC145231, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145231 BINDING SITE1 and LOC145231 BINDING SITE2, designated SEQ ID:40522 and SEQ ID:40523 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69055] Another function of VGAM1965 is therefore inhibition of LOC145231 (Accession XM_096740). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145231. LOC145497 (Accession XM_085150) is another VGAM1965 host target gene. LOC145497 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145497, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145497 BINDING SITE, designated SEQ ID:37874, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[69056] Another function of VGAM1965 is therefore inhibition of LOC145497 (Accession XM_085150). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145497. LOC145547 (Accession XM_085167) is another VGAM1965 host target gene. LOC145547 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145547, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145547 BINDING SITE, designated SEQ ID:37891, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69057] Another function of VGAM1965 is therefore inhibition of LOC145547 (Accession XM_085167). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145547. LOC145662 (Accession XM_085194) is another VGAM1965 host target gene. LOC145662 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145662, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145662 BINDING SITE, designated SEQ ID:37918, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69058] Another function of VGAM1965 is therefore inhibition of LOC145662 (Accession XM_085194). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145662. LOC145761 (Accession XM_096855) is another VGAM1965 host target gene. LOC145761 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145761, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145761 BINDING SITE, designated SEQ ID:40585, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69059] Another function of VGAM1965 is therefore inhibition of LOC145761 (Accession XM_096855). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC145761. LOC145955 (Accession XM_096912) is another VGAM1965 host target gene. LOC145955 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145955 BINDING SITE, designated SEQ ID:40646, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69060] Another function of VGAM1965 is therefore inhibition of LOC145955 (Accession XM_096912). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145955. LOC145988 (Accession XM_085290) is another VGAM1965 host target gene. LOC145988 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145988, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145988 BINDING SITE, designated SEQ ID:38043, to

the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69061] Another function of VGAM1965 is therefore inhibition of LOC145988 (Accession XM_085290). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145988. LOC146108 (Accession XM_085322) is another VGAM1965 host target gene. LOC146108 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146108, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146108 BINDING SITE, designated SEQ ID:38063, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69062] Another function of VGAM1965 is therefore inhibition of LOC146108 (Accession XM_085322). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146108. LOC146315 (Accession XM_027576) is another VGAM1965 host target gene. LOC146315 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC146315, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146315 BINDING SITE, designated SEQ ID:30535, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69063] Another function of VGAM1965 is therefore inhibition of LOC146315 (Accession XM_027576). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146315. LOC146336 (Accession XM_085421) is another VGAM1965 host target gene. LOC146336 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146336, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146336 BINDING SITE, designated SEQ ID:38134, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69064] Another function of VGAM1965 is therefore inhibition of LOC146336 (Accession XM_085421). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146336. LOC146445 (Accession XM_096999) is another VGAM1965 host target gene. LOC146445 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146445 BINDING SITE, designated SEQ ID:40699, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69065] Another function of VGAM1965 is therefore inhibition of LOC146445 (Accession XM_096999). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146445. LOC146745 (Accession XM_085577) is another VGAM1965 host target gene. LOC146745 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146745, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC146745 BINDING SITE, designated SEQ ID:38232, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69066] Another function of VGAM1965 is therefore inhibition of LOC146745 (Accession XM_085577). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146745. LOC146756 (Accession XM_097085) is another VGAM1965 host target gene. LOC146756 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146756, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146756 BINDING SITE, designated SEQ ID:40740, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69067] Another function of VGAM1965 is therefore inhibition of LOC146756 (Accession XM_097085). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146756. LOC146802 (Accession XM_085595) is another VGAM1965 host target gene. LOC146802 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146802, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146802 BINDING SITE, designated SEQ ID:38248, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69068] Another function of VGAM1965 is therefore inhibition of LOC146802 (Accession XM_085595). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146802. LOC146839 (Accession XM_097107) is another VGAM1965 host target gene. LOC146839 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146839, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146839 BINDING SITE, designated SEQ ID:40755, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69069] Another function of VGAM1965 is therefore inhibition of

LOC146839 (Accession XM_097107). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146839. LOC146880 (Accession XM_085627) is another VGAM1965 host target gene. LOC146880 BINDING SITE1 and LOC146880 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC146880, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146880 BINDING SITE1 and LOC146880 BINDING SITE2, designated SEQ ID:38262 and SEQ ID:38263 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69070] Another function of VGAM1965 is therefore inhibition of LOC146880 (Accession XM_085627). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146880. LOC147077 (Accession XM_085699) is another VGAM1965 host target gene. LOC147077 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147077, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147077 BINDING SITE, designated SEQ ID:38292, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69071] Another function of VGAM1965 is therefore inhibition of LOC147077 (Accession XM_085699). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147077. LOC147160 (Accession XM_097202) is another VGAM1965 host target gene. LOC147160 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147160 BINDING SITE, designated SEQ ID:40811, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69072] Another function of VGAM1965 is therefore inhibition of LOC147160 (Accession XM_097202). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC147160. LOC147229 (Accession XM_085742) is another VGAM1965 host target gene. LOC147229 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147229 BINDING SITE, designated SEQ ID:38323, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69073] Another function of VGAM1965 is therefore inhibition of LOC147229 (Accession XM_085742). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147229. LOC148029 (Accession XM_086014) is another VGAM1965 host target gene. LOC148029 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148029, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148029 BINDING SITE, designated SEQ ID:38446, to

the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69074] Another function of VGAM1965 is therefore inhibition of LOC148029 (Accession XM_086014). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148029. LOC148223 (Accession XM_086101) is another VGAM1965 host target gene. LOC148223 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148223, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148223 BINDING SITE, designated SEQ ID:38493, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69075] Another function of VGAM1965 is therefore inhibition of LOC148223 (Accession XM_086101). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148223. LOC148394 (Accession XM_097460) is another VGAM1965 host target gene. LOC148394 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC148394, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148394 BINDING SITE, designated SEQ ID:40882, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69076] Another function of VGAM1965 is therefore inhibition of LOC148394 (Accession XM_097460). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148394. LOC148479 (Accession XM_086204) is another VGAM1965 host target gene. LOC148479 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148479, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148479 BINDING SITE, designated SEQ ID:38543, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69077] Another function of VGAM1965 is therefore inhibition of LOC148479 (Accession XM_086204). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148479. LOC148823 (Accession NM_145278) is another VGAM1965 host target gene. LOC148823 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148823, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148823 BINDING SITE, designated SEQ ID:29796, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69078] Another function of VGAM1965 is therefore inhibition of LOC148823 (Accession NM_145278). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148823. LOC148887 (Accession XM_097537) is another VGAM1965 host target gene. LOC148887 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148887, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC148887 BINDING SITE, designated SEQ ID:40912, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69079] Another function of VGAM1965 is therefore inhibition of LOC148887 (Accession XM_097537). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148887. LOC149010 (Accession XM_086397) is another VGAM1965 host target gene. LOC149010 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149010, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149010 BINDING SITE, designated SEQ ID:38628, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69080] Another function of VGAM1965 is therefore inhibition of LOC149010 (Accession XM_086397). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149010. LOC149013 (Accession XM_086398) is another VGAM1965 host target gene. LOC149013 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149013, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149013 BINDING SITE, designated SEQ ID:38634, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69081] Another function of VGAM1965 is therefore inhibition of LOC149013 (Accession XM_086398). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149013. LOC149086 (Accession XM_097580) is another VGAM1965 host target gene. LOC149086 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149086, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149086 BINDING SITE, designated SEQ ID:40947, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69082] Another function of VGAM1965 is therefore inhibition of

LOC149086 (Accession XM_097580). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149086. LOC149127 (Accession XM_097584) is another VGAM1965 host target gene. LOC149127 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149127, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149127 BINDING SITE, designated SEQ ID:40950, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69083] Another function of VGAM1965 is therefore inhibition of LOC149127 (Accession XM_097584). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149127. LOC149153 (Accession XM_097599) is another VGAM1965 host target gene. LOC149153 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149153, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC149153 BINDING SITE, designated SEQ ID:40966, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69084] Another function of VGAM1965 is therefore inhibition of LOC149153 (Accession XM_097599). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149153. LOC149175 (Accession XM_086445) is another VGAM1965 host target gene. LOC149175 BINDING SITE1 and LOC149175 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC149175, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149175 BINDING SITE1 and LOC149175 BINDING SITE2, designated SEQ ID:38664 and SEQ ID:38665 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69085] Another function of VGAM1965 is therefore inhibition of LOC149175 (Accession XM_086445). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC149175. LOC149271 (Accession XM_086475) is another VGAM1965 host target gene. LOC149271 BINDING SITE1 and LOC149271 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC149271, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149271 BINDING SITE1 and LOC149271 BINDING SITE2, designated SEQ ID:38684 and SEQ ID:38683 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69086] Another function of VGAM1965 is therefore inhibition of LOC149271 (Accession XM_086475). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149271. LOC149319 (Accession XM_086495) is another VGAM1965 host target gene. LOC149319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149319, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC149319 BINDING SITE, designated SEQ ID:38713, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69087] Another function of VGAM1965 is therefore inhibition of LOC149319 (Accession XM_086495). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149319. LOC149464 (Accession XM_097645) is another VGAM1965 host target gene. LOC149464 BINDING SITE1 and LOC149464 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC149464, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149464 BINDING SITE1 and LOC149464 BINDING SITE2, designated SEQ ID:40995 and SEQ ID:40996 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69088] Another function of VGAM1965 is therefore inhibition of LOC149464 (Accession XM_097645). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC149464. LOC149606 (Accession XM_086600) is another VGAM1965 host target gene. LOC149606 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149606, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149606 BINDING SITE, designated SEQ ID:38785, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69089] Another function of VGAM1965 is therefore inhibition of LOC149606 (Accession XM_086600). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149606. LOC149684 (Accession XM_097710) is another VGAM1965 host target gene. LOC149684 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149684, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149684 BINDING SITE, designated SEQ ID:41049, to

the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69090] Another function of VGAM1965 is therefore inhibition of LOC149684 (Accession XM_097710). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149684. LOC149692 (Accession XM_097706) is another VGAM1965 host target gene. LOC149692 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149692, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149692 BINDING SITE, designated SEQ ID:41041, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69091] Another function of VGAM1965 is therefore inhibition of LOC149692 (Accession XM_097706). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149692. LOC149711 (Accession XM_097720) is another VGAM1965 host target gene. LOC149711 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC149711, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149711 BINDING SITE, designated SEQ ID:41076, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69092] Another function of VGAM1965 is therefore inhibition of LOC149711 (Accession XM_097720). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149711. LOC149722 (Accession XM_097709) is another VGAM1965 host target gene. LOC149722 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149722, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149722 BINDING SITE, designated SEQ ID:41045, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69093] Another function of VGAM1965 is therefore inhibition of LOC149722 (Accession XM_097709). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149722. LOC149773 (Accession XM_086628) is another VGAM1965 host target gene. LOC149773 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149773, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149773 BINDING SITE, designated SEQ ID:38801, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69094] Another function of VGAM1965 is therefore inhibition of LOC149773 (Accession XM_086628). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149773. LOC150150 (Accession XM_097820) is another VGAM1965 host target gene. LOC150150 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150150, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC150150 BINDING SITE, designated SEQ ID:41137, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69095] Another function of VGAM1965 is therefore inhibition of LOC150150 (Accession XM_097820). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150150. LOC150299 (Accession XM_097869) is another VGAM1965 host target gene. LOC150299 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150299, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150299 BINDING SITE, designated SEQ ID:41183, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69096] Another function of VGAM1965 is therefore inhibition of LOC150299 (Accession XM_097869). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150299. LOC150365 (Accession XM_086847) is another VGAM1965 host target gene. LOC150365 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150365, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150365 BINDING SITE, designated SEQ ID:38913, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69097] Another function of VGAM1965 is therefore inhibition of LOC150365 (Accession XM_086847). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150365. LOC150423 (Accession XM_086912) is another VGAM1965 host target gene. LOC150423 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150423, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150423 BINDING SITE, designated SEQ ID:38969, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69098] Another function of VGAM1965 is therefore inhibition of

LOC150423 (Accession XM_086912). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150423. LOC150468 (Accession XM_086926) is another VGAM1965 host target gene. LOC150468 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150468, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150468 BINDING SITE, designated SEQ ID:38976, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69099] Another function of VGAM1965 is therefore inhibition of LOC150468 (Accession XM_086926). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150468. LOC150848 (Accession XM_097959) is another VGAM1965 host target gene. LOC150848 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150848, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC150848 BINDING SITE, designated SEQ ID:41259, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69100] Another function of VGAM1965 is therefore inhibition of LOC150848 (Accession XM_097959). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150848. LOC150933 (Accession XM_097971) is another VGAM1965 host target gene. LOC150933 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150933, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150933 BINDING SITE, designated SEQ ID:41272, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69101] Another function of VGAM1965 is therefore inhibition of LOC150933 (Accession XM_097971). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150933. LOC150998 (Accession XM_097990) is an-

other VGAM1965 host target gene. LOC150998 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150998, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150998 BINDING SITE, designated SEQ ID:41288, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69102] Another function of VGAM1965 is therefore inhibition of LOC150998 (Accession XM_097990). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150998. LOC151124 (Accession XM_098006) is another VGAM1965 host target gene. LOC151124 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151124, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151124 BINDING SITE, designated SEQ ID:41303, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69103] Another function of VGAM1965 is therefore inhibition of LOC151124 (Accession XM_098006). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151124. LOC151126 (Accession XM_087103) is another VGAM1965 host target gene. LOC151126 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151126, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151126 BINDING SITE, designated SEQ ID:39059, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69104] Another function of VGAM1965 is therefore inhibition of LOC151126 (Accession XM_087103). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151126. LOC151146 (Accession XM_087106) is another VGAM1965 host target gene. LOC151146 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151146, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151146 BINDING SITE, designated SEQ ID:39062, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69105] Another function of VGAM1965 is therefore inhibition of LOC151146 (Accession XM_087106). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151146. LOC151201 (Accession XM_098021) is another VGAM1965 host target gene. LOC151201 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151201, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151201 BINDING SITE, designated SEQ ID:41322, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69106] Another function of VGAM1965 is therefore inhibition of LOC151201 (Accession XM_098021). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC151201. LOC151405 (Accession XM_098058) is another VGAM1965 host target gene. LOC151405 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151405, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151405 BINDING SITE, designated SEQ ID:41340, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69107] Another function of VGAM1965 is therefore inhibition of LOC151405 (Accession XM_098058). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151405. LOC151446 (Accession XM_098061) is another VGAM1965 host target gene. LOC151446 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151446, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151446 BINDING SITE, designated SEQ ID:41352, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[69108] Another function of VGAM1965 is therefore inhibition of LOC151446 (Accession XM_098061). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151446. LOC151568 (Accession NM_138483) is another VGAM1965 host target gene. LOC151568 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151568, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151568 BINDING SITE, designated SEQ ID:28839, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69109] Another function of VGAM1965 is therefore inhibition of LOC151568 (Accession NM_138483). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151568. LOC151602 (Accession XM_087247) is another VGAM1965 host target gene. LOC151602 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151602, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151602 BINDING SITE, designated SEQ ID:39140, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69110] Another function of VGAM1965 is therefore inhibition of LOC151602 (Accession XM_087247). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151602. LOC151643 (Accession XM_087259) is another VGAM1965 host target gene. LOC151643 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151643, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151643 BINDING SITE, designated SEQ ID:39152, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69111] Another function of VGAM1965 is therefore inhibition of LOC151643 (Accession XM_087259). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC151643. LOC151904 (Accession XM_087334) is another VGAM1965 host target gene. LOC151904 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151904, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151904 BINDING SITE, designated SEQ ID:39174, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69112] Another function of VGAM1965 is therefore inhibition of LOC151904 (Accession XM_087334). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151904. LOC151959 (Accession XM_098144) is another VGAM1965 host target gene. LOC151959 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151959, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151959 BINDING SITE, designated SEQ ID:41410, to

the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69113] Another function of VGAM1965 is therefore inhibition of LOC151959 (Accession XM_098144). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151959. LOC152018 (Accession XM_098156) is another VGAM1965 host target gene. LOC152018 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152018, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152018 BINDING SITE, designated SEQ ID:41423, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69114] Another function of VGAM1965 is therefore inhibition of LOC152018 (Accession XM_098156). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152018. LOC152137 (Accession XM_087392) is another VGAM1965 host target gene. LOC152137 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC152137, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152137 BINDING SITE, designated SEQ ID:39223, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69115] Another function of VGAM1965 is therefore inhibition of LOC152137 (Accession XM_087392). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152137. LOC152315 (Accession XM_087440) is another VGAM1965 host target gene. LOC152315 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152315, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152315 BINDING SITE, designated SEQ ID:39255, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69116] Another function of VGAM1965 is therefore inhibition of LOC152315 (Accession XM_087440). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152315. LOC152345 (Accession XM_087442) is another VGAM1965 host target gene. LOC152345 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152345, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152345 BINDING SITE, designated SEQ ID:39268, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69117] Another function of VGAM1965 is therefore inhibition of LOC152345 (Accession XM_087442). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152345. LOC152627 (Accession XM_087495) is another VGAM1965 host target gene. LOC152627 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152627, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC152627 BINDING SITE, designated SEQ ID:39296, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69118] Another function of VGAM1965 is therefore inhibition of LOC152627 (Accession XM_087495). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152627. LOC152804 (Accession XM_098266) is another VGAM1965 host target gene. LOC152804 BINDING SITE1 and LOC152804 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC152804, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152804 BINDING SITE1 and LOC152804 BINDING SITE2, designated SEQ ID:41557 and SEQ ID:41558 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69119] Another function of VGAM1965 is therefore inhibition of LOC152804 (Accession XM_098266). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC152804. LOC152860 (Accession XM_087539) is another VGAM1965 host target gene. LOC152860 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152860, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152860 BINDING SITE, designated SEQ ID:39326, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69120] Another function of VGAM1965 is therefore inhibition of LOC152860 (Accession XM_087539). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152860. LOC153516 (Accession NM_138491) is another VGAM1965 host target gene. LOC153516 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153516 BINDING SITE, designated SEQ ID:28843, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[69121] Another function of VGAM1965 is therefore inhibition of LOC153516 (Accession NM_138491). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153516. LOC153688 (Accession XM_098416) is another VGAM1965 host target gene. LOC153688 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153688, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153688 BINDING SITE, designated SEQ ID:41662, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69122] Another function of VGAM1965 is therefore inhibition of LOC153688 (Accession XM_098416). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153688. LOC153810 (Accession XM_087778) is another VGAM1965 host target gene. LOC153810 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153810, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153810 BINDING SITE, designated SEQ ID:39413, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69123] Another function of VGAM1965 is therefore inhibition of LOC153810 (Accession XM_087778). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153810. LOC153811 (Accession XM_087779) is another VGAM1965 host target gene. LOC153811 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153811, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153811 BINDING SITE, designated SEQ ID:39419, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69124] Another function of VGAM1965 is therefore inhibition of LOC153811 (Accession XM_087779). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC153811. LOC153910 (Accession XM_087801) is another VGAM1965 host target gene. LOC153910 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153910, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153910 BINDING SITE, designated SEQ ID:39440, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69125] Another function of VGAM1965 is therefore inhibition of LOC153910 (Accession XM_087801). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153910. LOC154222 (Accession XM_098497) is another VGAM1965 host target gene. LOC154222 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154222, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154222 BINDING SITE, designated SEQ ID:41694, to

the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69126] Another function of VGAM1965 is therefore inhibition of LOC154222 (Accession XM_098497). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154222. LOC154739 (Accession XM_098602) is another VGAM1965 host target gene. LOC154739 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154739, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154739 BINDING SITE, designated SEQ ID:41710, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69127] Another function of VGAM1965 is therefore inhibition of LOC154739 (Accession XM_098602). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154739. LOC155060 (Accession XM_098650) is another VGAM1965 host target gene. LOC155060 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC155060, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155060 BINDING SITE, designated SEQ ID:41751, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69128] Another function of VGAM1965 is therefore inhibition of LOC155060 (Accession XM_098650). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155060. LOC155179 (Accession XM_088169) is another VGAM1965 host target gene. LOC155179 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155179, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155179 BINDING SITE, designated SEQ ID:39561, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69129] Another function of VGAM1965 is therefore inhibition of LOC155179 (Accession XM_088169). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155179. LOC157381 (Accession XM_098754) is another VGAM1965 host target gene. LOC157381 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157381, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157381 BINDING SITE, designated SEQ ID:41791, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69130] Another function of VGAM1965 is therefore inhibition of LOC157381 (Accession XM_098754). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157381. LOC157506 (Accession XM_088311) is another VGAM1965 host target gene. LOC157506 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157506, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC157506 BINDING SITE, designated SEQ ID:39602, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69131] Another function of VGAM1965 is therefore inhibition of LOC157506 (Accession XM_088311). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157506. LOC157621 (Accession XM_098800) is another VGAM1965 host target gene. LOC157621 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157621, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157621 BINDING SITE, designated SEQ ID:41825, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69132] Another function of VGAM1965 is therefore inhibition of LOC157621 (Accession XM_098800). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157621. LOC157624 (Accession XM_098801) is another VGAM1965 host target gene. LOC157624 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157624, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157624 BINDING SITE, designated SEQ ID:41827, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69133] Another function of VGAM1965 is therefore inhibition of LOC157624 (Accession XM_098801). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157624. LOC158055 (Accession XM_088453) is another VGAM1965 host target gene. LOC158055 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158055, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158055 BINDING SITE, designated SEQ ID:39707, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69134] Another function of VGAM1965 is therefore inhibition of

LOC158055 (Accession XM_088453). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158055. LOC158056 (Accession XM_088463) is another VGAM1965 host target gene. LOC158056 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158056, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158056 BINDING SITE, designated SEQ ID:39715, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69135] Another function of VGAM1965 is therefore inhibition of LOC158056 (Accession XM_088463). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158056. LOC158301 (Accession XM_088543) is another VGAM1965 host target gene. LOC158301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC158301 BINDING SITE, designated SEQ ID:39812, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69136] Another function of VGAM1965 is therefore inhibition of LOC158301 (Accession XM_088543). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158301. LOC158308 (Accession XM_098917) is another VGAM1965 host target gene. LOC158308 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158308 BINDING SITE, designated SEQ ID:41942, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69137] Another function of VGAM1965 is therefore inhibition of LOC158308 (Accession XM_098917). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158308. LOC158332 (Accession XM_088554) is an-

other VGAM1965 host target gene. LOC158332 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158332, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158332 BINDING SITE, designated SEQ ID:39826, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69138] Another function of VGAM1965 is therefore inhibition of LOC158332 (Accession XM_088554). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158332. LOC158382 (Accession XM_098931) is another VGAM1965 host target gene. LOC158382 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158382, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158382 BINDING SITE, designated SEQ ID:41969, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69139] Another function of VGAM1965 is therefore inhibition of LOC158382 (Accession XM_098931). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158382. LOC158427 (Accession NM_139246) is another VGAM1965 host target gene. LOC158427 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158427, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158427 BINDING SITE, designated SEQ ID:29248, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69140] Another function of VGAM1965 is therefore inhibition of LOC158427 (Accession NM_139246). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158427. LOC158490 (Accession XM_088585) is another VGAM1965 host target gene. LOC158490 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158490, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158490 BINDING SITE, designated SEQ ID:39849, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69141] Another function of VGAM1965 is therefore inhibition of LOC158490 (Accession XM_088585). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158490. LOC158527 (Accession XM_088594) is another VGAM1965 host target gene. LOC158527 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158527, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158527 BINDING SITE, designated SEQ ID:39864, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69142] Another function of VGAM1965 is therefore inhibition of LOC158527 (Accession XM_088594). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC158527. LOC158987 (Accession XM_099015) is another VGAM1965 host target gene. LOC158987 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158987, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158987 BINDING SITE, designated SEQ ID:42051, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69143] Another function of VGAM1965 is therefore inhibition of LOC158987 (Accession XM_099015). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158987. LOC161527 (Accession XM_090960) is another VGAM1965 host target gene. LOC161527 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC161527, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161527 BINDING SITE, designated SEQ ID:40020, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[69144] Another function of VGAM1965 is therefore inhibition of LOC161527 (Accession XM_090960). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161527. LOC161829 (Accession XM_091161) is another VGAM1965 host target gene. LOC161829 BINDING SITE1 and LOC161829 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC161829, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161829 BINDING SITE1 and LOC161829 BINDING SITE2, designated SEQ ID:40036 and SEQ ID:40041 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69145] Another function of VGAM1965 is therefore inhibition of LOC161829 (Accession XM_091161). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161829. LOC162333 (Accession XM_102591) is another VGAM1965 host target gene. LOC162333 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC162333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162333 BINDING SITE, designated SEQ ID:42139, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69146] Another function of VGAM1965 is therefore inhibition of LOC162333 (Accession XM_102591). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162333. LOC170106 (Accession XM_093106) is another VGAM1965 host target gene. LOC170106 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC170106, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC170106 BINDING SITE, designated SEQ ID:40175, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69147] Another function of VGAM1965 is therefore inhibition of

LOC170106 (Accession XM_093106). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170106. LOC170409 (Accession XM_096330) is another VGAM1965 host target gene. LOC170409 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC170409, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC170409 BINDING SITE, designated SEQ ID:40316, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69148] Another function of VGAM1965 is therefore inhibition of LOC170409 (Accession XM_096330). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170409. LOC196477 (Accession XM_113728) is another VGAM1965 host target gene. LOC196477 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196477, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC196477 BINDING SITE, designated SEQ ID:42377, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69149] Another function of VGAM1965 is therefore inhibition of LOC196477 (Accession XM_113728). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196477. LOC196484 (Accession XM_031807) is another VGAM1965 host target gene. LOC196484 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC196484, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196484 BINDING SITE, designated SEQ ID:31486, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69150] Another function of VGAM1965 is therefore inhibition of LOC196484 (Accession XM_031807). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196484. LOC196955 (Accession XM_085210) is an-

other VGAM1965 host target gene. LOC196955 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC196955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196955 BINDING SITE, designated SEQ ID:37939, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69151] Another function of VGAM1965 is therefore inhibition of LOC196955 (Accession XM_085210). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196955. LOC197196 (Accession XM_117003) is another VGAM1965 host target gene. LOC197196 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC197196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197196 BINDING SITE, designated SEQ ID:43203, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69152] Another function of VGAM1965 is therefore inhibition of LOC197196 (Accession XM_117003). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197196. LOC197201 (Accession XM_113839) is another VGAM1965 host target gene. LOC197201 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197201, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197201 BINDING SITE, designated SEQ ID:42466, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69153] Another function of VGAM1965 is therefore inhibition of LOC197201 (Accession XM_113839). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197201. LOC197342 (Accession XM_113869) is another VGAM1965 host target gene. LOC197342 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197342, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197342 BINDING SITE, designated SEQ ID:42490, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69154] Another function of VGAM1965 is therefore inhibition of LOC197342 (Accession XM_113869). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197342. LOC199858 (Accession XM_114040) is another VGAM1965 host target gene. LOC199858 BINDING SITE1 and LOC199858 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC199858, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199858 BINDING SITE1 and LOC199858 BINDING SITE2, designated SEQ ID:42644 and SEQ ID:42645 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69155] Another function of VGAM1965 is therefore inhibition of LOC199858 (Accession XM_114040). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199858. LOC200488 (Accession XM_117240) is another VGAM1965 host target gene. LOC200488 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200488, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200488 BINDING SITE, designated SEQ ID:43314, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69156] Another function of VGAM1965 is therefore inhibition of LOC200488 (Accession XM_117240). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200488. LOC200830 (Accession XM_117287) is another VGAM1965 host target gene. LOC200830 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200830, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC200830 BINDING SITE, designated SEQ ID:43349, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69157] Another function of VGAM1965 is therefore inhibition of LOC200830 (Accession XM_117287). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200830. LOC200953 (Accession XM_117302) is another VGAM1965 host target gene. LOC200953 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200953, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200953 BINDING SITE, designated SEQ ID:43368, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69158] Another function of VGAM1965 is therefore inhibition of LOC200953 (Accession XM_117302). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200953. LOC201173 (Accession XM_113312) is another VGAM1965 host target gene. LOC201173 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201173, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201173 BINDING SITE, designated SEQ ID:42217, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69159] Another function of VGAM1965 is therefore inhibition of LOC201173 (Accession XM_113312). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201173. LOC201203 (Accession XM_113920) is another VGAM1965 host target gene. LOC201203 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201203, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201203 BINDING SITE, designated SEQ ID:42537, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69160] Another function of VGAM1965 is therefore inhibition of

LOC201203 (Accession XM_113920). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201203. LOC201220 (Accession XM_113321) is another VGAM1965 host target gene. LOC201220 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201220, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201220 BINDING SITE, designated SEQ ID:42226, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69161] Another function of VGAM1965 is therefore inhibition of LOC201220 (Accession XM_113321). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201220. LOC201243 (Accession XM_113935) is another VGAM1965 host target gene. LOC201243 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201243, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC201243 BINDING SITE, designated SEQ ID:42554, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69162] Another function of VGAM1965 is therefore inhibition of LOC201243 (Accession XM_113935). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201243. LOC201626 (Accession XM_114349) is another VGAM1965 host target gene. LOC201626 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201626, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201626 BINDING SITE, designated SEQ ID:42888, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69163] Another function of VGAM1965 is therefore inhibition of LOC201626 (Accession XM_114349). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201626. LOC201895 (Accession XM_114396) is an-

other VGAM1965 host target gene. LOC201895 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201895, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201895 BINDING SITE, designated SEQ ID:42928, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69164] Another function of VGAM1965 is therefore inhibition of LOC201895 (Accession XM_114396). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201895. LOC202134 (Accession XM_117365) is another VGAM1965 host target gene. LOC202134 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202134, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202134 BINDING SITE, designated SEQ ID:43415, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69165] Another function of VGAM1965 is therefore inhibition of LOC202134 (Accession XM_117365). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202134. LOC203235 (Accession XM_117514) is another VGAM1965 host target gene. LOC203235 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203235, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203235 BINDING SITE, designated SEQ ID:43479, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69166] Another function of VGAM1965 is therefore inhibition of LOC203235 (Accession XM_117514). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203235. LOC203248 (Accession XM_114659) is another VGAM1965 host target gene. LOC203248 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203248, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203248 BINDING SITE, designated SEQ ID:43019, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69167] Another function of VGAM1965 is therefore inhibition of LOC203248 (Accession XM_114659). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203248. LOC203339 (Accession XM_117534) is another VGAM1965 host target gene. LOC203339 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203339, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203339 BINDING SITE, designated SEQ ID:43526, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69168] Another function of VGAM1965 is therefore inhibition of LOC203339 (Accession XM_117534). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC203339. LOC203378 (Accession XM_117541) is another VGAM1965 host target gene. LOC203378 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203378, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203378 BINDING SITE, designated SEQ ID:43559, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69169] Another function of VGAM1965 is therefore inhibition of LOC203378 (Accession XM_117541). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203378. LOC203504 (Accession XM_117550) is another VGAM1965 host target gene. LOC203504 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203504, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203504 BINDING SITE, designated SEQ ID:43567, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[69170] Another function of VGAM1965 is therefore inhibition of LOC203504 (Accession XM_117550). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203504. LOC205251 (Accession XM_119554) is another VGAM1965 host target gene. LOC205251 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC205251, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC205251 BINDING SITE, designated SEQ ID:43591, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69171] Another function of VGAM1965 is therefore inhibition of LOC205251 (Accession XM_119554). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC205251. LOC219540 (Accession XM_168047) is another VGAM1965 host target gene. LOC219540 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219540, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219540 BINDING SITE, designated SEQ ID:44959, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69172] Another function of VGAM1965 is therefore inhibition of LOC219540 (Accession XM_168047). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219540. LOC219627 (Accession XM_166402) is another VGAM1965 host target gene. LOC219627 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219627, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219627 BINDING SITE, designated SEQ ID:44275, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69173] Another function of VGAM1965 is therefore inhibition of LOC219627 (Accession XM_166402). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC219627. LOC219690 (Accession XM_167572) is another VGAM1965 host target gene. LOC219690 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219690, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219690 BINDING SITE, designated SEQ ID:44707, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69174] Another function of VGAM1965 is therefore inhibition of LOC219690 (Accession XM_167572). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219690. LOC219735 (Accession XM_167601) is another VGAM1965 host target gene. LOC219735 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219735, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219735 BINDING SITE, designated SEQ ID:44722, to

the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69175] Another function of VGAM1965 is therefore inhibition of LOC219735 (Accession XM_167601). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219735. LOC219920 (Accession XM_167787) is another VGAM1965 host target gene. LOC219920 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219920, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219920 BINDING SITE, designated SEQ ID:44813, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69176] Another function of VGAM1965 is therefore inhibition of LOC219920 (Accession XM_167787). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219920. LOC219942 (Accession XM_167790) is another VGAM1965 host target gene. LOC219942 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC219942, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219942 BINDING SITE, designated SEQ ID:44823, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69177] Another function of VGAM1965 is therefore inhibition of LOC219942 (Accession XM_167790). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219942. LOC220073 (Accession XM_167847) is another VGAM1965 host target gene. LOC220073 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220073, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220073 BINDING SITE, designated SEQ ID:44875, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69178] Another function of VGAM1965 is therefore inhibition of LOC220073 (Accession XM_167847). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220073. LOC220143 (Accession XM_168046) is another VGAM1965 host target gene. LOC220143 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220143, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220143 BINDING SITE, designated SEQ ID:44955, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69179] Another function of VGAM1965 is therefore inhibition of LOC220143 (Accession XM_168046). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220143. LOC220692 (Accession XM_165991) is another VGAM1965 host target gene. LOC220692 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220692, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC220692 BINDING SITE, designated SEQ ID:43832, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69180] Another function of VGAM1965 is therefore inhibition of LOC220692 (Accession XM_165991). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220692. LOC221002 (Accession XM_166156) is another VGAM1965 host target gene. LOC221002 BINDING SITE1 and LOC221002 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC221002, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221002 BINDING SITE1 and LOC221002 BINDING SITE2, designated SEQ ID:43974 and SEQ ID:43978 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69181] Another function of VGAM1965 is therefore inhibition of LOC221002 (Accession XM_166156). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC221002. LOC221178 (Accession XM_167936) is another VGAM1965 host target gene. LOC221178 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221178 BINDING SITE, designated SEQ ID:44930, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69182] Another function of VGAM1965 is therefore inhibition of LOC221178 (Accession XM_167936). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221178. LOC221288 (Accession XM_168058) is another VGAM1965 host target gene. LOC221288 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221288 BINDING SITE, designated SEQ ID:44971, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[69183] Another function of VGAM1965 is therefore inhibition of LOC221288 (Accession XM_168058). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221288. LOC221421 (Accession XM_166428) is another VGAM1965 host target gene. LOC221421 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221421, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221421 BINDING SITE, designated SEQ ID:44324, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69184] Another function of VGAM1965 is therefore inhibition of LOC221421 (Accession XM_166428). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221421. LOC221466 (Accession XM_168087) is another VGAM1965 host target gene. LOC221466 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221466, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221466 BINDING SITE, designated SEQ ID:44995, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69185] Another function of VGAM1965 is therefore inhibition of LOC221466 (Accession XM_168087). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221466. LOC221495 (Accession XM_168136) is another VGAM1965 host target gene. LOC221495 BINDING SITE1 through LOC221495 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC221495, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221495 BINDING SITE1 through LOC221495 BINDING SITE3, designated SEQ ID:45059, SEQ ID:45060 and SEQ ID:45061 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69186] Another function of VGAM1965 is therefore inhibition of

LOC221495 (Accession XM_168136). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221495. LOC221641 (Accession XM_168090) is another VGAM1965 host target gene. LOC221641 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221641, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221641 BINDING SITE, designated SEQ ID:45010, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69187] Another function of VGAM1965 is therefore inhibition of LOC221641 (Accession XM_168090). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221641. LOC221662 (Accession XM_166466) is another VGAM1965 host target gene. LOC221662 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221662, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC221662 BINDING SITE, designated SEQ ID:44389, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69188] Another function of VGAM1965 is therefore inhibition of LOC221662 (Accession XM_166466). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221662. LOC221712 (Accession XM_168059) is another VGAM1965 host target gene. LOC221712 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221712, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221712 BINDING SITE, designated SEQ ID:44974, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69189] Another function of VGAM1965 is therefore inhibition of LOC221712 (Accession XM_168059). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221712. LOC221760 (Accession XM_168105) is an-

other VGAM1965 host target gene. LOC221760 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221760, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221760 BINDING SITE, designated SEQ ID:45033, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69190] Another function of VGAM1965 is therefore inhibition of LOC221760 (Accession XM_168105). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221760. LOC221773 (Accession XM_165802) is another VGAM1965 host target gene. LOC221773 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221773, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221773 BINDING SITE, designated SEQ ID:43765, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69191] Another function of VGAM1965 is therefore inhibition of LOC221773 (Accession XM_165802). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221773. LOC221955 (Accession NM_139179) is another VGAM1965 host target gene. LOC221955 BINDING SITE1 and LOC221955 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC221955, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221955 BINDING SITE1 and LOC221955 BINDING SITE2, designated SEQ ID:29193 and SEQ ID:29194 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69192] Another function of VGAM1965 is therefore inhibition of LOC221955 (Accession NM_139179). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221955. LOC222128 (Accession XM_166560) is another VGAM1965 host target gene. LOC222128 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC222128, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222128 BINDING SITE, designated SEQ ID:44540, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69193] Another function of VGAM1965 is therefore inhibition of LOC222128 (Accession XM_166560). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222128. LOC222256 (Accession XM_168571) is another VGAM1965 host target gene. LOC222256 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222256, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222256 BINDING SITE, designated SEQ ID:45250, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69194] Another function of VGAM1965 is therefore inhibition of LOC222256 (Accession XM_168571). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222256. LOC222671 (Accession XM_167094) is another VGAM1965 host target gene. LOC222671 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222671, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222671 BINDING SITE, designated SEQ ID:44604, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69195] Another function of VGAM1965 is therefore inhibition of LOC222671 (Accession XM_167094). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222671. LOC253216 (Accession XM_170765) is another VGAM1965 host target gene. LOC253216 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253216, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC253216 BINDING SITE, designated SEQ ID:45522, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69196] Another function of VGAM1965 is therefore inhibition of LOC253216 (Accession XM_170765). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253216. LOC253264 (Accession XM_170639) is another VGAM1965 host target gene. LOC253264 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253264, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253264 BINDING SITE, designated SEQ ID:45418, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69197] Another function of VGAM1965 is therefore inhibition of LOC253264 (Accession XM_170639). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253264. LOC253612 (Accession XM_172985) is another VGAM1965 host target gene. LOC253612 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253612, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253612 BINDING SITE, designated SEQ ID:46257, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69198] Another function of VGAM1965 is therefore inhibition of LOC253612 (Accession XM_172985). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253612. LOC253758 (Accession XM_173067) is another VGAM1965 host target gene. LOC253758 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253758, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253758 BINDING SITE, designated SEQ ID:46320, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69199] Another function of VGAM1965 is therefore inhibition of

LOC253758 (Accession XM_173067). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253758. LOC253912 (Accession XM_173222) is another VGAM1965 host target gene. LOC253912 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253912, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253912 BINDING SITE, designated SEQ ID:46485, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69200] Another function of VGAM1965 is therefore inhibition of LOC253912 (Accession XM_173222). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253912. LOC253926 (Accession XM_170741) is another VGAM1965 host target gene. LOC253926 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253926, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC253926 BINDING SITE, designated SEQ ID:45500, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69201] Another function of VGAM1965 is therefore inhibition of LOC253926 (Accession XM_170741). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253926. LOC254015 (Accession XM_172977) is another VGAM1965 host target gene. LOC254015 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254015, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254015 BINDING SITE, designated SEQ ID:46247, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69202] Another function of VGAM1965 is therefore inhibition of LOC254015 (Accession XM_172977). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254015. LOC254143 (Accession XM_172880) is an-

other VGAM1965 host target gene. LOC254143 BINDING SITE1 and LOC254143 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC254143, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254143 BINDING SITE1 and LOC254143 BINDING SITE2, designated SEQ ID:46159 and SEQ ID:46160 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69203] Another function of VGAM1965 is therefore inhibition of LOC254143 (Accession XM_172880). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254143. LOC254266 (Accession XM_173221) is another VGAM1965 host target gene. LOC254266 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254266 BINDING SITE, designated SEQ ID:46482, to

the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69204] Another function of VGAM1965 is therefore inhibition of LOC254266 (Accession XM_173221). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254266. LOC254351 (Accession XM_170774) is another VGAM1965 host target gene. LOC254351 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254351, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254351 BINDING SITE, designated SEQ ID:45543, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69205] Another function of VGAM1965 is therefore inhibition of LOC254351 (Accession XM_170774). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254351. LOC254413 (Accession XM_173141) is another VGAM1965 host target gene. LOC254413 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC254413, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254413 BINDING SITE, designated SEQ ID:46405, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69206] Another function of VGAM1965 is therefore inhibition of LOC254413 (Accession XM_173141). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254413. LOC254719 (Accession XM_171166) is another VGAM1965 host target gene. LOC254719 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254719, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254719 BINDING SITE, designated SEQ ID:45952, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69207] Another function of VGAM1965 is therefore inhibition of LOC254719 (Accession XM_171166). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254719. LOC254896 (Accession XM_171201) is another VGAM1965 host target gene. LOC254896 BINDING SITE1 and LOC254896 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC254896, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254896 BINDING SITE1 and LOC254896 BINDING SITE2, designated SEQ ID:45988 and SEQ ID:45990 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69208] Another function of VGAM1965 is therefore inhibition of LOC254896 (Accession XM_171201). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254896. LOC255104 (Accession XM_170911) is another VGAM1965 host target gene. LOC255104 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255104, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255104 BINDING SITE, designated SEQ ID:45685, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69209] Another function of VGAM1965 is therefore inhibition of LOC255104 (Accession XM_170911). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255104. LOC255177 (Accession XM_172941) is another VGAM1965 host target gene. LOC255177 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255177, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255177 BINDING SITE, designated SEQ ID:46202, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69210] Another function of VGAM1965 is therefore inhibition of LOC255177 (Accession XM_172941). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC255177. LOC255252 (Accession XM_170779) is another VGAM1965 host target gene. LOC255252 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255252, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255252 BINDING SITE, designated SEQ ID:45548, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69211] Another function of VGAM1965 is therefore inhibition of LOC255252 (Accession XM_170779). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255252. LOC255320 (Accession XM_170777) is another VGAM1965 host target gene. LOC255320 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255320, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255320 BINDING SITE, designated SEQ ID:45544, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[69212] Another function of VGAM1965 is therefore inhibition of LOC255320 (Accession XM_170777). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255320. LOC255327 (Accession XM_171236) is another VGAM1965 host target gene. LOC255327 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255327, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255327 BINDING SITE, designated SEQ ID:46023, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69213] Another function of VGAM1965 is therefore inhibition of LOC255327 (Accession XM_171236). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255327. LOC255338 (Accession XM_171105) is another VGAM1965 host target gene. LOC255338 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255338, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255338 BINDING SITE, designated SEQ ID:45913, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69214] Another function of VGAM1965 is therefore inhibition of LOC255338 (Accession XM_171105). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255338. LOC255426 (Accession XM_173155) is another VGAM1965 host target gene. LOC255426 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255426 BINDING SITE, designated SEQ ID:46410, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69215] Another function of VGAM1965 is therefore inhibition of LOC255426 (Accession XM_173155). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC255426. LOC255533 (Accession XM_173073) is another VGAM1965 host target gene. LOC255533 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255533, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255533 BINDING SITE, designated SEQ ID:46332, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69216] Another function of VGAM1965 is therefore inhibition of LOC255533 (Accession XM_173073). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255533. LOC255975 (Accession XM_171083) is another VGAM1965 host target gene. LOC255975 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255975, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255975 BINDING SITE, designated SEQ ID:45892, to

the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69217] Another function of VGAM1965 is therefore inhibition of LOC255975 (Accession XM_171083). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255975. LOC256096 (Accession XM_173164) is another VGAM1965 host target gene. LOC256096 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256096, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256096 BINDING SITE, designated SEQ ID:46420, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69218] Another function of VGAM1965 is therefore inhibition of LOC256096 (Accession XM_173164). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256096. LOC256207 (Accession XM_170837) is another VGAM1965 host target gene. LOC256207 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC256207, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256207 BINDING SITE, designated SEQ ID:45622, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69219] Another function of VGAM1965 is therefore inhibition of LOC256207 (Accession XM_170837). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256207. LOC256337 (Accession XM_170643) is another VGAM1965 host target gene. LOC256337 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256337, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256337 BINDING SITE, designated SEQ ID:45420, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69220] Another function of VGAM1965 is therefore inhibition of LOC256337 (Accession XM_170643). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256337. LOC256867 (Accession XM_170694) is another VGAM1965 host target gene. LOC256867 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256867, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256867 BINDING SITE, designated SEQ ID:45477, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69221] Another function of VGAM1965 is therefore inhibition of LOC256867 (Accession XM_170694). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256867. LOC256905 (Accession XM_173031) is another VGAM1965 host target gene. LOC256905 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256905, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC256905 BINDING SITE, designated SEQ ID:46298, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69222] Another function of VGAM1965 is therefore inhibition of LOC256905 (Accession XM_173031). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256905. LOC257302 (Accession XM_171750) is another VGAM1965 host target gene. LOC257302 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257302, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257302 BINDING SITE, designated SEQ ID:46064, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69223] Another function of VGAM1965 is therefore inhibition of LOC257302 (Accession XM_171750). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257302. LOC257358 (Accession XM_173138) is another VGAM1965 host target gene. LOC257358 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257358, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257358 BINDING SITE, designated SEQ ID:46389, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69224] Another function of VGAM1965 is therefore inhibition of LOC257358 (Accession XM_173138). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257358. LOC257431 (Accession XM_088764) is another VGAM1965 host target gene. LOC257431 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257431, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257431 BINDING SITE, designated SEQ ID:39947, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69225] Another function of VGAM1965 is therefore inhibition of

LOC257431 (Accession XM_088764). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257431. LOC257464 (Accession XM_116972) is another VGAM1965 host target gene. LOC257464 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257464, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257464 BINDING SITE, designated SEQ ID:43167, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69226] Another function of VGAM1965 is therefore inhibition of LOC257464 (Accession XM_116972). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257464. LOC257476 (Accession XM_028610) is another VGAM1965 host target gene. LOC257476 BINDING SITE1 and LOC257476 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC257476, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257476 BINDING SITE1 and LOC257476 BINDING SITE2, designated SEQ ID:30716 and SEQ ID:30717 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69227] Another function of VGAM1965 is therefore inhibition of LOC257476 (Accession XM_028610). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257476. LOC257596 (Accession XM_175296) is another VGAM1965 host target gene. LOC257596 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257596, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257596 BINDING SITE, designated SEQ ID:46755, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69228] Another function of VGAM1965 is therefore inhibition of LOC257596 (Accession XM_175296). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC257596. LOC257601 (Accession XM_175231) is another VGAM1965 host target gene. LOC257601 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257601, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257601 BINDING SITE, designated SEQ ID:46697, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69229] Another function of VGAM1965 is therefore inhibition of LOC257601 (Accession XM_175231). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257601. LOC257615 (Accession XM_175293) is another VGAM1965 host target gene. LOC257615 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257615, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257615 BINDING SITE, designated SEQ ID:46744, to

the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69230] Another function of VGAM1965 is therefore inhibition of LOC257615 (Accession XM_175293). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257615. LOC51134 (Accession NM_016122) is another VGAM1965 host target gene. LOC51134 BINDING SITE1 and LOC51134 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC51134, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51134 BINDING SITE1 and LOC51134 BINDING SITE2, designated SEQ ID:18212 and SEQ ID:18211 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69231] Another function of VGAM1965 is therefore inhibition of LOC51134 (Accession NM_016122). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51134. LOC51301 (Accession NM_016591) is another

VGAM1965 host target gene. LOC51301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51301 BINDING SITE, designated SEQ ID:18672, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69232] Another function of VGAM1965 is therefore inhibition of LOC51301 (Accession NM_016591). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51301. LOC51308 (Accession NM_016606) is another VGAM1965 host target gene. LOC51308 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51308 BINDING SITE, designated SEQ ID:18709, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69233] Another function of VGAM1965 is therefore inhibition of LOC51308 (Accession NM_016606). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51308. LOC51580 (Accession NM_015874) is another VGAM1965 host target gene. LOC51580 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51580, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51580 BINDING SITE, designated SEQ ID:18016, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69234] Another function of VGAM1965 is therefore inhibition of LOC51580 (Accession NM_015874). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51580. LOC51696 (Accession NM_016217) is another VGAM1965 host target gene. LOC51696 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51696, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51696 BINDING SITE, designated SEQ ID:18316, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69235] Another function of VGAM1965 is therefore inhibition of LOC51696 (Accession NM_016217). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51696. LOC56920 (Accession NM_020163) is another VGAM1965 host target gene. LOC56920 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC56920, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56920 BINDING SITE, designated SEQ ID:21383, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69236] Another function of VGAM1965 is therefore inhibition of LOC56920 (Accession NM_020163). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC56920. LOC57805 (Accession NM_021174) is another VGAM1965 host target gene. LOC57805 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57805, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57805 BINDING SITE, designated SEQ ID:22150, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69237] Another function of VGAM1965 is therefore inhibition of LOC57805 (Accession NM_021174). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57805. LOC58525 (Accession XM_086045) is another VGAM1965 host target gene. LOC58525 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC58525, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC58525 BINDING SITE, designated SEQ ID:38460, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[69238] Another function of VGAM1965 is therefore inhibition of LOC58525 (Accession XM_086045). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC58525. LOC90019 (Accession NM_138567) is another VGAM1965 host target gene. LOC90019 BINDING SITE1 through LOC90019 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC90019, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90019 BINDING SITE1 through LOC90019 BINDING SITE3, designated SEQ ID:28874, SEQ ID:28875 and SEQ ID:28876 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69239] Another function of VGAM1965 is therefore inhibition of LOC90019 (Accession NM_138567). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90019. LOC90092 (Accession XM_028862) is another VGAM1965 host target gene. LOC90092 BINDING SITE1

and LOC90092 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC90092, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90092 BINDING SITE1 and LOC90092 BINDING SITE2, designated SEQ ID:30782 and SEQ ID:30793 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69240] Another function of VGAM1965 is therefore inhibition of LOC90092 (Accession XM_028862). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90092. LOC90246 (Accession XM_030283) is another VGAM1965 host target gene. LOC90246 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90246, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90246 BINDING SITE, designated SEQ ID:31003, to the nucleotide sequence of VGAM1965 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4676.

[69241] Another function of VGAM1965 is therefore inhibition of LOC90246 (Accession XM_030283). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90246. LOC90379 (Accession XM_031308) is another VGAM1965 host target gene. LOC90379 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90379, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90379 BINDING SITE, designated SEQ ID:31338, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69242] Another function of VGAM1965 is therefore inhibition of LOC90379 (Accession XM_031308). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90379. LOC90459 (Accession XM_031826) is another VGAM1965 host target gene. LOC90459 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90459, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90459 BINDING SITE, designated SEQ ID:31493, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69243] Another function of VGAM1965 is therefore inhibition of LOC90459 (Accession XM_031826). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90459. LOC90509 (Accession XM_032209) is another VGAM1965 host target gene. LOC90509 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90509, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90509 BINDING SITE, designated SEQ ID:31610, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69244] Another function of VGAM1965 is therefore inhibition of LOC90509 (Accession XM_032209). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC90509. LOC90529 (Accession XM_032350) is another VGAM1965 host target gene. LOC90529 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90529, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90529 BINDING SITE, designated SEQ ID:31639, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69245] Another function of VGAM1965 is therefore inhibition of LOC90529 (Accession XM_032350). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90529. LOC90538 (Accession XM_032401) is another VGAM1965 host target gene. LOC90538 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90538, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90538 BINDING SITE, designated SEQ ID:31660, to the

nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69246] Another function of VGAM1965 is therefore inhibition of LOC90538 (Accession XM_032401). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90538. LOC90670 (Accession XM_033352) is another VGAM1965 host target gene. LOC90670 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90670, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90670 BINDING SITE, designated SEQ ID:31884, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69247] Another function of VGAM1965 is therefore inhibition of LOC90670 (Accession XM_033352). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90670. LOC90750 (Accession XM_033868) is another VGAM1965 host target gene. LOC90750 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC90750, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90750 BINDING SITE, designated SEQ ID:31970, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69248] Another function of VGAM1965 is therefore inhibition of LOC90750 (Accession XM_033868). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90750. LOC90918 (Accession XM_034863) is another VGAM1965 host target gene. LOC90918 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90918, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90918 BINDING SITE, designated SEQ ID:32177, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69249] Another function of VGAM1965 is therefore inhibition of LOC90918 (Accession XM_034863). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90918. LOC91040 (Accession XM_035641) is another VGAM1965 host target gene. LOC91040 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91040 BINDING SITE, designated SEQ ID:32324, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69250] Another function of VGAM1965 is therefore inhibition of LOC91040 (Accession XM_035641). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91040. LOC91069 (Accession XM_035824) is another VGAM1965 host target gene. LOC91069 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91069, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC91069 BINDING SITE, designated SEQ ID:32347, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69251] Another function of VGAM1965 is therefore inhibition of LOC91069 (Accession XM_035824). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91069. LOC91149 (Accession XM_036480) is another VGAM1965 host target gene. LOC91149 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91149, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91149 BINDING SITE, designated SEQ ID:32459, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69252] Another function of VGAM1965 is therefore inhibition of LOC91149 (Accession XM_036480). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91149. LOC91408 (Accession XM_038290) is another VGAM1965 host target gene. LOC91408 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91408, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91408 BINDING SITE, designated SEQ ID:32793, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69253] Another function of VGAM1965 is therefore inhibition of LOC91408 (Accession XM_038290). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91408. LOC91445 (Accession XM_018516) is another VGAM1965 host target gene. LOC91445 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91445 BINDING SITE, designated SEQ ID:30373, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69254] Another function of VGAM1965 is therefore inhibition of

LOC91445 (Accession XM_018516). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91445. LOC91464 (Accession XM_038589) is another VGAM1965 host target gene. LOC91464 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91464, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91464 BINDING SITE, designated SEQ ID:32875, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69255] Another function of VGAM1965 is therefore inhibition of LOC91464 (Accession XM_038589). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91464. LOC91948 (Accession XM_041723) is another VGAM1965 host target gene. LOC91948 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91948, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC91948 BINDING SITE, designated SEQ ID:33576, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69256] Another function of VGAM1965 is therefore inhibition of LOC91948 (Accession XM_041723). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91948. LOC92078 (Accession XM_042684) is another VGAM1965 host target gene. LOC92078 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92078, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92078 BINDING SITE, designated SEQ ID:33748, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69257] Another function of VGAM1965 is therefore inhibition of LOC92078 (Accession XM_042684). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92078. LOC92140 (Accession XM_043070) is another

VGAM1965 host target gene. LOC92140 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92140 BINDING SITE, designated SEQ ID:33888, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69258] Another function of VGAM1965 is therefore inhibition of LOC92140 (Accession XM_043070). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92140. LOC92181 (Accession XM_043394) is another VGAM1965 host target gene. LOC92181 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92181, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92181 BINDING SITE, designated SEQ ID:33945, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69259] Another function of VGAM1965 is therefore inhibition of LOC92181 (Accession XM_043394). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92181. LOC92249 (Accession XM_043814) is another VGAM1965 host target gene. LOC92249 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92249, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92249 BINDING SITE, designated SEQ ID:34026, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69260] Another function of VGAM1965 is therefore inhibition of LOC92249 (Accession XM_043814). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92249. LOC92267 (Accession XM_043979) is another VGAM1965 host target gene. LOC92267 BINDING SITE1 and LOC92267 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC92267, corresponding to HOST TARGET binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92267 BINDING SITE1 and LOC92267 BINDING SITE2, designated SEQ ID:34056 and SEQ ID:34059 respectively, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69261] Another function of VGAM1965 is therefore inhibition of LOC92267 (Accession XM_043979). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92267. LOC92379 (Accession XM_044712) is another VGAM1965 host target gene. LOC92379 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92379, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92379 BINDING SITE, designated SEQ ID:34267, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69262] Another function of VGAM1965 is therefore inhibition of LOC92379 (Accession XM_044712). Accordingly, utilities

of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92379. LOC92661 (Accession XM_046465) is another VGAM1965 host target gene. LOC92661 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92661, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92661 BINDING SITE, designated SEQ ID:34723, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69263] Another function of VGAM1965 is therefore inhibition of LOC92661 (Accession XM_046465). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92661. LOC92771 (Accession NM_033424) is another VGAM1965 host target gene. LOC92771 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92771, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC92771 BINDING SITE, designated SEQ ID:27248, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69264] Another function of VGAM1965 is therefore inhibition of LOC92771 (Accession NM_033424). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92771. LOC93052 (Accession XM_048905) is another VGAM1965 host target gene. LOC93052 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93052, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93052 BINDING SITE, designated SEQ ID:35301, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69265] Another function of VGAM1965 is therefore inhibition of LOC93052 (Accession XM_048905). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93052. LOC93070 (Accession XM_049046) is another VGAM1965 host target gene. LOC93070 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93070, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93070 BINDING SITE, designated SEQ ID:35324, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69266] Another function of VGAM1965 is therefore inhibition of LOC93070 (Accession XM_049046). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93070. LOC93622 (Accession NM_138699) is another VGAM1965 host target gene. LOC93622 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93622, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93622 BINDING SITE, designated SEQ ID:28949, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69267] Another function of VGAM1965 is therefore inhibition of

LOC93622 (Accession NM_138699). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93622. LOC93624 (Accession XM_052624) is another VGAM1965 host target gene. LOC93624 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93624, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93624 BINDING SITE, designated SEQ ID:36015, to the nucleotide sequence of VGAM1965 RNA, herein designated VGAM RNA, also designated SEQ ID:4676.

[69268] Another function of VGAM1965 is therefore inhibition of LOC93624 (Accession XM_052624). Accordingly, utilities of VGAM1965 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93624. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1966 (VGAM1966) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[69269] VGAM1966 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1966 was detected is described hereinabove with reference to Figs. 1-8.

[69270] VGAM1966 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM1966 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69271] VGAM1966 gene encodes a VGAM1966 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1966 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1966 precursor RNA is designated SEQ ID:1952, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1952 is located at position 88719 relative to the genome of Rana Tigrina Ranavirus.

[69272] VGAM1966 precursor RNA folds onto itself, forming VGAM1966 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69273] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1966 folded precursor RNA into VGAM1966 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM1966 RNA is designated SEQ ID:4677, and is provided hereinbelow with reference to the sequence listing part.

[69274] VGAM1966 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1966 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1966 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69275] VGAM1966 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1966 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1966 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1966 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1966 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[69276] The complementary binding of VGAM1966 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1966 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1966 host target RNA into VGAM1966 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69277] It is appreciated that VGAM1966 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1966 host target genes. The mRNA of each one of this plurality of VGAM1966 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1966 RNA, herein designated VGAM RNA, and which when bound by VGAM1966 RNA causes inhibition of translation of respective one or more VGAM1966 host target proteins.

[69278] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1966 gene, herein designated VGAM GENE, on one

or more VGAM1966 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69279] It is yet further appreciated that a function of VGAM1966 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1966 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM1966 correlate with, and may be deduced from, the identity of the host target genes which VGAM1966 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69280] Nucleotide sequences of the VGAM1966 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1966 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1966 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1966 are further described hereinbelow with reference to Table 1.

[69281] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1966 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1966 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69282] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1966 gene, herein designated VGAM is inhibition of expression of VGAM1966 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1966 correlate with, and may be deduced from, the identity of the target genes which VGAM1966 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69283] Surfeit 6 (SURF6, Accession NM_006753) is a VGAM1966

host target gene. SURF6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SURF6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SURF6 BINDING SITE, designated SEQ ID:13608, to the nucleotide sequence of VGAM1966 RNA, herein designated VGAM RNA, also designated SEQ ID:4677.

[69284] A function of VGAM1966 is therefore inhibition of Surfeit 6 (SURF6, Accession NM_006753). Accordingly, utilities of VGAM1966 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SURF6. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1967 (VGAM1967) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69285] VGAM1967 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1967 was detected is described hereinabove with reference to Figs. 1-8.

[69286] VGAM1967 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM1967 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69287] VGAM1967 gene encodes a VGAM1967 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1967 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1967 precursor RNA is designated SEQ ID:1953, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1953 is located at position 96311 relative to the genome of Rana Tigrina Ranavirus.

[69288] VGAM1967 precursor RNA folds onto itself, forming VGAM1967 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[69289] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1967 folded precursor RNA into VGAM1967 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM1967 RNA is designated SEQ ID:4678, and is provided hereinbelow with reference to the sequence listing part.

[69290] VGAM1967 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1967 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1967 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69291] VGAM1967 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1967 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1967 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1967 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1967 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69292] The complementary binding of VGAM1967 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1967 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1967 host target RNA into VGAM1967 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69293] It is appreciated that VGAM1967 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1967 host target genes. The mRNA of each one of this plurality of VGAM1967 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1967 RNA, herein designated VGAM RNA, and which when bound by VGAM1967 RNA causes inhibition of translation of respective one or more VGAM1967 host target proteins.

[69294] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1967 gene, herein designated VGAM GENE, on one or more VGAM1967 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69295] It is yet further appreciated that a function of VGAM1967 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM1967 correlate with, and may be deduced from, the identity of the host target genes which VGAM1967 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69296] Nucleotide sequences of the VGAM1967 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1967 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1967 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1967 are further described hereinbelow with reference to Table 1.

[69297] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1967 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1967 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69298] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1967 gene, herein designated VGAM is inhibition of expression of VGAM1967 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1967 correlate with, and may be deduced from, the identity of the target genes which VGAM1967 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69299] Dual Oxidase 1 (DUOX1, Accession NM_017434) is a VGAM1967 host target gene. DUOX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DUOX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of DUOX1 BINDING SITE, designated SEQ ID:18888, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69300] A function of VGAM1967 is therefore inhibition of Dual Oxidase 1 (DUOX1, Accession NM_017434), a gene which is a component of the thyroid hydrogen peroxide generating system. Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUOX1. The function of DUOX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1188.Growth Differentiation Factor 2 (GDF2, Accession NM_016204) is another VGAM1967 host target gene. GDF2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GDF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GDF2 BINDING SITE, designated SEQ ID:18299, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69301] Another function of VGAM1967 is therefore inhibition of Growth Differentiation Factor 2 (GDF2, Accession NM_016204), a gene which could be involved in bone formation. Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GDF2. The function of GDF2 has been established by previous studies. Bone morphogenetic proteins (BMPs, e.g., BMP2; 112261) are members of the highly conserved transforming growth factor-beta (TGFB; OMIM Ref. No. 190180) superfamily. BMP signaling is important during development and growth, and BMPs and their type I (e.g., BMPR1A; 601299) and type II (e.g., BMPR2; 600799) receptors are expressed in numerous cell types. BMP ligands bring type I and type II receptors together, allowing the ser/thr kinase activity of the type II receptor to phosphorylate and activate the type I ser/thr kinase. The activated receptor then initiates intracellular signaling. By ribonuclease protection analysis, Miller et al. (2000) found that Bmp9, also called Gdf2, is expressed in adult rat predominantly in the Kupffer cells (KC), endothelial cells (EC), and stellate cells, but not the parenchymal cells, of liver, with little expression in other tissues. Western blot analysis showed that a 13-kD Bmp9 protein is

expressed in KC and liver EC. KC and liver EC bound Bmp9 but not other BMPs, suggesting that BMP9 acts in an autocrine and/or paracrine manner. Liver EC and KC also internalized labeled Bmp9 under physiologic conditions.

[69302] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69303] Lopez-Coviella, I.; Berse, B.; Krauss, R.; Thies, R. S.; Blusztajn, J. K. : Induction and maintenance of the neuronal cholinergic phenotype in the central nervous system by BMP-9. Science 289: 313-316, 2000. ; and

[69304] Miller, A. F.; Harvey, S. A. K.; Thies, R. S.; Olson, M. S. : Bone morphogenetic protein-9: an autocrine/paracrine cytokine in the liver. J. Biol. Chem. 275: 17937-17945, 2000.

[69305] Further studies establishing the function and utilities of GDF2 are found in John Hopkins OMIM database record ID 605120, and in sited publications numbered 696 and 7080-7081 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Jun B Proto-oncogene (JUNB, Accession NM_002229) is another VGAM1967 host target gene. JUNB BINDING SITE is HOST TARGET binding site found in the 5` untranslated region

of mRNA encoded by JUNB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JUNB BINDING SITE, designated SEQ ID:8011, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69306] Another function of VGAM1967 is therefore inhibition of Jun B Proto-oncogene (JUNB, Accession NM_002229), a gene which may be a key transcriptional regulator of myelopoiesis. Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JUNB. The function of JUNB has been established by previous studies. Jacobs-Helber et al. (2002) studied the role of JUNB in erythroid differentiation in an erythropoietin (EPO; 133170)-dependent cell line and in primary mouse and human erythroid cells. They identified an initial EPO-dependent induction of JUNB expression that was insufficient to induce differentiation. A second EPO-independent peak of JUNB expression was associated with erythroid cell differentiation as measured by increased expression of erythroid-specific proteins. Mathas et al. (2002) found AP1 constitutively activated,

with robust JUN (OMIM Ref. No. 165160) and JUNB overexpression, in all cell lines derived from patients with classical Hodgkin lymphoma (OMIM Ref. No. 236000) and anaplastic large cell lymphoma (ALCL), but not in other lymphoma types. AP1 supported proliferation of Hodgkin cells, but suppressed apoptosis of ALCL cells. Mathas et al. (2002) noted that, whereas JUN is upregulated by an autoregulatory process, JUNB is under the control of nuclear factor kappa-B (NFKB; 164011). They found that AP1 and NFKB cooperate and stimulate expression of the cell cycle regulator cyclin D2 (OMIM Ref. No. 123833), the protooncogene MET (OMIM Ref. No. 164860), and the lymphocyte homing receptor CCR7 (OMIM Ref. No. 600242), which are all strongly expressed in primary Hodgkin/Reed-Sternberg (HRS) cells Jacobs-Helber et al. (2002) studied the role of JUNB in erythroid differentiation in an erythropoietin (EPO; 133170)-dependent cell line and in primary mouse and human erythroid cells. They identified an initial EPO-dependent induction of JUNB expression that was insufficient to induce differentiation. A second EPO-independent peak of JUNB expression was associated with erythroid cell differentiation as measured by increased expression of erythroid-specific proteins.

Mathas et al. (2002) found AP1 constitutively activated, with robust JUN (OMIM Ref. No. 165160) and JUNB overexpression, in all cell lines derived from patients with classical Hodgkin lymphoma (OMIM Ref. No. 236000) and anaplastic large cell lymphoma (ALCL), but not in other lymphoma types. AP1 supported proliferation of Hodgkin cells, but suppressed apoptosis of ALCL cells. Mathas et al. (2002) noted that, whereas JUN is upregulated by an autoregulatory process, JUNB is under the control of nuclear factor kappa-B (NFKB; 164011). They found that AP1 and NFKB cooperate and stimulate expression of the cell cycle regulator cyclin D2 (OMIM Ref. No. 123833), the protooncogene MET (OMIM Ref. No. 164860), and the lymphocyte homing receptor CCR7 (OMIM Ref. No. 600242), which are all strongly expressed in primary Hodgkin/Reed-Sternberg (HRS) cells Animal model experiments lend further support to the function of JUNB. The JUN and JUNB components of the AP1 transcription factor are known to have antagonistic functions. Passegue et al. (2002) showed, by a knockin strategy and a transgenic complementation approach, that JunB can substitute for absence of Jun during mouse development. JunB can rescue both liver and cardiac defects in Jun-null mice in a

manner dependent on gene dosage. JunB restores the expression of genes regulated by Jun/Fos (OMIM Ref. No. 164810), but not those regulated by Jun/ATF (ATF1; 123803), thereby rescuing Jun-dependent defects in vivo as well as in primary fibroblasts and fetal hepatoblasts in vitro. Thus, the transcriptionally less active JunB has the potential to substitute for Jun, indicating that the spatial and temporal regulation of expression of the transcription factor AP1 may be more important than the coding sequence of its components.

[69307] It is appreciated that the abovementioned animal model for JUNB is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[69308] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69309] Passegue, E.; Jochum, W.; Behrens, A.; Ricci, R.; Wagner, E. F. : JunB can substitute for Jun in mouse development and cell proliferation. Nature Genet. 30: 158-166, 2002. ; and

[69310] Jacobs-Helber, S. M.; Abutin, R. M.; Tian, C.; Bondurant, M.; Wickrema, A.; Sawyer, S. T. : Role of JunB in erythroid differentiation. J. Biol. Chem. 277: 4859-4866, 2002.

[69311] Further studies establishing the function and utilities of JUNB are found in John Hopkins OMIM database record ID 165161, and in sited publications numbered 5122-512 and 4710 listed in the bibliography section hereinbelow, which are also hereby incorporated by refer-ence.Palmitoyl-protein Thioesterase 2 (PPT2, Accession NM_138934) is another VGAM1967 host target gene. PPT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPT2, corre-sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-trates the complementarity of the nucleotide sequences of PPT2 BINDING SITE, designated SEQ ID:29062, to the nu-cleotide sequence of VGAM1967 RNA, herein designated

VGAM RNA, also designated SEQ ID:4678.

[69312] Another function of VGAM1967 is therefore inhibition of Palmitoyl-protein Thioesterase 2 (PPT2, Accession NM_138934), a gene which is a palmitoyl-protein thioesterase 2 which possesses a different substrate specificity than PPT1. Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPT2. The function of PPT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM120.Ribonucleotide Reductase M2 Polypeptide (RRM2, Accession NM_001034) is another VGAM1967 host target gene. RRM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RRM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RRM2 BINDING SITE, designated SEQ ID:6698, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69313] Another function of VGAM1967 is therefore inhibition of

Ribonucleotide Reductase M2 Polypeptide (RRM2, Accession NM_001034). Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RRM2. DKFZP434I2117 (Accession NM_031478) is another VGAM1967 host target gene. DKFZP434I2117 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434I2117, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434I2117 BINDING SITE, designated SEQ ID:25556, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69314] Another function of VGAM1967 is therefore inhibition of DKFZP434I2117 (Accession NM_031478). Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434I2117. DKFZp564A176 (Accession NM_032242) is another VGAM1967 host target gene. DKFZp564A176 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp564A176, corresponding to a HOST TARGET bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp564A176 BINDING SITE, designated SEQ ID:25979, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69315] Another function of VGAM1967 is therefore inhibition of DKFZp564A176 (Accession NM_032242). Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp564A176. GNB4 (Accession NM_021629) is another VGAM1967 host target gene. GNB4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GNB4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNB4 BINDING SITE, designated SEQ ID:22270, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69316] Another function of VGAM1967 is therefore inhibition of GNB4 (Accession NM_021629). Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with GNB4. KIAA0323 (Accession XM_032634) is another VGAM1967 host target gene. KIAA0323 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0323 BINDING SITE, designated SEQ ID:31692, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69317] Another function of VGAM1967 is therefore inhibition of KIAA0323 (Accession XM_032634). Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0323. SARM (Accession NM_015077) is another VGAM1967 host target gene. SARM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SARM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SARM BINDING SITE, designated SEQ ID:17456, to the nucleotide sequence of

VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69318] Another function of VGAM1967 is therefore inhibition of SARM (Accession NM_015077). Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SARM. LOC149345 (Accession XM_086502) is another VGAM1967 host target gene. LOC149345 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149345, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149345 BINDING SITE, designated SEQ ID:38715, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69319] Another function of VGAM1967 is therefore inhibition of LOC149345 (Accession XM_086502). Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149345. LOC152275 (Accession XM_098186) is another VGAM1967 host target gene. LOC152275 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC152275, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152275 BINDING SITE, designated SEQ ID:41457, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69320] Another function of VGAM1967 is therefore inhibition of LOC152275 (Accession XM_098186). Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152275. LOC152286 (Accession XM_098188) is another VGAM1967 host target gene. LOC152286 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152286, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152286 BINDING SITE, designated SEQ ID:41463, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69321] Another function of VGAM1967 is therefore inhibition of LOC152286 (Accession XM_098188). Accordingly, utilities

of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152286. LOC160646 (Accession XM_090413) is another VGAM1967 host target gene. LOC160646 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC160646, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC160646 BINDING SITE, designated SEQ ID:40004, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69322] Another function of VGAM1967 is therefore inhibition of LOC160646 (Accession XM_090413). Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC160646. LOC84548 (Accession XM_048904) is another VGAM1967 host target gene. LOC84548 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC84548, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC84548 BINDING SITE, designated SEQ ID:35297, to the nucleotide sequence of VGAM1967 RNA, herein designated VGAM RNA, also designated SEQ ID:4678.

[69323] Another function of VGAM1967 is therefore inhibition of LOC84548 (Accession XM_048904). Accordingly, utilities of VGAM1967 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC84548. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1968 (VGAM1968) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69324] VGAM1968 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1968 was detected is described hereinabove with reference to Figs. 1-8.

[69325] VGAM1968 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM1968 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69326] VGAM1968 gene encodes a VGAM1968 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1968 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1968 precursor RNA is designated SEQ ID:1954, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1954 is located at position 97726 relative to the genome of Rana Tigrina Ranavirus.

[69327] VGAM1968 precursor RNA folds onto itself, forming VGAM1968 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69328] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1968 folded precursor RNA into VGAM1968 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1968 RNA is designated SEQ ID:4679, and is provided hereinbelow with reference to the sequence listing part.

[69329] VGAM1968 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1968 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1968 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69330] VGAM1968 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1968 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1968 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1968 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1968 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69331] The complementary binding of VGAM1968 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1968 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1968 host target RNA into VGAM1968 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69332] It is appreciated that VGAM1968 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1968 host target genes. The mRNA of each one of this plurality of VGAM1968 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1968 RNA, herein designated VGAM RNA, and which when bound by VGAM1968 RNA causes inhibition of translation of respective one or more VGAM1968 host target proteins.

[69333] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1968 gene, herein designated VGAM GENE, on one or more VGAM1968 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69334] It is yet further appreciated that a function of VGAM1968 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM1968 correlate with, and may be deduced from, the identity of the host target genes which VGAM1968 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69335] Nucleotide sequences of the VGAM1968 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1968 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1968 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1968 are further described hereinbelow with reference to Table 1.

[69336] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1968 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM1968 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69337] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1968 gene, herein designated VGAM is inhibition of expression of VGAM1968 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1968 correlate with, and may be deduced from, the identity of the target genes which VGAM1968 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69338] Adaptor-related Protein Complex 1, Gamma 1 Subunit (AP1G1, Accession NM_001128) is a VGAM1968 host target gene. AP1G1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP1G1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP1G1 BINDING SITE, designated SEQ ID:6801, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69339] A function of VGAM1968 is therefore inhibition of Adaptor-related Protein Complex 1, Gamma 1 Subunit (AP1G1, Accession NM_001128), a gene which promotes the formation of clathrin-coated pits and vesicles. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1G1. The function of AP1G1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM316.ASIC4 (Accession NM_018674) is another VGAM1968 host target gene. ASIC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ASIC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ASIC4 BINDING SITE, designated SEQ ID:20748, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69340] Another function of VGAM1968 is therefore inhibition of ASIC4 (Accession NM_018674), a gene which is a proton-gated, amiloride-sensitive sodium channel. Accordingly, utilities of VGAM1968 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with ASIC4. The function of ASIC4 has been established by previous studies. Grunder et al. (2000) isolated a cDNA corresponding to the human ASIC4 gene from a pituitary gland-specific cDNA library. Human ASIC4 protein shares 97% identity with its rat homolog. Dot-blot analysis and abundance of ASIC4 cDNAs in the pituitary cDNA library indicated strong expression in pituitary gland. By RT-PCR, Grunder et al. (2000) demonstrated expression in vestibular system and very faint expression in organ of Corti. ASIC4 could not be activated by a drop in extracellular pH in Xenopus oocytes, suggesting association with other subunits or activation by a ligand other than protons As the ASIC4 gene mapped in close proximity to the locus for paroxysmal dystonic choreoathetosis (PDC; 118800) on chromosome 2q, Grunder et al. (2001) sequenced the entire coding region and adjacent intronic sequences in an affected member of a large PDC family in which the disorder had been shown to be linked to the PDC locus on chromosome 2. Although 3 amino acid substitution polymorphisms were identified, none was disease-specific.

[69341] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[69342] Grunder, S.; Geisler, H.-S.; Rainer, S.; Fink, J. K. : Acid-sensing ion channel (ASIC) 4 gene: physical mapping, genomic organisation, and evaluation as a candidate for paroxysmal dystonia. Europ. J. Hum. Genet. 9: 672-676, 2001. ; and

[69343] Grunder, S.; Geissler, H.-S.; Bassler, E.-L.; Ruppersberg, J. P. : A new member of acid-sensing ion channels from pituitary gland. Neuroreport 11: 1607-1611, 2000.

[69344] Further studies establishing the function and utilities of ASIC4 are found in John Hopkins OMIM database record ID 606715, and in sited publications numbered 11920 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.ATPase, Cu++ Transporting, Beta Polypeptide (Wilson disease) (ATP7B, Accession NM_000053) is another VGAM1968 host target gene. ATP7B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP7B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP7B BINDING SITE, designated SEQ ID:5505, to the nucleotide sequence of VGAM1968 RNA, herein

designated VGAM RNA, also designated SEQ ID:4679.

[69345] Another function of VGAM1968 is therefore inhibition of ATPase, Cu++ Transporting, Beta Polypeptide (Wilson disease) (ATP7B, Accession NM_000053). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7B. B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6, Accession NM_001706) is another VGAM1968 host target gene. BCL6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BCL6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL6 BINDING SITE, designated SEQ ID:7432, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69346] Another function of VGAM1968 is therefore inhibition of B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6, Accession NM_001706), a gene which is involved in the generation and maintenance of both T and B cells during immune responses. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with BCL6. The function of BCL6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM481.BLAME (Accession NM_020125) is another VGAM1968 host target gene. BLAME BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BLAME, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BLAME BINDING SITE, designated SEQ ID:21310, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69347] Another function of VGAM1968 is therefore inhibition of BLAME (Accession NM_020125). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BLAME. Breast Cancer 1, Early Onset (BRCA1, Accession NM_007301) is another VGAM1968 host target gene. BRCA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BRCA1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRCA1 BINDING SITE, designated SEQ ID:14203, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69348] Another function of VGAM1968 is therefore inhibition of Breast Cancer 1, Early Onset (BRCA1, Accession NM_007301). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRCA1. Bassoon (presynaptic cytomatrix protein) (BSN, Accession NM_003458) is another VGAM1968 host target gene. BSN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BSN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BSN BINDING SITE, designated SEQ ID:9518, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69349] Another function of VGAM1968 is therefore inhibition of Bassoon (presynaptic cytomatrix protein) (BSN, Accession

NM_003458), a gene which may be involved in cytomatrix organization at the site of neurotransmitter release. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BSN. The function of BSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM638.BUB3 Budding Uninhibited By Benzimidazoles 3 Homolog (yeast) (BUB3, Accession NM_004725) is another VGAM1968 host target gene. BUB3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BUB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BUB3 BINDING SITE, designated SEQ ID:11095, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69350] Another function of VGAM1968 is therefore inhibition of BUB3 Budding Uninhibited By Benzimidazoles 3 Homolog (yeast) (BUB3, Accession NM_004725), a gene which has a role in the mitotic spindle checkpoint. Accordingly, utilities of VGAM1968 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with BUB3. The function of BUB3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1361.Cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1, Accession NM_053056) is another VGAM1968 host target gene. CCND1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CCND1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCND1 BINDING SITE, designated SEQ ID:27599, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69351] Another function of VGAM1968 is therefore inhibition of Cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1, Accession NM_053056), a gene which is involved in the control of cell cycle and is required for Schwann cell proliferation to proceed normally during Wallerian degeneration. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCND1. The function of CCND1

and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM220.CIAO1 (Accession NM_004804) is another VGAM1968 host target gene. CIAO1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CIAO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CIAO1 BINDING SITE, designated SEQ ID:11226, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69352] Another function of VGAM1968 is therefore inhibition of CIAO1 (Accession NM_004804), a gene which interacts in regulating cell cycle progression and apoptosis. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIAO1. The function of CIAO1 has been established by previous studies. The Wilms tumor gene (WT1; 607102) on 11p13 is involved in regulating cell cycle progression and apoptosis. In an attempt to dissect the molecular mechanisms of transcriptional activation and

repression by WT1, and to identify other proteins that may be involved in kidney and hematopoietic cell tumorigenesis, several groups have studied WT1-interacting proteins. WT1 binds in vivo and in vitro to p53 (OMIM Ref. No. 191170), resulting in WT1 functioning as a transcriptional repressor. Mutations in p53 increase the aggressiveness of Wilms tumors, resulting in poorer patient prognosis, but are not thought to be a primary genetic cause of Wilms tumor formation. WT1 also interacts with and regulates the transcriptional activity of steroidogenic factor-1 (OMIM Ref. No. 184757), a key molecule in gonadal development. Johnstone et al. (1996) identified a protein called PAWR (OMIM Ref. No. 601936), the gene for which maps to 12q21, that is capable of modulating the transcriptional activities of WT1. Johnstone et al. (1998) identified a second protein, which they named CIAO1 after the Chinese word for "bridge," that is also capable of modulating the transcriptional activities of WT1. CIAO1 is a 339-amino acid polypeptide containing 7 WD40 or beta-transducin repeats. It can inhibit the transcriptional activation function of WT1, but does not affect WT1-mediated transcriptional repression. Johnstone et al. (1998) demonstrated that the yeast Ciao1 homolog is an essential pro-

tein that appears to be highly evolutionarily conserved. Johnstone et al. (1999) described the structural organization of the CIAO1 gene, with the intron/exon boundaries closely matching the consensus 5-prime donor/3-prime acceptor splice site sequences. By FISH and radiation hybrid analysis, Johnstone et al. (1999) mapped the CIAO1 gene to the pericentric region of chromosome 2. They stated that the probable location is 2q11.2 based on the gene's inclusion within a previously mapped BAC clone (GenBank AC004020).

[69353] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69354] Johnstone, R. W.; See, R. H.; Sells, S. F.; Wang, J.; Muthukkumar, S.; Englert, C.; Haber, D. A.; Licht, J. D.; Sugrue, S. P.; Roberts, T.; Rangnekar, V. M.; Shi, Y. : A novel repressor, par-4, modulates transcription and growth suppression functions of the Wilms' tumor suppressor WT1. Molec. Cell. Biol. 16: 6945-6956, 1996. ; and

[69355] Johnstone, R. W.; Tommerup, N.; Hansen, C.; Vissing, H.; Shi, Y. : Structural organization, tissue expression, and chromosomal localization of Ciao 1, a functional modula-

tor of the Wilm.

[69356] Further studies establishing the function and utilities of CIAO1 are found in John Hopkins OMIM database record ID 604333, and in sited publications numbered 93 and 4985-4986 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Coronin, Actin Binding Protein, 1C (CORO1C, Accession NM_014325) is another VGAM1968 host target gene. CORO1C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CORO1C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CORO1C BINDING SITE, designated SEQ ID:15630, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69357] Another function of VGAM1968 is therefore inhibition of Coronin, Actin Binding Protein, 1C (CORO1C, Accession NM_014325). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CORO1C. Carboxypeptidase D (CPD, Accession NM_001304) is another VGAM1968

host target gene. CPD BINDING SITE1 and CPD BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CPD, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPD BINDING SITE1 and CPD BINDING SITE2, designated SEQ ID:6984 and SEQ ID:6985 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69358] Another function of VGAM1968 is therefore inhibition of Carboxypeptidase D (CPD, Accession NM_001304), a gene which is a membrane-bound metalloprotease. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPD. The function of CPD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM596.D1S155E (Accession NM_007158) is another VGAM1968 host target gene. D1S155E BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by D1S155E, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of D1S155E BINDING SITE, designated SEQ ID:14005, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69359] Another function of VGAM1968 is therefore inhibition of D1S155E (Accession NM_007158), a gene which regulates development of the testis. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with D1S155E. The function of D1S155E has been established by previous studies. While investigating NRAS (OMIM Ref. No. 164790), Jeffers et al. (1990) isolated cDNAs that originated from a closely linked upstream gene on chromosome 1. RNase protection assays showed that this gene, termed UNR by them, is transcribed in the same direction as NRAS and that its 3-prime end is located only 130 bp from the transcription initiation site of NRAS. The close spatial relationship was conserved in all species from which the NRAS gene had been isolated. The UNR cDNA contained an open reading frame capable of encoding a protein of 798 amino acids. Neither the primary pro-

tein structure nor the nucleic acid sequence of UNR was homologous to any known gene, including NRAS. UNR transcripts were detected in mouse, rat, and human cells. Only a single copy of UNR was detected in the mouse. The gene produced multiple transcripts that differed in their 3-prime ends and apparently resulted from the differential use of multiple polyadenylation sites located in the 3-prime untranslated region of the gene. Both UNR and NRAS were expressed in all tissues examined and the 2 genes may be coordinately regulated. UNR was first isolated by Doniger and DiPaolo (1988) in tumorigenic guinea pig cells. They designated the gene UNR (for 'upstream of NRAS'). (This should not be confused with the gene encoding ubiquitously expressed nuclear receptor (UNR; 600380) on chromosome 19.)

[69360] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69361] Doniger, J.; DiPaolo, J. A. : Coordinate N-RAS mRNA up-regulation with mutational activation in tumorigenic guinea pig cells. Nucleic Acids Res. 16: 969-980, 1988. ; and

[69362] Jeffers, M.; Paciucci, R.; Pellicer, A. : Characterization of

UNR: a gene closely linked to N-RAS. Nucleic Acids Res. 18: 4891-4899, 1990.

[69363] Further studies establishing the function and utilities of D1S155E are found in John Hopkins OMIM database record ID 191510, and in sited publications numbered 12356-12357 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Development and Differentiation Enhancing Factor 2 (DDEF2, Accession NM_003887) is another VGAM1968 host target gene. DDEF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DDEF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDEF2 BINDING SITE, designated SEQ ID:9967, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69364] Another function of VGAM1968 is therefore inhibition of Development and Differentiation Enhancing Factor 2 (DDEF2, Accession NM_003887), a gene which interacts with members of the Arf and Src family. Accordingly, utilities of VGAM1968 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DDEF2. The function of DDEF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM464.DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 3 (DDX3, Accession NM_001356) is another VGAM1968 host target gene. DDX3 BINDING SITE1 through DDX3 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DDX3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDX3 BINDING SITE1 through DDX3 BINDING SITE3, designated SEQ ID:7035, SEQ ID:7036 and SEQ ID:23432 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69365] Another function of VGAM1968 is therefore inhibition of DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 3 (DDX3, Accession NM_001356), a gene which interacts with hepatitis c virus core protein resulting a change in intracellular location. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with DDX3. The function of DDX3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM232.DnaJ (Hsp40) Homolog, Subfmaily B, Member 1 (DNAJB1, Accession NM_006145) is another VGAM1968 host target gene. DNAJB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DNAJB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNAJB1 BINDING SITE, designated SEQ ID:12789, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69366] Another function of VGAM1968 is therefore inhibition of DnaJ (Hsp40) Homolog, Subfmaily B, Member 1 (DNAJB1, Accession NM_006145), a gene which may prevent aggregation of newly translated proteins. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAJB1. The function of DNAJB1 and its association with various diseases and clinical conditions, has been estab-

lished by previous studies, as described hereinabove with reference to VGAM1778.Deoxyribonuclease I (DNASE1, Accession NM_005223) is another VGAM1968 host target gene. DNASE1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DNASE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNASE1 BINDING SITE, designated SEQ ID:11715, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69367] Another function of VGAM1968 is therefore inhibition of Deoxyribonuclease I (DNASE1, Accession NM_005223), a gene which seems to be involved in cell death. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNASE1. The function of DNASE1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM492.Ephrin-B1 (EFNB1, Accession NM_004429) is another VGAM1968 host target gene. EFNB1 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by EFNB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFNB1 BINDING SITE, designated SEQ ID:10712, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69368] Another function of VGAM1968 is therefore inhibition of Ephrin-B1 (EFNB1, Accession NM_004429), a gene which is a transmembrane ligand of Eph-related receptor tyrosine kinases, has a role in cell adhesion. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFNB1. The function of EFNB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM390.V-erb-b2 Erythroblastic Leukemia Viral Oncogene Homolog 2, Neuro/glioblastoma Derived Oncogene Homolog (avian) (ERBB2, Accession NM_004448) is another VGAM1968 host target gene. ERBB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERBB2,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERBB2 BINDING SITE, designated SEQ ID:10746, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69369] Another function of VGAM1968 is therefore inhibition of V-erb-b2 Erythroblastic Leukemia Viral Oncogene Homolog 2, Neuro/glioblastoma Derived Oncogene Homolog (avian) (ERBB2, Accession NM_004448), a gene which Tyrosine kinase receptor. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERBB2. The function of ERBB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1366.Fucosyltransferase 5 (alpha (1,3) Fucosyltransferase) (FUT5, Accession NM_002034) is another VGAM1968 host target gene. FUT5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FUT5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FUT5 BINDING SITE, designated SEQ ID:7789, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69370] Another function of VGAM1968 is therefore inhibition of Fucosyltransferase 5 (alpha (1,3) Fucosyltransferase) (FUT5, Accession NM_002034), a gene which may catalyse alpha-1,3 glycosidic linkages involved in the expression of vim-2, lewis x/ssea-1 and sialyl lewis x antigens. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUT5. The function of FUT5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1519.Growth Arrest-specific 7 (GAS7, Accession NM_003644) is another VGAM1968 host target gene. GAS7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GAS7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAS7 BINDING SITE,

designated SEQ ID:9715, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69371] Another function of VGAM1968 is therefore inhibition of Growth Arrest-specific 7 (GAS7, Accession NM_003644), a gene which may play a role in promoting maturation and morphological differentiation of cerebellar neurons. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAS7. The function of GAS7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM232.G1 to S Phase Transition 1 (GSPT1, Accession NM_002094) is another VGAM1968 host target gene. GSPT1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GSPT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GSPT1 BINDING SITE, designated SEQ ID:7883, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69372] Another function of VGAM1968 is therefore inhibition of G1 to S Phase Transition 1 (GSPT1, Accession NM_002094), a gene which involves in regulation of mammalian cell growth. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSPT1. The function of GSPT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1707.Glutathione S-transferase M5 (GSTM5, Accession NM_000851) is another VGAM1968 host target gene. GSTM5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GSTM5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GSTM5 BINDING SITE, designated SEQ ID:6520, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69373] Another function of VGAM1968 is therefore inhibition of Glutathione S-transferase M5 (GSTM5, Accession NM_000851), a gene which conjugates reduced glu-

tathione to a wide number of exogenous and endogenous hydrophobic electrophiles. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GSTM5. The function of GSTM5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1957.H3 Histone, Family 3B (H3.3B) (H3F3B, Accession NM_005324) is another VGAM1968 host target gene. H3F3B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by H3F3B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H3F3B BINDING SITE, designated SEQ ID:11795, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69374] Another function of VGAM1968 is therefore inhibition of H3 Histone, Family 3B (H3.3B) (H3F3B, Accession NM_005324). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H3F3B. High Mobility Group

AT-hook 2 (HMGA2, Accession NM_003483) is another VGAM1968 host target gene. HMGA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HMGA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMGA2 BINDING SITE, designated SEQ ID:9568, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69375] Another function of VGAM1968 is therefore inhibition of High Mobility Group AT-hook 2 (HMGA2, Accession NM_003483), a gene which may affect transcription and cell differentiation; shares common DNA-binding motif with other HMG HMG I/Y family members. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMGA2. The function of HMGA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM552.Hairless Homolog (mouse) (HR, Accession NM_005144) is another VGAM1968 host target gene. HR BINDING SITE is HOST TARGET binding

site found in the 5` untranslated region of mRNA encoded by HR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HR BINDING SITE, designated SEQ ID:11616, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69376] Another function of VGAM1968 is therefore inhibition of Hairless Homolog (mouse) (HR, Accession NM_005144). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HR. Heparan Sulfate 2-O-sulfotransferase 1 (HS2ST1, Accession NM_012262) is another VGAM1968 host target gene. HS2ST1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HS2ST1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HS2ST1 BINDING SITE, designated SEQ ID:14573, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69377] Another function of VGAM1968 is therefore inhibition of

Heparan Sulfate 2-O-sulfotransferase 1 (HS2ST1, Accession NM_012262). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HS2ST1. Potassium Inwardly-rectifying Channel, Subfamily J, Member 15 (KCNJ15, Accession NM_002243) is another VGAM1968 host target gene. KCNJ15 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCNJ15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNJ15 BINDING SITE, designated SEQ ID:8029, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69378] Another function of VGAM1968 is therefore inhibition of Potassium Inwardly-rectifying Channel, Subfamily J, Member 15 (KCNJ15, Accession NM_002243). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ15. Kinesin Heavy Chain Member 2 (KIF2, Accession NM_004520) is another VGAM1968 host target gene. KIF2 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by KIF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIF2 BINDING SITE, designated SEQ ID:10848, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69379] Another function of VGAM1968 is therefore inhibition of Kinesin Heavy Chain Member 2 (KIF2, Accession NM_004520). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF2. Leukocyte Tyrosine Kinase (LTK, Accession NM_002344) is another VGAM1968 host target gene. LTK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LTK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LTK BINDING SITE, designated SEQ ID:8143, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69380] Another function of VGAM1968 is therefore inhibition of

Leukocyte Tyrosine Kinase (LTK, Accession NM_002344), a gene which is probably a receptor with a tyrosine-protein kinase activity. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LTK. The function of LTK has been established by previous studies. Ben-Neriah and Bauskin (1988) isolated and characterized the complementary DNA for the mouse leukocyte tyrosine kinase locus. They used the insulin receptor-related avian sarcoma oncogene v-ros (OMIM Ref. No. 165020) as a probe to isolate the cDNA from a mouse pre-B lymphocyte cDNA library. Northern analysis revealed expression of the gene in thymus, spleen, and kidney. Sequence analysis of the gene revealed similarities with several tyrosine kinase receptor genes of the insulin receptor family. The LTK gene, however, is unique in that it encodes a transmembrane protein that lacks an extracellular domain. The authors suggested that LTK may encode a signal transduction subunit for one or more of the hematopoietic receptors. Krolewski et al. (1990) mapped TYK1 to human chromosome 15 by Southern analysis of somatic cell hybrid DNAs. Richard et al. (1994) mapped many loci on chromosome 15, which they subdivided into 5 regions. By PCR,

they concluded that the LTK gene is located in their region III: 15q15.1-q21.1. Liao et al. (1996) found that the mouse Ltk gene is closely linked to the Tyro3 gene (OMIM Ref. No. 600341) which maps to mouse chromosome 2. Toyoshima et al. (1993) cloned a set of cDNAs representing differently spliced human LTK mRNAs. These cDNAs predicted a truncated receptor protein that lacks the tyrosine kinase domain and a soluble receptor protein that has neither a transmembrane nor a tyrosine kinase domain. A cDNA clone containing the complete open reading frame demonstrated that the extracellular domain of the receptor protein is larger than previously predicted. Thus, the LTK gene produces not only the putative receptor tyrosine kinase for an unknown ligand but also multiple protein products that may have different functions

[69381] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69382] Liao, X.; Zhou, R.; Gilbert, D. J.; Copeland, N. G.; Jenkins, N. A. : Receptor tyrosine kinase gene Tyro3 maps to mouse chromosome 2, closely linked to Ltk. Mammalian Genome 7: 395-396, 1996. ; and

[69383] Richard, I.; Broux, O.; Chiannilkulchai, N.; Fougerousse, F.;

Allamand, V.; Bourg, N.; Brenguier, L.; Devaud, C.; Pasturaud, P.; Roudaut, C.; Lorenzo, F.; Sebastiani-Kabatchis, C.; Schul.

[69384] Further studies establishing the function and utilities of LTK are found in John Hopkins OMIM database record ID 151520, and in sited publications numbered 5077-5079, 212 and 5080 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Mitogen-activated Protein Kinase Kinase Kinase 7 (MAP3K7, Accession NM_003188) is another VGAM1968 host target gene. MAP3K7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K7 BINDING SITE, designated SEQ ID:9164, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69385] Another function of VGAM1968 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 7 (MAP3K7, Accession NM_003188), a gene which can phosphorylate and activate yet undefined mapkks. media-

tor of tgf-beta signal transduction. stimulates nf-kappa b activation. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K7. The function of MAP3K7 has been established by previous studies. The MAP kinase (MAPK) cascades constitute functional units that couple upstream input signals to a variety of outputs through pathways that involve 3 protein kinases. MAPKKK (MAP3K; OMIM Ref. No. 602448) phosphorylates MAPKK (MAP2K; OMIM Ref. No. 176872), which in turn phosphorylates and activates MAPK (see OMIM Ref. No. 176948). One MAPK pathway in S. cerevisiae controls the response to mating pheromone. Yamaguchi et al. (1995) screened a mouse cDNA library for clones that could act as MAPKKKs, suppressing a defect in the mating pheromone response pathway. They identified a cDNA that encodes a predicted 579-amino acid protein, which they named TAK1 (TGF-beta-activated kinase). TAK1 has a putative N-terminal protein kinase domain. In mammalian cells, TAK1 regulates transcription by transforming growth factor-beta (TGFB; 190180). Only TAK1 protein missing the N-terminal 22 amino acids suppressed the yeast defect. This activated form also signaled in the absence of TGFB in

mammalian cells Kondo et al. (1998) identified human ESTs that were homologous to mouse TAK1 and used the resulting sequence information to clone human TAK1 from lung cDNA. The predicted 579-amino acid human TAK1 protein is 99% identical to the mouse TAK1 protein. On Northern blots, TAK1 was expressed as a 3-kb mRNA in all tissues tested. Kondo et al. (1998) found 2 isoforms of TAK1 that differed by an insertion of 27 amino acids after amino acid 403

[69386] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69387] Yamaguchi, K.; Shirakabe, K.; Shibuya, H.; Irie, K.; Oishi, I.; Ueno, N.; Taniguchi, T.; Nishida, E.; Matsumoto, K. : Identification of a member of the MAPKKK family as a potential mediator of TGF-beta signal transduction. Science 270: 2008-2011, 1995. ; and

[69388] Kondo, M.; Osada, H.; Uchida, K.; Yanagisawa, K.; Masuda, A.; Takagi, K.; Takahashi, T.; Takahashi, T. : Molecular cloning of human TAK1 and its mutational analysis in human lung cancer.

[69389] Further studies establishing the function and utilities of MAP3K7 are found in John Hopkins OMIM database record

ID 602614, and in sited publications numbered 9048-9050, 902 and 9051 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Matrix Metalloproteinase 14 (membrane-inserted) (MMP14, Accession NM_004995) is another VGAM1968 host target gene. MMP14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MMP14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MMP14 BINDING SITE, designated SEQ ID:11433, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69390] Another function of VGAM1968 is therefore inhibition of Matrix Metalloproteinase 14 (membrane-inserted) (MMP14, Accession NM_004995). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMP14. Myosin, Light Polypeptide Kinase (MYLK, Accession XM_173098) is another VGAM1968 host target gene. MYLK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYLK,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYLK BINDING SITE, designated SEQ ID:46358, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69391] Another function of VGAM1968 is therefore inhibition of Myosin, Light Polypeptide Kinase (MYLK, Accession XM_173098), a gene which is involved in contraction of smooth muscle. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLK. The function of MYLK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM793.NDRG Family Member 3 (NDRG3, Accession NM_032013) is another VGAM1968 host target gene. NDRG3 BINDING SITE1 and NDRG3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NDRG3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDRG3 BINDING SITE1 and NDRG3 BINDING

SITE2, designated SEQ ID:25723 and SEQ ID:22847 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69392] Another function of VGAM1968 is therefore inhibition of NDRG Family Member 3 (NDRG3, Accession NM_032013). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG3. Nuclear Factor of Kappa Light Polypeptide Gene Enhancer In B-cells Inhibitor-like 2 (NFKBIL2, Accession NM_013432) is another VGAM1968 host target gene. NFKBIL2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NFKBIL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFKBIL2 BINDING SITE, designated SEQ ID:15086, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69393] Another function of VGAM1968 is therefore inhibition of Nuclear Factor of Kappa Light Polypeptide Gene Enhancer In B-cells Inhibitor-like 2 (NFKBIL2, Accession

NM_013432), a gene which may have a role in regulating NF-kappa B function in epithelial cells. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFKBIL2. The function of NFKBIL2 has been established by previous studies. By means of subtractive hybridization of lung fibroblast cDNAs from a lung epithelial cell line cDNA, degenerate PCR, and HeLa cell cDNA screening, Ray et al. (1995) identified a novel cDNA, which they called I-kappa-B-related (IKBR). IKBR cDNA encodes a deduced 481-amino acid protein containing 3 ankyrin-repeat motifs. Northern blot analysis revealed an approximately 5.5-kb transcript in lung and trachea epithelial but not fibroblast cells. In whole tissues, the transcript was detected in skeletal muscle and heart but not in lung (where epithelial cells constitute only 10% of adult alveolar epithelium), liver, kidney, pancreas, brain, or placenta. Western blot analysis demonstrated a 52-kD protein in HeLa cell lysates. In electrophoretic mobility shift assays, DNA binding by NFKB/RELA was inhibited in the presence of NFKBIL2. Norman and Barton (2000) showed that the NFKBIL2 gene contains 13 exons, spanning 6,550 bp of genomic sequence. They reported a revised mRNA and

protein sequence for IKBR, which predicted that the protein is larger than originally described.

[69394] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69395] Norman, D. A. M.; Barton, P. J. R. : Isolation, sequence, and chromosomal localisation of the human I(kappa)BR gene. Ann. Hum. Genet. 64: 15-23, 2000. ; and

[69396] Ray, P.; Zhang, D.-H.; Elias, J. A.; Ray, A. : Cloning of a differentially expressed I-kappa-B-related protein. J. Biol. Chem. 270: 10680-10685, 1995.

[69397] Further studies establishing the function and utilities of NFKBIL2 are found in John Hopkins OMIM database record ID 604546, and in sited publications numbered 7464-7465 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Nucleoporin 98kDa (NUP98, Accession NM_016320) is another VGAM1968 host target gene. NUP98 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUP98, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

NUP98 BINDING SITE, designated SEQ ID:18443, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69398] Another function of VGAM1968 is therefore inhibition of Nucleoporin 98kDa (NUP98, Accession NM_016320), a gene which functions in the nuclear transport of protein and RNA. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUP98. The function of NUP98 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.OIP2 (Accession XM_085017) is another VGAM1968 host target gene. OIP2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by OIP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OIP2 BINDING SITE, designated SEQ ID:37794, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69399] Another function of VGAM1968 is therefore inhibition of OIP2 (Accession XM_085017), a gene which belongs to a

family of outer membrane proteins involved in gonococcal adhesion to and invasion of human cells. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OIP2. The function of OIP2 has been established by previous studies. Neisseria gonorrhoeae opacity-associated (Opa) proteins are a family of outer membrane proteins involved in gonococcal adhesion to and invasion of human cells. Opa expression appears to be necessary for gonococcal disease. Using the yeast 2-hybrid system to screen a HeLa cell cDNA library with an N. gonorrhoeae Opa protein as bait, Williams et al. (1998) identified partial cDNAs encoding Opa-interacting protein-1 (OIP1, or TRIP6; 602933), OIP2, OIP3 (PK3; 179050), OIP4 (PRAME; 606021), and OIP5 (OMIM Ref. No. 606020). Sequence analysis predicted that the partial OIP2 cDNA encodes a 265-amino acid peptide that is likely to be the C terminus of a longer protein. OIP2 contains a cluster of basic residues, but unlike OIP1, OIP4, and OIP5, it has no cysteine motif. Inherently unstable mammalian mRNAs contain AU-rich elements (AREs) within their 3-prime untranslated regions. In yeast, 3-prime-to-5-prime mRNA degradation is mediated by the exosome, a multisubunit

particle. Chen et al. (2001) purified and characterized the human exosome by mass spectrometry and found its composition to be similar to its yeast counterpart. They identified the following protein subunits within the human exosome: p7, which is homologous to the yeast Rrp4 protein (OMIM Ref. No. 602238); p8, which is homologous to the yeast Rrp42 protein (OMIM Ref. No. 606488); p9, which is homologous to the yeast Rrp43 protein (OIP2); p10, which is homologous to the yeast Rrp40 protein (OMIM Ref. No. 606489); p11, which is homologous to the yeast Mtr3 protein (OMIM Ref. No. 606490); p12A, which is homologous to the yeast Rrp41 protein (OMIM Ref. No. 606491); p12B, which is homologous to the yeast Rrp46 protein (OMIM Ref. No. 606492); and p13, which is homologous to the yeast Csl4 protein (OMIM Ref. No. 606493). They also identified 2 exosome-associated factors, p1 (OMIM Ref. No. 600478) and p14 (MPP6; 605500), that were not homologous to any yeast exosome components.

[69400] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69401] Chen, C.-Y.; Gherzi, R.; Ong, S.-E.; Chan, E. L.; Raijmak-

ers, R.; Pruijn, G. J. M.; Stoecklin, G.; Moroni, C.; Mann, M.; Karin, M. : AU binding proteins recruit the exosome to degrade ARE-containing mRNAs. Cell 107: 451-464, 2001. ; and

[69402] Williams, J. M.; Chen, G.-C.; Zhu, L.; Rest, R. F. : Using the yeast two-hybrid system to identify human epithelial cell proteins that bind gonococcal Opa proteins: intracellular gonoc.

[69403] Further studies establishing the function and utilities of OIP2 are found in John Hopkins OMIM database record ID 606019, and in sited publications numbered 9518 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.poly(A) Binding Protein, Nuclear 1 (PABPN1, Accession NM_004643) is another VGAM1968 host target gene. PABPN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PABPN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PABPN1 BINDING SITE, designated SEQ ID:11018, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69404] Another function of VGAM1968 is therefore inhibition of poly(A) Binding Protein, Nuclear 1 (PABPN1, Accession NM_004643), a gene which binds to Poly(A). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PABPN1. The function of PABPN1 has been established by previous studies. In a search for a gene mutant in oculopharyngeal muscular dystrophy (OPMD; 164300), which maps to 14q11, Brais et al. (1998) isolated a promising candidate, a gene homologous to the bovine poly(A)-binding protein-2 gene. The authors called the human gene PABP2. PABP2 was considered a good candidate for OPMD because it maps to the genetically defined candidate interval in 14q11, its mRNA is highly expressed in skeletal muscle, and the PABP2 protein is exclusively localized to the nucleus, where it acts as a factor in mRNA polyadenylation. Brais et al. (1998) identified short N-terminal trinucleotide expansions (GCG) in the PABP2 gene of OPMD patients (e.g., 602279.0001) Using both immunoelectron microscopy and fluorescence confocal microscopy, Calado et al. (2000) determined that the OPMD-specific nuclear inclusions were stained anti-PABP2 antibodies. In addition, the inclusions were labeled with anti-

bodies directed against ubiquitin and the subunits of the proteasome, and contained a less soluble form of PABP2 as well as poly(A) RNA. The authors suggested that the polyalanine expansions in PABP2 induce a misfolding and aggregation of the protein into insoluble inclusions, similarly to events in neurodegenerative diseases caused by CAG/polyglutamine expansions, and that in OPMD the polyalanine expansions in the PABP2 protein may interfere with the cellular traffic of poly(A) RNA.

[69405] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69406] Brais, B.; Bouchard, J.-P.; Xie, Y.-G.; Rochefort, D. L.; Chretien, N.; Tome, F. M. S.; Lafreniere, R. G.; Rommens, J. M.; Uyama, E.; Nohira, O.; Blumen, S.; Korczyn, A. D.; Heutink, P.; Mathieu, J.; Duranceau, A.; Codere, F.; Fardeau, M.; Rouleau, G. A. : Short GCG expansions in the PABP2 gene cause oculopharyngeal muscular dystrophy. Nature Genet. 18: 164-167, 1998. Note: Erratum: Nature Genet. 19: 404 only, 1998. ; and

[69407] Calado, A.; Tome, F. M. S.; Brais, B.; Rouleau, G. A.; Kuhn, U.; Wahle, E.; Carmo-Fonseca, M. : Nuclear inclusions in oculopharyngeal muscular dystrophy consist of poly(A)

binding protei.

[69408] Further studies establishing the function and utilities of PABPN1 are found in John Hopkins OMIM database record ID 602279, and in sited publications numbered 8568-8569, 10685, 1114 and 11606 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Platelet-derived Growth Factor Beta Polypeptide (simian sarcoma viral (v-sis) Oncogene Homolog) (PDGFB, Accession NM_002608) is another VGAM1968 host target gene. PDGFB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDGFB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDGFB BINDING SITE, designated SEQ ID:8470, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69409] Another function of VGAM1968 is therefore inhibition of Platelet-derived Growth Factor Beta Polypeptide (simian sarcoma viral (v-sis) Oncogene Homolog) (PDGFB, Accession NM_002608), a gene which plays an important role in stimulating adjacent cells to grow and thereby heal the

wound. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFB. The function of PDGFB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM173.Placental Growth Factor, Vascular Endothelial Growth Factor-related Protein (PGF, Accession NM_002632) is another VGAM1968 host target gene. PGF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PGF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PGF BINDING SITE, designated SEQ ID:8493, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69410] Another function of VGAM1968 is therefore inhibition of Placental Growth Factor, Vascular Endothelial Growth Factor-related Protein (PGF, Accession NM_002632), a gene which is a growth factor active in angiogenesis, and endothelial cell growth, stimulating cell proliferation and migration. it binds to receptor vegfr-1/fl. Accordingly,

utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PGF. The function of PGF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1420.Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 3 (p55, gamma) (PIK3R3, Accession XM_027982) is another VGAM1968 host target gene. PIK3R3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIK3R3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIK3R3 BINDING SITE, designated SEQ ID:30606, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69411] Another function of VGAM1968 is therefore inhibition of Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 3 (p55, gamma) (PIK3R3, Accession XM_027982). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3R3. Pinin, Desmosome Associated

Protein (PNN, Accession XM_048719) is another VGAM1968 host target gene. PNN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PNN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PNN BINDING SITE, designated SEQ ID:35233, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69412] Another function of VGAM1968 is therefore inhibition of Pinin, Desmosome Associated Protein (PNN, Accession XM_048719), a gene which reinforces the intermediate filament-desmosome complex. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNN. The function of PNN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM120.Polymerase (DNA directed), Eta (POLH, Accession NM_006502) is another VGAM1968 host target gene. POLH BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

POLH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POLH BINDING SITE, designated SEQ ID:13251, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69413] Another function of VGAM1968 is therefore inhibition of Polymerase (DNA directed), Eta (POLH, Accession NM_006502). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLH. Protein Kinase, Y-linked (PRKY, Accession NM_002760) is another VGAM1968 host target gene. PRKY BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRKY, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKY BINDING SITE, designated SEQ ID:8647, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69414] Another function of VGAM1968 is therefore inhibition of Protein Kinase, Y-linked (PRKY, Accession NM_002760), a

gene which is a putative protein kinase. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKY. The function of PRKY has been established by previous studies. PRKX (OMIM Ref. No. 300083) is a novel serine/threonine subtype of protein kinase that appears to encode a protein related to the catalytic subunit of the cAMP-dependent protein kinases, which are key players in the cellular responses to the second messenger cAMP. Klink et al. (1995) found that somatic cell hybrid analysis of PRKX under high stringency conditions revealed at least 3 further loci closely related to this gene in the human, constituting a small subfamily. Schiebel et al. (1997) isolated and characterized the PRKY gene, which is highly homologous to the PRKX gene on Xp22.3 and represents a member of the cAMP-dependent serine/threonine protein kinase gene family. Abnormal interchange can occur anywhere between Xp and Yp proximal to SRY (OMIM Ref. No. 480000). Schiebel et al. (1997) demonstrated that abnormal interchange in XX males (OMIM Ref. No. 278850) and XY females (OMIM Ref. No. 306100) happens particularly frequently between PRKX and PRKY. In a collection of 26 XX males and 4 XY females, between 27 and 35% of the

interchanges took place between PRK homologs, but at different sites within the gene. PRKY and PRKX are located far from the pseudoautosomal region, where XY exchange normally takes place. Schiebel et al. (1997) stated that the unprecedented high sequence identity and identical orientation of PRKY to its homologous partner on the X chromosome, PRKX, explains the high frequency of abnormal pairing and the subsequent ectopic recombination, leading to XX males and XY females and to the highest rate of recombination outside the pseudoautosomal region. Schiebel et al. (1997) used FISH analysis to map the PRKY gene to Yp11.2 in close proximity to AMELY (OMIM Ref. No. 410000); the autosomal copy, a pseudogene (OMIM Ref. No. PRKXP1), to 15q26; and a further X-linked pseudogene (OMIM Ref. No. PRKXP2) to Xq12-q13.

[69415] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69416] Schiebel, K.; Mertz, A.; Winkelmann, B.; Glaser, B.; Schempp, W.; Rappold, G. : FISH localization of the human Y-homolog of protein kinase PRKX (PRKY) to Yp11.2 and two pseudogenes to 15q26 and Xq12-q13. Cytogenet. Cell Genet. 76: 49-52, 1997. ; and

[69417] Schiebel, K.; Winkelmann, M.; Mertz, A.; Xu, X.; Page, D. C.; Weil, D.; Petit, C.; Rappold, G. A. : Abnormal XY inter-change between a novel isolated protein kinase gene, PRKY, and its h.

[69418] Further studies establishing the function and utilities of PRKY are found in John Hopkins OMIM database record ID 400008, and in sited publications numbered 10972-1097 and 8834 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.RAB5A, Member RAS Oncogene Family (RAB5A, Accession NM_004162) is another VGAM1968 host target gene. RAB5A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB5A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB5A BINDING SITE, designated SEQ ID:10372, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69419] Another function of VGAM1968 is therefore inhibition of RAB5A, Member RAS Oncogene Family (RAB5A, Accession NM_004162), a gene which is a rate-limiting component

of the machinery regulating the kinetics of membrane traffic. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB5A. The function of RAB5A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1342.Regulator of Nonsense Transcripts 1 (RENT1, Accession NM_002911) is another VGAM1968 host target gene. RENT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RENT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RENT1 BINDING SITE, designated SEQ ID:8815, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69420] Another function of VGAM1968 is therefore inhibition of Regulator of Nonsense Transcripts 1 (RENT1, Accession NM_002911), a gene which eliminates the production of nonsense-containing RNAs in mammalian cells. Accordingly, utilities of VGAM1968 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with RENT1. The function of RENT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.SH3-domain Binding Protein 2 (SH3BP2, Accession NM_003023) is another VGAM1968 host target gene. SH3BP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3BP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3BP2 BINDING SITE, designated SEQ ID:8947, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69421] Another function of VGAM1968 is therefore inhibition of SH3-domain Binding Protein 2 (SH3BP2, Accession NM_003023). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BP2. SUSP1 (Accession NM_015571) is another VGAM1968 host target gene. SUSP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SUSP1,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SUSP1 BINDING SITE, designated SEQ ID:17844, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69422] Another function of VGAM1968 is therefore inhibition of SUSP1 (Accession NM_015571), a gene which may play a role in the regulation of SUMO-1-mediated cellular processes particularly related to reproduction. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUSP1. The function of SUSP1 has been established by previous studies. By screening human brain cDNAs for the potential to encode proteins that are at least 50 kD, Nagase et al. (1998) isolated a partial SUSP1 cDNA, which they called KIAA0797, that lacks 5-prime coding sequence. The deduced partial SUSP1 protein has 1,084 amino acids. RT-PCR followed by ELISA detected SUSP1 expression in all 10 human tissues examined, with highest expression in ovary and lowest expression in spleen. By 5-prime-anchored PCR using the KIAA0797 cDNA iso-

lated by Nagase et al. (1998), Kim et al. (2000) determined the complete SUSP1 coding sequence. The deduced 1,112-amino acid SUSP1 protein is a cysteine protease containing the conserved histidine, aspartic acid, and cysteine residues of the catalytic triad and the invariant glutamine residue that helps form the oxyanion hole. The sequence similarity of SUSP1 to other known UBL-specific proteases was largely restricted to the active site domains. Recombinant SUSP1 expressed in bacteria efficiently released SUMO1 from a SUMO1-beta-galactosidase fusion protein but not from a RANGAP1-SUMO1 conjugate, suggesting a role for SUSP1 in the generation of mature SUMO1 specifically from its precursor. SUSP1 showed a tight substrate specificity for SUMO1. Recombinant SUSP1 was exclusively localized to the cytoplasm of mammalian cells. Northern blot analysis detected a 4.4-kb SUSP1 transcript in various human tissues. The highest expression of SUSP1 was in reproductive organs, namely testis, ovary, and prostate. SUSP1 was also expressed in colon and peripheral blood leukocytes. Little or no SUSP1 transcripts were detected in brain, liver, lung, kidney, pancreas, spleen, thymus, heart, and skeletal muscle. Kim et al. (2000) suggested that SUSP1 may play a role in the

regulation of SUMO1-mediated cellular processes particularly related to reproduction.

[69423] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69424] Kim, K. I.; Baek, S. H.; Jeon, Y.-J.; Nishimori, S.; Suzuki, T.; Uchida, S.; Shimbara, N.; Saitoh, H.; Tanaka, K.; Chung, C. H. : A new SUMO-1-specific protease, SUSP1, that is highly expressed in reproductive organs. J. Biol. Chem. 275: 14102-14106, 2000. ; and

[69425] Nagase, T.; Ishikawa, K.; Suyama, M.; Kikuno, R.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. : Prediction of the coding sequences of unidentified human genes. XI. The.

[69426] Further studies establishing the function and utilities of SUSP1 are found in John Hopkins OMIM database record ID 605003, and in sited publications numbered 291 and 7048 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Transducin (beta)-like 1X-linked (TBL1X, Accession NM_005647) is another VGAM1968 host target gene. TBL1X BINDING SITE1 and TBL1X BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by

TBL1X, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBL1X BINDING SITE1 and TBL1X BINDING SITE2, designated SEQ ID:12185 and SEQ ID:12186 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69427] Another function of VGAM1968 is therefore inhibition of Transducin (beta)-like 1X-linked (TBL1X, Accession NM_005647), a gene which activates latent HDAC3 activity. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBL1X. The function of TBL1X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1151.Transmembrane, Prostate Androgen Induced RNA (TMEPAI, Accession NM_020182) is another VGAM1968 host target gene. TMEPAI BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TMEPAI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMEPAI BINDING SITE, designated SEQ ID:21407, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69428] Another function of VGAM1968 is therefore inhibition of Transmembrane, Prostate Androgen Induced RNA (TMEPAI, Accession NM_020182). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMEPAI. Transformation/transcription Domain-associated Protein (TRRAP, Accession NM_003496) is another VGAM1968 host target gene. TRRAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRRAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRRAP BINDING SITE, designated SEQ ID:9589, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69429] Another function of VGAM1968 is therefore inhibition of Transformation/transcription Domain-associated Protein

(TRRAP, Accession NM_003496). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRRAP. Uncoupling Protein 3 (mitochondrial, proton carrier) (UCP3, Accession NM_003356) is another VGAM1968 host target gene. UCP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UCP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UCP3 BINDING SITE, designated SEQ ID:9385, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69430] Another function of VGAM1968 is therefore inhibition of Uncoupling Protein 3 (mitochondrial, proton carrier) (UCP3, Accession NM_003356), a gene which is a mitochondrial transporter protein that creates proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UCP3. The function of UCP3 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1317.WAS Protein Family, Member 3 (WASF3, Accession NM_006646) is another VGAM1968 host target gene. WASF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WASF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WASF3 BINDING SITE, designated SEQ ID:13442, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69431] Another function of VGAM1968 is therefore inhibition of WAS Protein Family, Member 3 (WASF3, Accession NM_006646), a gene which stimulates actin polymerization. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WASF3. The function of WASF3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1692.Tyrosine 3-monooxygenase/tryptophan

5-monooxygenase Activation Protein, Epsilon Polypeptide (YWHAE, Accession NM_006761) is another VGAM1968 host target gene. YWHAE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by YWHAE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YWHAE BINDING SITE, designated SEQ ID:13614, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69432] Another function of VGAM1968 is therefore inhibition of Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, Epsilon Polypeptide (YWHAE, Accession NM_006761), a gene which binds to cdc25 and may facilitate cdc25 interaction with Raf-1 in vivo. Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YWHAE. The function of YWHAE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM656.AD-020 (Accession NM_020141) is another VGAM1968 host target

gene. AD-020 BINDING SITE1 and AD-020 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AD-020, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AD-020 BINDING SITE1 and AD-020 BINDING SITE2, designated SEQ ID:21340 and SEQ ID:29870 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69433] Another function of VGAM1968 is therefore inhibition of AD-020 (Accession NM_020141). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AD-020. Adaptor-related Protein Complex 3, Delta 1 Subunit (AP3D1, Accession NM_003938) is another VGAM1968 host target gene. AP3D1 BINDING SITE1 and AP3D1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AP3D1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP3D1 BINDING SITE1 and AP3D1 BINDING SITE2, desig-

nated SEQ ID:10047 and SEQ ID:18509 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69434] Another function of VGAM1968 is therefore inhibition of Adaptor-related Protein Complex 3, Delta 1 Subunit (AP3D1, Accession NM_003938). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP3D1. Chromosome 17 Open Reading Frame 31 (C17orf31, Accession NM_017575) is another VGAM1968 host target gene. C17orf31 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C17orf31, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C17orf31 BINDING SITE, designated SEQ ID:19006, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69435] Another function of VGAM1968 is therefore inhibition of Chromosome 17 Open Reading Frame 31 (C17orf31, Accession NM_017575). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with C17orf31. Chromosome 19 Open Reading Frame 7 (C19orf7, Accession XM_028253) is another VGAM1968 host target gene. C19orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C19orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C19orf7 BINDING SITE, designated SEQ ID:30636, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69436] Another function of VGAM1968 is therefore inhibition of Chromosome 19 Open Reading Frame 7 (C19orf7, Accession XM_028253). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C19orf7. Chromosome 20 Open Reading Frame 100 (C20orf100, Accession NM_032883) is another VGAM1968 host target gene. C20orf100 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf100, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of C20orf100 BINDING SITE, designated SEQ ID:26704, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69437] Another function of VGAM1968 is therefore inhibition of Chromosome 20 Open Reading Frame 100 (C20orf100, Accession NM_032883). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf100. Chromosome 21 Open Reading Frame 25 (C21orf25, Accession XM_032945) is another VGAM1968 host target gene. C21orf25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C21orf25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C21orf25 BINDING SITE, designated SEQ ID:31801, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69438] Another function of VGAM1968 is therefore inhibition of Chromosome 21 Open Reading Frame 25 (C21orf25, Ac-

cession XM_032945). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf25. Chromosome 21 Open Reading Frame 59 (C21orf59, Accession NM_017835) is another VGAM1968 host target gene. C21orf59 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C21orf59, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C21orf59 BINDING SITE, designated SEQ ID:19501, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69439] Another function of VGAM1968 is therefore inhibition of Chromosome 21 Open Reading Frame 59 (C21orf59, Accession NM_017835). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf59. Chemokine (C-C motif) Receptor 6 (CCR6, Accession NM_031409) is another VGAM1968 host target gene. CCR6 BINDING SITE1 and CCR6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of

mRNA encoded by CCR6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCR6 BINDING SITE1 and CCR6 BINDING SITE2, designated SEQ ID:25370 and SEQ ID:10577 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69440] Another function of VGAM1968 is therefore inhibition of Chemokine (C-C motif) Receptor 6 (CCR6, Accession NM_031409). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCR6. DJ37E16.5 (Accession NM_020315) is another VGAM1968 host target gene. DJ37E16.5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DJ37E16.5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DJ37E16.5 BINDING SITE, designated SEQ ID:21576, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69441] Another function of VGAM1968 is therefore inhibition of DJ37E16.5 (Accession NM_020315). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DJ37E16.5. DKFZP434E2135 (Accession NM_030804) is another VGAM1968 host target gene. DKFZP434E2135 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434E2135, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434E2135 BINDING SITE, designated SEQ ID:25115, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69442] Another function of VGAM1968 is therefore inhibition of DKFZP434E2135 (Accession NM_030804). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434E2135. DKFZP434F091 (Accession NM_015453) is another VGAM1968 host target gene. DKFZP434F091 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

DKFZP434F091, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434F091 BINDING SITE, designated SEQ ID:17739, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69443] Another function of VGAM1968 is therefore inhibition of DKFZP434F091 (Accession NM_015453). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F091. DKFZP564B1162 (Accession NM_031305) is another VGAM1968 host target gene. DKFZP564B1162 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP564B1162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564B1162 BINDING SITE, designated SEQ ID:25337, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69444] Another function of VGAM1968 is therefore inhibition of

DKFZP564B1162 (Accession NM_031305). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564B1162. DKFZP586A0522 (Accession NM_014033) is another VGAM1968 host target gene. DKFZP586A0522 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586A0522, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586A0522 BINDING SITE, designated SEQ ID:15262, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69445] Another function of VGAM1968 is therefore inhibition of DKFZP586A0522 (Accession NM_014033). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586A0522. F-box Only Protein 21 (FBXO21, Accession NM_033624) is another VGAM1968 host target gene. FBXO21 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXO21, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXO21 BINDING SITE, designated SEQ ID:27324, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69446] Another function of VGAM1968 is therefore inhibition of F-box Only Protein 21 (FBXO21, Accession NM_033624). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO21. FLJ10199 (Accession XM_048840) is another VGAM1968 host target gene. FLJ10199 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10199, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10199 BINDING SITE, designated SEQ ID:35285, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69447] Another function of VGAM1968 is therefore inhibition of FLJ10199 (Accession XM_048840). Accordingly, utilities of

VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10199. FLJ11269 (Accession XM_052193) is another VGAM1968 host target gene. FLJ11269 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11269, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11269 BINDING SITE, designated SEQ ID:35954, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69448] Another function of VGAM1968 is therefore inhibition of FLJ11269 (Accession XM_052193). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11269. FLJ12783 (Accession NM_031426) is another VGAM1968 host target gene. FLJ12783 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12783, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12783

BINDING SITE, designated SEQ ID:25418, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69449] Another function of VGAM1968 is therefore inhibition of FLJ12783 (Accession NM_031426). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12783. FLJ13441 (Accession NM_023924) is another VGAM1968 host target gene. FLJ13441 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13441, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13441 BINDING SITE, designated SEQ ID:23393, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69450] Another function of VGAM1968 is therefore inhibition of FLJ13441 (Accession NM_023924). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13441. FLJ13646 (Accession NM_024584) is another VGAM1968 host target gene. FLJ13646 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13646, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13646 BINDING SITE, designated SEQ ID:23813, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69451] Another function of VGAM1968 is therefore inhibition of FLJ13646 (Accession NM_024584). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13646. FLJ14803 (Accession NM_032842) is another VGAM1968 host target gene. FLJ14803 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14803, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14803 BINDING SITE, designated SEQ ID:26627, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69452] Another function of VGAM1968 is therefore inhibition of

FLJ14803 (Accession NM_032842). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14803. FLJ20445 (Accession NM_017824) is another VGAM1968 host target gene. FLJ20445 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20445 BINDING SITE, designated SEQ ID:19481, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69453] Another function of VGAM1968 is therefore inhibition of FLJ20445 (Accession NM_017824). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20445. FLJ20548 (Accession NM_017873) is another VGAM1968 host target gene. FLJ20548 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20548, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ20548 BINDING SITE, designated SEQ ID:19545, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69454] Another function of VGAM1968 is therefore inhibition of FLJ20548 (Accession NM_017873). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20548. FLJ22479 (Accession NM_024900) is another VGAM1968 host target gene. FLJ22479 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22479, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22479 BINDING SITE, designated SEQ ID:24386, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69455] Another function of VGAM1968 is therefore inhibition of FLJ22479 (Accession NM_024900). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22479. FLJ22679 (Accession NM_032227) is another

VGAM1968 host target gene. FLJ22679 BINDING SITE1 and FLJ22679 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ22679, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22679 BINDING SITE1 and FLJ22679 BINDING SITE2, designated SEQ ID:25950 and SEQ ID:19263 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69456] Another function of VGAM1968 is therefore inhibition of FLJ22679 (Accession NM_032227). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22679. GS3955 (Accession NM_021643) is another VGAM1968 host target gene. GS3955 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GS3955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GS3955 BINDING SITE, designated SEQ ID:22301, to the nucleotide

sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69457] Another function of VGAM1968 is therefore inhibition of GS3955 (Accession NM_021643). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GS3955. HCA4 (Accession XM_085287) is another VGAM1968 host target gene. HCA4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCA4 BINDING SITE, designated SEQ ID:38024, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69458] Another function of VGAM1968 is therefore inhibition of HCA4 (Accession XM_085287). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCA4. HDAC9-PENDING (Accession NM_058176) is another VGAM1968 host target gene. HDAC9-PENDING BINDING SITE1 through HDAC9-PENDING BINDING SITE3 are HOST

TARGET binding sites found in untranslated regions of mRNA encoded by HDAC9-PENDING, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HDAC9-PENDING BINDING SITE1 through HDAC9-PENDING BINDING SITE3, designated SEQ ID:27728, SEQ ID:27729 and SEQ ID:16251 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69459] Another function of VGAM1968 is therefore inhibition of HDAC9-PENDING (Accession NM_058176). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HDAC9-PENDING. Potassium Channel, Subfamily T, Member 1 (KCNT1, Accession XM_029962) is another VGAM1968 host target gene. KCNT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNT1 BINDING SITE, designated SEQ ID:30976, to the nucleotide se-

quence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69460] Another function of VGAM1968 is therefore inhibition of Potassium Channel, Subfamily T, Member 1 (KCNT1, Accession XM_029962). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNT1. KIAA0057 (Accession NM_012288) is another VGAM1968 host target gene. KIAA0057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0057 BINDING SITE, designated SEQ ID:14622, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69461] Another function of VGAM1968 is therefore inhibition of KIAA0057 (Accession NM_012288). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0057. KIAA0335 (Accession NM_014803) is another VGAM1968 host target gene. KIAA0335 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0335, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0335 BINDING SITE, designated SEQ ID:16732, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69462] Another function of VGAM1968 is therefore inhibition of KIAA0335 (Accession NM_014803). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0335. KIAA0446 (Accession XM_044155) is another VGAM1968 host target gene. KIAA0446 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0446, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0446 BINDING SITE, designated SEQ ID:34150, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69463] Another function of VGAM1968 is therefore inhibition of

KIAA0446 (Accession XM_044155). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0446. KIAA0534 (Accession XM_049349) is another VGAM1968 host target gene. KIAA0534 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0534, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0534 BINDING SITE, designated SEQ ID:35385, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69464] Another function of VGAM1968 is therefore inhibition of KIAA0534 (Accession XM_049349). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0534. KIAA0843 (Accession NM_014945) is another VGAM1968 host target gene. KIAA0843 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0843, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0843 BINDING SITE, designated SEQ ID:17260, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69465] Another function of VGAM1968 is therefore inhibition of KIAA0843 (Accession NM_014945). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0843. KIAA0892 (Accession XM_048457) is another VGAM1968 host target gene. KIAA0892 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0892, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0892 BINDING SITE, designated SEQ ID:35172, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69466] Another function of VGAM1968 is therefore inhibition of KIAA0892 (Accession XM_048457). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0892. KIAA0894 (Accession NM_014896) is another

VGAM1968 host target gene. KIAA0894 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0894, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0894 BINDING SITE, designated SEQ ID:17056, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69467] Another function of VGAM1968 is therefore inhibition of KIAA0894 (Accession NM_014896). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0894. KIAA0981 (Accession XM_028867) is another VGAM1968 host target gene. KIAA0981 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0981, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0981 BINDING SITE, designated SEQ ID:30799, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69468] Another function of VGAM1968 is therefore inhibition of KIAA0981 (Accession XM_028867). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0981. KIAA1157 (Accession XM_051093) is another VGAM1968 host target gene. KIAA1157 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1157, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1157 BINDING SITE, designated SEQ ID:35751, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69469] Another function of VGAM1968 is therefore inhibition of KIAA1157 (Accession XM_051093). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1157. KIAA1274 (Accession XM_166125) is another VGAM1968 host target gene. KIAA1274 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1274, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1274 BINDING SITE, designated SEQ ID:43911, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69470] Another function of VGAM1968 is therefore inhibition of KIAA1274 (Accession XM_166125). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1274. KIAA1529 (Accession XM_047336) is another VGAM1968 host target gene. KIAA1529 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1529, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1529 BINDING SITE, designated SEQ ID:34947, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69471] Another function of VGAM1968 is therefore inhibition of KIAA1529 (Accession XM_047336). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1529. KIAA1538 (Accession XM_049474) is another VGAM1968 host target gene. KIAA1538 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1538, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1538 BINDING SITE, designated SEQ ID:35437, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69472] Another function of VGAM1968 is therefore inhibition of KIAA1538 (Accession XM_049474). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1538. KIAA1576 (Accession XM_038186) is another VGAM1968 host target gene. KIAA1576 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1576, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1576 BINDING SITE, designated SEQ ID:32775, to the nucleotide sequence of VGAM1968 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4679.

[69473] Another function of VGAM1968 is therefore inhibition of KIAA1576 (Accession XM_038186). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1576. KIAA1821 (Accession XM_050101) is another VGAM1968 host target gene. KIAA1821 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1821, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1821 BINDING SITE, designated SEQ ID:35551, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69474] Another function of VGAM1968 is therefore inhibition of KIAA1821 (Accession XM_050101). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1821. KIAA1894 (Accession XM_058025) is another VGAM1968 host target gene. KIAA1894 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1894, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1894 BINDING SITE, designated SEQ ID:36561, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69475] Another function of VGAM1968 is therefore inhibition of KIAA1894 (Accession XM_058025). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1894. V-maf Musculoaponeurotic Fibrosarcoma Oncogene Homolog B (avian) (MAFB, Accession NM_005461) is another VGAM1968 host target gene. MAFB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAFB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAFB BINDING SITE, designated SEQ ID:11943, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69476] Another function of VGAM1968 is therefore inhibition of V-maf Musculoaponeurotic Fibrosarcoma Oncogene Ho-

molog B (avian) (MAFB, Accession NM_005461). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAFB. Mitogen-activated Protein Kinase Kinase 6 (MAP2K6, Accession NM_002758) is another VGAM1968 host target gene. MAP2K6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAP2K6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP2K6 BINDING SITE, designated SEQ ID:8641, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69477] Another function of VGAM1968 is therefore inhibition of Mitogen-activated Protein Kinase Kinase 6 (MAP2K6, Accession NM_002758). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP2K6. MGC2628 (Accession NM_024076) is another VGAM1968 host target gene. MGC2628 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2628, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2628 BINDING SITE, designated SEQ ID:23511, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69478] Another function of VGAM1968 is therefore inhibition of MGC2628 (Accession NM_024076). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2628. MGC30052 (Accession NM_144721) is another VGAM1968 host target gene. MGC30052 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC30052, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC30052 BINDING SITE, designated SEQ ID:29544, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69479] Another function of VGAM1968 is therefore inhibition of MGC30052 (Accession NM_144721). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC30052. MGC4294 (Accession NM_024314) is another VGAM1968 host target gene. MGC4294 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC4294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4294 BINDING SITE, designated SEQ ID:23608, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69480] Another function of VGAM1968 is therefore inhibition of MGC4294 (Accession NM_024314). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4294. Oxysterol Binding Protein-like 5 (OSBPL5, Accession XM_052567) is another VGAM1968 host target gene. OSBPL5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL5 BINDING SITE, designated SEQ

ID:35991, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69481] Another function of VGAM1968 is therefore inhibition of Oxysterol Binding Protein-like 5 (OSBPL5, Accession XM_052567). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL5. pcnp (Accession NM_020357) is another VGAM1968 host target gene. pcnp BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by pcnp, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of pcnp BINDING SITE, designated SEQ ID:21628, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69482] Another function of VGAM1968 is therefore inhibition of pcnp (Accession NM_020357). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with pcnp. PDZ Domain Containing 2 (PDZD2, Accession XM_087705) is another VGAM1968 host target gene. PDZD2 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PDZD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDZD2 BINDING SITE, designated SEQ ID:39391, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69483] Another function of VGAM1968 is therefore inhibition of PDZ Domain Containing 2 (PDZD2, Accession XM_087705). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDZD2. Paraneoplastic Antigen MA3 (PNMA3, Accession NM_013364) is another VGAM1968 host target gene. PNMA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PNMA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PNMA3 BINDING SITE, designated SEQ ID:15010, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69484] Another function of VGAM1968 is therefore inhibition of Paraneoplastic Antigen MA3 (PNMA3, Accession NM_013364). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNMA3. Polymerase I and Transcript Release Factor (PTRF, Accession XM_032852) is another VGAM1968 host target gene. PTRF BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PTRF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTRF BINDING SITE, designated SEQ ID:31784, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69485] Another function of VGAM1968 is therefore inhibition of Polymerase I and Transcript Release Factor (PTRF, Accession XM_032852). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTRF. RAB14, Member RAS Oncogene Family (RAB14, Accession NM_016322) is another VGAM1968 host target gene. RAB14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by RAB14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB14 BINDING SITE, designated SEQ ID:18448, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69486] Another function of VGAM1968 is therefore inhibition of RAB14, Member RAS Oncogene Family (RAB14, Accession NM_016322). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB14. RAS Guanyl Releasing Protein 4 (RASGRP4, Accession NM_052949) is another VGAM1968 host target gene. RASGRP4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RASGRP4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RASGRP4 BINDING SITE, designated SEQ ID:27504, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69487] Another function of VGAM1968 is therefore inhibition of

RAS Guanyl Releasing Protein 4 (RASGRP4, Accession NM_052949). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASGRP4. Retinoblastoma Binding Protein 1 (RBBP1, Accession NM_023001) is another VGAM1968 host target gene. RBBP1 BINDING SITE1 and RBBP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RBBP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBBP1 BINDING SITE1 and RBBP1 BINDING SITE2, designated SEQ ID:23261 and SEQ ID:8800 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69488] Another function of VGAM1968 is therefore inhibition of Retinoblastoma Binding Protein 1 (RBBP1, Accession NM_023001). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP1. RNAH (Accession XM_030392) is another VGAM1968 host target gene. RNAH BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by RNAH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNAH BINDING SITE, designated SEQ ID:31039, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69489] Another function of VGAM1968 is therefore inhibition of RNAH (Accession XM_030392). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNAH. Ring Finger Protein 11 (RNF11, Accession NM_014372) is another VGAM1968 host target gene. RNF11 BINDING SITE1 and RNF11 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RNF11, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF11 BINDING SITE1 and RNF11 BINDING SITE2, designated SEQ ID:15705 and SEQ ID:15706 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69490] Another function of VGAM1968 is therefore inhibition of Ring Finger Protein 11 (RNF11, Accession NM_014372). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF11. SAST (Accession XM_032034) is another VGAM1968 host target gene. SAST BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SAST, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SAST BINDING SITE, designated SEQ ID:31542, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69491] Another function of VGAM1968 is therefore inhibition of SAST (Accession XM_032034). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SAST. Sema Domain, Transmembrane Domain (TM), and Cytoplasmic Domain, (semaphorin) 6B (SEMA6B, Accession NM_032108) is another VGAM1968 host target gene. SEMA6B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

SEMA6B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEMA6B BINDING SITE, designated SEQ ID:25801, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69492] Another function of VGAM1968 is therefore inhibition of Sema Domain, Transmembrane Domain (TM), and Cytoplasmic Domain, (semaphorin) 6B (SEMA6B, Accession NM_032108). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA6B. Solute Carrier Family 6 (neurotransmitter transporter), Member 14 (SLC6A14, Accession NM_007231) is another VGAM1968 host target gene. SLC6A14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC6A14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC6A14 BINDING SITE, designated SEQ ID:14103, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4679.

[69493] Another function of VGAM1968 is therefore inhibition of Solute Carrier Family 6 (neurotransmitter transporter), Member 14 (SLC6A14, Accession NM_007231). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A14. STATI2 (Accession XM_170547) is another VGAM1968 host target gene. STATI2 BINDING SITE1 and STATI2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by STATI2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STATI2 BINDING SITE1 and STATI2 BINDING SITE2, designated SEQ ID:45371 and SEQ ID:9960 respectively, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69494] Another function of VGAM1968 is therefore inhibition of STATI2 (Accession XM_170547). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STATI2. TA-PP2C (Accession NM_139283) is another VGAM1968

host target gene. TA-PP2C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TA-PP2C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TA-PP2C BINDING SITE, designated SEQ ID:29283, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69495] Another function of VGAM1968 is therefore inhibition of TA-PP2C (Accession NM_139283). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TA-PP2C. TBLR1 (Accession NM_024665) is another VGAM1968 host target gene. TBLR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBLR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBLR1 BINDING SITE, designated SEQ ID:23966, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69496] Another function of VGAM1968 is therefore inhibition of TBLR1 (Accession NM_024665). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBLR1. TIP-1 (Accession NM_014604) is another VGAM1968 host target gene. TIP-1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TIP-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIP-1 BINDING SITE, designated SEQ ID:15968, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69497] Another function of VGAM1968 is therefore inhibition of TIP-1 (Accession NM_014604). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIP-1. TOLLIP (Accession NM_019009) is another VGAM1968 host target gene. TOLLIP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOLLIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOLLIP BINDING SITE, designated SEQ ID:21091, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69498] Another function of VGAM1968 is therefore inhibition of TOLLIP (Accession NM_019009). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOLLIP. Tripartite Motif-containing 4 (TRIM4, Accession NM_033017) is another VGAM1968 host target gene. TRIM4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM4 BINDING SITE, designated SEQ ID:26904, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69499] Another function of VGAM1968 is therefore inhibition of Tripartite Motif-containing 4 (TRIM4, Accession NM_033017). Accordingly, utilities of VGAM1968 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM4. TRIP-Br2 (Accession NM_014755) is another VGAM1968 host target gene. TRIP-Br2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIP-Br2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIP-Br2 BINDING SITE, designated SEQ ID:16483, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69500] Another function of VGAM1968 is therefore inhibition of TRIP-Br2 (Accession NM_014755). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIP-Br2. TSPAN-5 (Accession NM_005723) is another VGAM1968 host target gene. TSPAN-5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TSPAN-5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TSPAN-5

BINDING SITE, designated SEQ ID:12276, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69501] Another function of VGAM1968 is therefore inhibition of TSPAN-5 (Accession NM_005723). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSPAN-5. LOC115073 (Accession XM_055193) is another VGAM1968 host target gene. LOC115073 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115073, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115073 BINDING SITE, designated SEQ ID:36233, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69502] Another function of VGAM1968 is therefore inhibition of LOC115073 (Accession XM_055193). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115073. LOC115219 (Accession XM_055499) is another VGAM1968 host target gene. LOC115219 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC115219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115219 BINDING SITE, designated SEQ ID:36281, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69503] Another function of VGAM1968 is therefore inhibition of LOC115219 (Accession XM_055499). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115219. LOC118709 (Accession XM_058338) is another VGAM1968 host target gene. LOC118709 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC118709, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC118709 BINDING SITE, designated SEQ ID:36600, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69504] Another function of VGAM1968 is therefore inhibition of

LOC118709 (Accession XM_058338). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118709. LOC126353 (Accession XM_059034) is another VGAM1968 host target gene. LOC126353 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126353, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126353 BINDING SITE, designated SEQ ID:36830, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69505] Another function of VGAM1968 is therefore inhibition of LOC126353 (Accession XM_059034). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126353. LOC126661 (Accession XM_059061) is another VGAM1968 host target gene. LOC126661 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126661, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC126661 BINDING SITE, designated SEQ ID:36853, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69506] Another function of VGAM1968 is therefore inhibition of LOC126661 (Accession XM_059061). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126661. LOC132321 (Accession XM_059585) is another VGAM1968 host target gene. LOC132321 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC132321, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132321 BINDING SITE, designated SEQ ID:37027, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69507] Another function of VGAM1968 is therefore inhibition of LOC132321 (Accession XM_059585). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132321. LOC133686 (Accession XM_059667) is an-

other VGAM1968 host target gene. LOC133686 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC133686, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133686 BINDING SITE, designated SEQ ID:37053, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69508] Another function of VGAM1968 is therefore inhibition of LOC133686 (Accession XM_059667). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133686. LOC144317 (Accession XM_084813) is another VGAM1968 host target gene. LOC144317 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144317, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144317 BINDING SITE, designated SEQ ID:37718, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69509] Another function of VGAM1968 is therefore inhibition of LOC144317 (Accession XM_084813). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144317. LOC144848 (Accession XM_056770) is another VGAM1968 host target gene. LOC144848 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144848, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144848 BINDING SITE, designated SEQ ID:36421, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69510] Another function of VGAM1968 is therefore inhibition of LOC144848 (Accession XM_056770). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144848. LOC145317 (Accession XM_096760) is another VGAM1968 host target gene. LOC145317 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145317, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145317 BINDING SITE, designated SEQ ID:40531, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69511] Another function of VGAM1968 is therefore inhibition of LOC145317 (Accession XM_096760). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145317. LOC145844 (Accession XM_085255) is another VGAM1968 host target gene. LOC145844 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145844, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145844 BINDING SITE, designated SEQ ID:38001, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69512] Another function of VGAM1968 is therefore inhibition of LOC145844 (Accession XM_085255). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC145844. LOC150185 (Accession XM_097834) is another VGAM1968 host target gene. LOC150185 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150185, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150185 BINDING SITE, designated SEQ ID:41152, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69513] Another function of VGAM1968 is therefore inhibition of LOC150185 (Accession XM_097834). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150185. LOC150407 (Accession XM_086906) is another VGAM1968 host target gene. LOC150407 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150407, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150407 BINDING SITE, designated SEQ ID:38952, to the nucleotide sequence of VGAM1968 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4679.

[69514] Another function of VGAM1968 is therefore inhibition of LOC150407 (Accession XM_086906). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150407. LOC151405 (Accession XM_098058) is another VGAM1968 host target gene. LOC151405 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151405, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151405 BINDING SITE, designated SEQ ID:41339, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69515] Another function of VGAM1968 is therefore inhibition of LOC151405 (Accession XM_098058). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151405. LOC157660 (Accession XM_098805) is another VGAM1968 host target gene. LOC157660 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157660, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157660 BINDING SITE, designated SEQ ID:41830, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69516] Another function of VGAM1968 is therefore inhibition of LOC157660 (Accession XM_098805). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157660. LOC158434 (Accession XM_098939) is another VGAM1968 host target gene. LOC158434 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158434, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158434 BINDING SITE, designated SEQ ID:41986, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69517] Another function of VGAM1968 is therefore inhibition of LOC158434 (Accession XM_098939). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC158434. LOC164173 (Accession XM_089424) is another VGAM1968 host target gene. LOC164173 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC164173, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164173 BINDING SITE, designated SEQ ID:39975, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69518] Another function of VGAM1968 is therefore inhibition of LOC164173 (Accession XM_089424). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164173. LOC165741 (Accession XM_105272) is another VGAM1968 host target gene. LOC165741 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC165741, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC165741 BINDING SITE, designated SEQ ID:42192, to

the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69519] Another function of VGAM1968 is therefore inhibition of LOC165741 (Accession XM_105272). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC165741. LOC196047 (Accession XM_116883) is another VGAM1968 host target gene. LOC196047 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC196047, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196047 BINDING SITE, designated SEQ ID:43145, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69520] Another function of VGAM1968 is therefore inhibition of LOC196047 (Accession XM_116883). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196047. LOC196529 (Accession XM_113746) is another VGAM1968 host target gene. LOC196529 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC196529, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196529 BINDING SITE, designated SEQ ID:42409, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69521] Another function of VGAM1968 is therefore inhibition of LOC196529 (Accession XM_113746). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196529. LOC200942 (Accession XM_114323) is another VGAM1968 host target gene. LOC200942 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200942, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200942 BINDING SITE, designated SEQ ID:42873, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69522] Another function of VGAM1968 is therefore inhibition of LOC200942 (Accession XM_114323). Accordingly, utilities

of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200942. LOC201685 (Accession XM_117325) is another VGAM1968 host target gene. LOC201685 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201685, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201685 BINDING SITE, designated SEQ ID:43386, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69523] Another function of VGAM1968 is therefore inhibition of LOC201685 (Accession XM_117325). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201685. LOC202020 (Accession XM_114419) is another VGAM1968 host target gene. LOC202020 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202020, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC202020 BINDING SITE, designated SEQ ID:42954, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69524] Another function of VGAM1968 is therefore inhibition of LOC202020 (Accession XM_114419). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202020. LOC202934 (Accession XM_117486) is another VGAM1968 host target gene. LOC202934 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202934, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE, designated SEQ ID:43469, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69525] Another function of VGAM1968 is therefore inhibition of LOC202934 (Accession XM_117486). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202934. LOC220672 (Accession XM_017177) is another VGAM1968 host target gene. LOC220672 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220672, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220672 BINDING SITE, designated SEQ ID:30309, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69526] Another function of VGAM1968 is therefore inhibition of LOC220672 (Accession XM_017177). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220672. LOC254158 (Accession XM_172799) is another VGAM1968 host target gene. LOC254158 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254158, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254158 BINDING SITE, designated SEQ ID:46082, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69527] Another function of VGAM1968 is therefore inhibition of

LOC254158 (Accession XM_172799). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254158. LOC255045 (Accession XM_171243) is another VGAM1968 host target gene. LOC255045 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255045, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255045 BINDING SITE, designated SEQ ID:46033, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69528] Another function of VGAM1968 is therefore inhibition of LOC255045 (Accession XM_171243). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255045. LOC256536 (Accession XM_170651) is another VGAM1968 host target gene. LOC256536 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256536, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC256536 BINDING SITE, designated SEQ ID:45428, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69529] Another function of VGAM1968 is therefore inhibition of LOC256536 (Accession XM_170651). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256536. LOC257017 (Accession XM_173227) is another VGAM1968 host target gene. LOC257017 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257017, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257017 BINDING SITE, designated SEQ ID:46496, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69530] Another function of VGAM1968 is therefore inhibition of LOC257017 (Accession XM_173227). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257017. LOC56912 (Accession NM_020153) is an-

other VGAM1968 host target gene. LOC56912 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC56912, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56912 BINDING SITE, designated SEQ ID:21365, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69531] Another function of VGAM1968 is therefore inhibition of LOC56912 (Accession NM_020153). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56912. LOC85414 (Accession NM_033102) is another VGAM1968 host target gene. LOC85414 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC85414, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC85414 BINDING SITE, designated SEQ ID:26952, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69532] Another function of VGAM1968 is therefore inhibition of LOC85414 (Accession NM_033102). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC85414. LOC90183 (Accession XM_029709) is another VGAM1968 host target gene. LOC90183 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90183, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90183 BINDING SITE, designated SEQ ID:30926, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69533] Another function of VGAM1968 is therefore inhibition of LOC90183 (Accession XM_029709). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90183. LOC91272 (Accession XM_037317) is another VGAM1968 host target gene. LOC91272 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91272, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91272 BINDING SITE, designated SEQ ID:32612, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69534] Another function of VGAM1968 is therefore inhibition of LOC91272 (Accession XM_037317). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91272. LOC91301 (Accession XM_037564) is another VGAM1968 host target gene. LOC91301 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91301 BINDING SITE, designated SEQ ID:32651, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69535] Another function of VGAM1968 is therefore inhibition of LOC91301 (Accession XM_037564). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC91301. LOC91516 (Accession XM_038924) is another VGAM1968 host target gene. LOC91516 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91516 BINDING SITE, designated SEQ ID:32956, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69536] Another function of VGAM1968 is therefore inhibition of LOC91516 (Accession XM_038924). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91516. LOC91585 (Accession XM_039395) is another VGAM1968 host target gene. LOC91585 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91585, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91585 BINDING SITE, designated SEQ ID:33076, to the nucleotide sequence of VGAM1968 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4679.

[69537] Another function of VGAM1968 is therefore inhibition of LOC91585 (Accession XM_039395). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91585. LOC93166 (Accession XM_049619) is another VGAM1968 host target gene. LOC93166 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93166, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93166 BINDING SITE, designated SEQ ID:35462, to the nucleotide sequence of VGAM1968 RNA, herein designated VGAM RNA, also designated SEQ ID:4679.

[69538] Another function of VGAM1968 is therefore inhibition of LOC93166 (Accession XM_049619). Accordingly, utilities of VGAM1968 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93166. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1969 (VGAM1969) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69539] VGAM1969 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1969 was detected is described hereinabove with reference to Figs. 1-8.

[69540] VGAM1969 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM1969 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69541] VGAM1969 gene encodes a VGAM1969 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1969 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1969 precursor RNA is designated SEQ ID:1955, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1955 is located at position 88273 relative to the genome of Rana Tigrina Ranavirus.

[69542] VGAM1969 precursor RNA folds onto itself, forming

VGAM1969 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69543] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1969 folded precursor RNA into VGAM1969 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of VGAM1969 RNA is designated SEQ ID:4680, and is provided hereinbelow with reference to the sequence listing part.

[69544] VGAM1969 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1969 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1969 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69545] VGAM1969 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1969 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1969 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1969 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1969 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69546] The complementary binding of VGAM1969 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1969 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1969 host target RNA into VGAM1969 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69547] It is appreciated that VGAM1969 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1969 host target genes. The mRNA of each one of this plurality of VGAM1969 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1969 RNA, herein designated VGAM RNA, and which when bound by VGAM1969 RNA causes inhibition of translation of respective one or more VGAM1969 host target proteins.

[69548] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1969 gene, herein designated VGAM GENE, on one or more VGAM1969 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69549] It is yet further appreciated that a function of VGAM1969 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1969 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM1969 correlate with, and may be deduced from, the identity of the host target genes which VGAM1969 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[69550] Nucleotide sequences of the VGAM1969 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1969 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1969 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1969 are further described hereinbelow with reference to Table 1.

[69551] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1969 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1969 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69552] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1969 gene, herein designated VGAM is inhibition of expression of VGAM1969 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1969 correlate with, and may be deduced from, the identity of the target genes which VGAM1969 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[69553] FLJ21432 (Accession NM_024551) is a VGAM1969 host target gene. FLJ21432 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21432, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21432 BINDING SITE, designated SEQ ID:23767, to the nucleotide sequence of VGAM1969 RNA, herein designated VGAM RNA, also designated SEQ ID:4680.

[69554] A function of VGAM1969 is therefore inhibition of FLJ21432 (Accession NM_024551). Accordingly, utilities of VGAM1969 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21432. KIAA1538 (Accession XM_049474) is another VGAM1969 host target gene. KIAA1538 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1538, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1538 BINDING SITE, designated SEQ ID:35432, to the

nucleotide sequence of VGAM1969 RNA, herein designated VGAM RNA, also designated SEQ ID:4680.

[69555] Another function of VGAM1969 is therefore inhibition of KIAA1538 (Accession XM_049474). Accordingly, utilities of VGAM1969 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1538. LOC143914 (Accession XM_084654) is another VGAM1969 host target gene. LOC143914 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143914, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143914 BINDING SITE, designated SEQ ID:37635, to the nucleotide sequence of VGAM1969 RNA, herein designated VGAM RNA, also designated SEQ ID:4680.

[69556] Another function of VGAM1969 is therefore inhibition of LOC143914 (Accession XM_084654). Accordingly, utilities of VGAM1969 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143914. LOC146795 (Accession XM_085593) is another VGAM1969 host target gene. LOC146795 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC146795, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146795 BINDING SITE, designated SEQ ID:38243, to the nucleotide sequence of VGAM1969 RNA, herein designated VGAM RNA, also designated SEQ ID:4680.

[69557] Another function of VGAM1969 is therefore inhibition of LOC146795 (Accession XM_085593). Accordingly, utilities of VGAM1969 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146795. LOC154860 (Accession XM_098623) is another VGAM1969 host target gene. LOC154860 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154860, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154860 BINDING SITE, designated SEQ ID:41736, to the nucleotide sequence of VGAM1969 RNA, herein designated VGAM RNA, also designated SEQ ID:4680.

[69558] Another function of VGAM1969 is therefore inhibition of LOC154860 (Accession XM_098623). Accordingly, utilities

of VGAM1969 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154860. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1970 (VGAM1970) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69559] VGAM1970 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1970 was detected is described hereinabove with reference to Figs. 1-8.

[69560] VGAM1970 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM1970 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69561] VGAM1970 gene encodes a VGAM1970 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1970 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM1970 precursor RNA is designated SEQ ID:1956, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1956 is located at position 98318 relative to the genome of Rana Tigrina Ranavirus.

[69562] VGAM1970 precursor RNA folds onto itself, forming VGAM1970 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69563] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1970 folded precursor RNA into VGAM1970 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of VGAM1970 RNA is designated SEQ ID:4681, and

is provided hereinbelow with reference to the sequence listing part.

[69564] VGAM1970 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1970 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1970 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69565] VGAM1970 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1970 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1970 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM1970 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1970 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69566] The complementary binding of VGAM1970 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1970 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1970 host target RNA into VGAM1970 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69567] It is appreciated that VGAM1970 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1970 host target genes. The mRNA of each one of this plurality of VGAM1970 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM1970 RNA, herein designated VGAM RNA, and which when bound by VGAM1970 RNA causes inhibition of translation of respective one or more VGAM1970 host target proteins.

[69568] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1970 gene, herein designated VGAM GENE, on one or more VGAM1970 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69569] It is yet further appreciated that a function of VGAM1970 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1970 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM1970 correlate with, and may be deduced from, the identity of the host target genes which VGAM1970 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69570] Nucleotide sequences of the VGAM1970 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1970 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1970 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1970 are further described hereinbelow with reference to Table 1.

[69571] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1970 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1970 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69572] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM1970 gene, herein designated VGAM is inhibition of expression of VGAM1970 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1970 correlate with, and may be deduced from, the identity of the target genes which VGAM1970 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69573] Casein Kinase 1, Gamma 2 (CSNK1G2, Accession NM_001319) is a VGAM1970 host target gene. CSNK1G2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSNK1G2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSNK1G2 BINDING SITE, designated SEQ ID:7006, to the nucleotide sequence of VGAM1970 RNA, herein designated VGAM RNA, also designated SEQ ID:4681.

[69574] A function of VGAM1970 is therefore inhibition of Casein Kinase 1, Gamma 2 (CSNK1G2, Accession NM_001319). Accordingly, utilities of VGAM1970 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK1G2. Zinc Finger Protein 200

(ZNF200, Accession NM_003454) is another VGAM1970 host target gene. ZNF200 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF200, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF200 BINDING SITE, designated SEQ ID:9504, to the nucleotide sequence of VGAM1970 RNA, herein designated VGAM RNA, also designated SEQ ID:4681.

[69575] Another function of VGAM1970 is therefore inhibition of Zinc Finger Protein 200 (ZNF200, Accession NM_003454). Accordingly, utilities of VGAM1970 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF200. BLP1 (Accession NM_031940) is another VGAM1970 host target gene. BLP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BLP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BLP1 BINDING SITE, designated SEQ ID:25686, to the nucleotide sequence of VGAM1970 RNA, herein designated

VGAM RNA, also designated SEQ ID:4681.

[69576] Another function of VGAM1970 is therefore inhibition of BLP1 (Accession NM_031940). Accordingly, utilities of VGAM1970 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BLP1. GFR (Accession NM_012294) is another VGAM1970 host target gene. GFR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GFR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GFR BINDING SITE, designated SEQ ID:14633, to the nucleotide sequence of VGAM1970 RNA, herein designated VGAM RNA, also designated SEQ ID:4681.

[69577] Another function of VGAM1970 is therefore inhibition of GFR (Accession NM_012294). Accordingly, utilities of VGAM1970 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GFR. Interleukin 1 Receptor Accessory Protein-like 1 (IL1RAPL1, Accession NM_014271) is another VGAM1970 host target gene. IL1RAPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by IL1RAPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1RAPL1 BINDING SITE, designated SEQ ID:15551, to the nucleotide sequence of VGAM1970 RNA, herein designated VGAM RNA, also designated SEQ ID:4681.

[69578] Another function of VGAM1970 is therefore inhibition of Interleukin 1 Receptor Accessory Protein-like 1 (IL1RAPL1, Accession NM_014271). Accordingly, utilities of VGAM1970 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1RAPL1. LOC143187 (Accession NM_145206) is another VGAM1970 host target gene. LOC143187 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143187, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143187 BINDING SITE, designated SEQ ID:29746, to the nucleotide sequence of VGAM1970 RNA, herein designated VGAM RNA, also designated SEQ ID:4681.

[69579] Another function of VGAM1970 is therefore inhibition of

LOC143187 (Accession NM_145206). Accordingly, utilities of VGAM1970 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143187. LOC149711 (Accession XM_097720) is another VGAM1970 host target gene. LOC149711 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149711, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149711 BINDING SITE, designated SEQ ID:41070, to the nucleotide sequence of VGAM1970 RNA, herein designated VGAM RNA, also designated SEQ ID:4681.

[69580] Another function of VGAM1970 is therefore inhibition of LOC149711 (Accession XM_097720). Accordingly, utilities of VGAM1970 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149711. LOC90906 (Accession XM_034809) is another VGAM1970 host target gene. LOC90906 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of LOC90906 BINDING SITE, designated SEQ ID:32151, to the nucleotide sequence of VGAM1970 RNA, herein designated VGAM RNA, also designated SEQ ID:4681.

[69581] Another function of VGAM1970 is therefore inhibition of LOC90906 (Accession XM_034809). Accordingly, utilities of VGAM1970 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90906. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1971 (VGAM1971) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69582] VGAM1971 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1971 was detected is described hereinabove with reference to Figs. 1-8.

[69583] VGAM1971 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM1971 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[69584] VGAM1971 gene encodes a VGAM1971 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1971 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1971 precursor RNA is designated SEQ ID:1957, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1957 is located at position 90823 relative to the genome of Rana Tigrina Ranavirus.

[69585] VGAM1971 precursor RNA folds onto itself, forming VGAM1971 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69586] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1971 folded precursor RNA into VGAM1971 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1971 RNA is designated SEQ ID:4682, and is provided hereinbelow with reference to the sequence listing part.

[69587] VGAM1971 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1971 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1971 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69588] VGAM1971 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1971 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1971 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1971 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1971 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69589] The complementary binding of VGAM1971 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1971 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1971 host target RNA into VGAM1971 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69590] It is appreciated that VGAM1971 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1971 host target genes. The mRNA of each one of this plurality of VGAM1971 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1971 RNA, herein designated VGAM RNA, and which when bound by VGAM1971 RNA causes inhibition of translation of respective one or more VGAM1971 host target proteins.

[69591] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1971 gene, herein designated VGAM GENE, on one or more VGAM1971 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69592] It is yet further appreciated that a function of VGAM1971 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM1971 correlate with, and may be deduced from, the identity of the host target genes which VGAM1971 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69593] Nucleotide sequences of the VGAM1971 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1971 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1971 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1971 are further described hereinbelow with reference to Table 1.

[69594] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM1971 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1971 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69595] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1971 gene, herein designated VGAM is inhibition of expression of VGAM1971 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1971 correlate with, and may be deduced from, the identity of the target genes which VGAM1971 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69596] Androgen Receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) (AR, Accession NM_000044) is a VGAM1971 host target gene. AR BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AR BINDING SITE, designated SEQ ID:5487, to the nucleotide sequence of

VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69597] A function of VGAM1971 is therefore inhibition of Androgen Receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) (AR, Accession NM_000044), a gene which are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AR. The function of AR has been established by previous studies. The length of a polymorphic CAG repeat sequence occurring in the androgen receptor gene is inversely correlated with transcriptional activity by the androgen receptor. Men who possess exceptionally long CAG repeat lengths experience clinical androgen insensitivity, presumably related to reduced transcriptional activity of the receptor. Prostate carcinogenesis is dependent on androgens. Because shorter CAG repeat lengths are associated with high transcriptional activity of AR, Irvine et al. (1995) proposed that men with shorter repeat lengths will be at higher risk for prostate cancer. Some indirect evidence is consistent with

this hypothesis. African-Americans, who have generally shorter CAG repeat lengths in the AR gene, have a higher incidence and mortality rate from prostate cancer (Coetzee and Ross, 1994). Moreover, because of X linkage, a history of disease in a brother carries greater risk than paternal history. Against this background, Giovannucci et al. (1997) conducted within the Physician's Health Study a nested case-controlled study of 587 newly diagnosed cases of prostate cancer detected between 1982 and 1995, and 588 controls without prostate cancer. They found an association between fewer androgen receptor gene CAG repeats and higher risk of total prostate cancer. In particular, a shorter CAG repeat sequence was associated with cancers characterized by extraprostatic extension, distant metastases, or high histologic grade. Variability in the CAG repeat length was not associated with low-grade or low-stage disease. Animal model experiments lend further support to the function of AR. Abel et al. (2001) created transgenic mice that developed many of the motor symptoms of SBMA and had a truncated, highly expanded androgen receptor gene driven by the neurofilament light chain (OMIM Ref. No. 162280) promoter. In addition, transgenic mice created with the prion protein

(OMIM Ref. No. 176640) promoter developed widespread neurologic disease, reminiscent of juvenile forms of other polyglutamine diseases. The distribution of neurologic symptoms depended on the expression level and pattern of the promoter used, rather than on specific characteristics of androgen receptor metabolism or function. The transgenic mice that were generated developed neuronal intranuclear inclusions (NIIs), a hallmark of SBMA and the other polyglutamine diseases. These inclusions were ubiquitinated and sequestered molecular chaperones, components of the 26S proteasome (OMIM Ref. No. 604449) and the transcriptional activator CREB-binding protein. Apart from the presence of NIIs, evidence of neuropathology or neurogenic muscle atrophy was absent, suggesting to the authors that the neurologic phenotypes observed were the result of neuronal dysfunction rather than neuronal degeneration.

[69598] It is appreciated that the abovementioned animal model for AR is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[69599] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[69600] Abel, A.; Walcott, J.; Woods, J.; Duda, J.; Merry, D. E. : Expression of expanded repeat androgen receptor produces neurologic disease in transgenic mice. Hum. Molec. Genet. 10: 107-116, 2001. ; and

[69601] Irvine, R. A.; Yu, M. C.; Ross, R. K.; Coetzee, G. A. : The CAG and GGC microsatellites of the androgen receptor gene are in linkage disequilibrium in men with prostate cancer. Cancer.

[69602] Further studies establishing the function and utilities of AR are found in John Hopkins OMIM database record ID 313700, and in sited publications numbered 8395-8396, 9166-8409, 8413, 8431-8439, 1634, 8440-8449, 9181-8455, 9182, 8805, 9183, 9184, 8809, 9185, 9186-9187, 8811, 9188-8818, 1230, 8819, 9189, 9190-8825, 8229, 8838, 8976-8981, 311 and 8982-8995 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Insulin Receptor-related Receptor (INSRR, Accession XM_043563) is another VGAM1971 host target gene. INSRR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by INSRR, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of INSRR BINDING SITE, designated SEQ ID:33962, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69603] Another function of VGAM1971 is therefore inhibition of Insulin Receptor-related Receptor (INSRR, Accession XM_043563), a gene which phosphorylates the insulin receptor substrates irs-1 and irs-2. Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INSRR. The function of INSRR has been established by previous studies. Shier and Watt (1989) isolated genomic DNA that appeared to encode a novel receptor that was structurally as similar to the insulin receptor (OMIM Ref. No. 147670) and the IGF1 receptor (OMIM Ref. No. 147370) as the last two are to each other. This similarity suggested that the insulin receptor-related receptor (IRR) mediates the action of a ligand that is identical or very similar to insulin, IGF1, or IGF2. Kurachi et al. (1992) isolated IRR cDNA from rat brain and examined the expression of IRR mRNA in a variety of rat tissues. They demonstrated that, in contrast to the wide distribution of the insulin receptor and the IGF1

receptor mRNAs, the IRR mRNA is expressed preferentially in the kidney, which indicates that it has unique functions as a member of the insulin receptor family. Using genomic DNA encoding part of IRR in Southern blot analysis of DNA from human-mouse cell hybrids, Shier et al. (1990) assigned the INSRR gene to human chromosome 1. By radiation hybrid analysis, Whitmore et al. (1999) mapped the gene to chromosome 1q21-q23

[69604] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69605] Shier, P.; Willard, H. F.; Watt, V. M. : Localization of the insulin receptor-related receptor gene to human chromosome 1. Cytogenet. Cell Genet. 54: 80-81, 1990. ; and

[69606] Whitmore, T. E.; Maurer, M. F.; Day, H. L.; Jelmberg, A. C.; Dasovich, M. M.; Sundborg, L. M.; Burkhead, S. K.; Heipel, M. D.; Madden, K. L.; Kramer, J. M.; Kuijper, J. L.; Xu, W. F.; Ja.

[69607] Further studies establishing the function and utilities of INSRR are found in John Hopkins OMIM database record ID 147671, and in sited publications numbered 3210-3213 listed in the bibliography section hereinbelow, which are also hereby incorporated by refer-

ence.6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (PFKFB4, Accession NM_004567) is another VGAM1971 host target gene. PFKFB4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PFKFB4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PFKFB4 BINDING SITE, designated SEQ ID:10910, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69608] Another function of VGAM1971 is therefore inhibition of 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (PFKFB4, Accession NM_004567), a gene which catalizes synthesis and degradation of fructose 2,6-bisphosphate. Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PFKFB4. The function of PFKFB4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1316.Phosphomannomutase 2 (PMM2, Accession XM_050755) is another VGAM1971 host target gene.

PMM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PMM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMM2 BINDING SITE, designated SEQ ID:35682, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69609] Another function of VGAM1971 is therefore inhibition of Phosphomannomutase 2 (PMM2, Accession XM_050755). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMM2. Protein Kinase C, Alpha Binding Protein (PRKCABP, Accession NM_012407) is another VGAM1971 host target gene. PRKCABP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRKCABP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKCABP BINDING SITE, designated SEQ ID:14788, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM

RNA, also designated SEQ ID:4682.

[69610] Another function of VGAM1971 is therefore inhibition of Protein Kinase C, Alpha Binding Protein (PRKCABP, Accession NM_012407), a gene which may interact with the catalytic domain of protein C kinase. Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKCABP. The function of PRKCABP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Parathyroid Hormone-like Hormone (PTHLH, Accession NM_002820) is another VGAM1971 host target gene. PTHLH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTHLH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTHLH BINDING SITE, designated SEQ ID:8687, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69611] Another function of VGAM1971 is therefore inhibition of Parathyroid Hormone-like Hormone (PTHLH, Accession

NM_002820), a gene which plays a physiological role in lactation, possibly as a hormone for the mobilization and/or transfer of calcium to the milk. Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTHLH. The function of PTHLH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1590.Chromosome 2 Open Reading Frame 6 (C2orf6, Accession NM_018221) is another VGAM1971 host target gene. C2orf6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C2orf6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C2orf6 BINDING SITE, designated SEQ ID:20142, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69612] Another function of VGAM1971 is therefore inhibition of Chromosome 2 Open Reading Frame 6 (C2orf6, Accession NM_018221). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with C2orf6. DKFZp547I014 (Accession NM_020217) is another VGAM1971 host target gene. DKFZp547I014 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp547I014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547I014 BINDING SITE, designated SEQ ID:21467, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69613] Another function of VGAM1971 is therefore inhibition of DKFZp547I014 (Accession NM_020217). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547I014. EDR2 (Accession XM_018136) is another VGAM1971 host target gene. EDR2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EDR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EDR2 BINDING SITE, designated SEQ ID:30339, to the nucleotide se-

quence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69614] Another function of VGAM1971 is therefore inhibition of EDR2 (Accession XM_018136). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EDR2. FLJ10700 (Accession NM_018182) is another VGAM1971 host target gene. FLJ10700 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10700, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10700 BINDING SITE, designated SEQ ID:20020, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69615] Another function of VGAM1971 is therefore inhibition of FLJ10700 (Accession NM_018182). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10700. FLJ11160 (Accession NM_018344) is another VGAM1971 host target gene. FLJ11160 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ11160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11160 BINDING SITE, designated SEQ ID:20353, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69616] Another function of VGAM1971 is therefore inhibition of FLJ11160 (Accession NM_018344). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11160. FLJ12270 (Accession NM_030581) is another VGAM1971 host target gene. FLJ12270 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12270, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12270 BINDING SITE, designated SEQ ID:24954, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69617] Another function of VGAM1971 is therefore inhibition of FLJ12270 (Accession NM_030581). Accordingly, utilities of

VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12270. FLJ12294 (Accession NM_025100) is another VGAM1971 host target gene. FLJ12294 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12294 BINDING SITE, designated SEQ ID:24746, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69618] Another function of VGAM1971 is therefore inhibition of FLJ12294 (Accession NM_025100). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12294. FLJ14297 (Accession NM_024903) is another VGAM1971 host target gene. FLJ14297 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14297, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14297

BINDING SITE, designated SEQ ID:24392, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69619] Another function of VGAM1971 is therefore inhibition of FLJ14297 (Accession NM_024903). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14297. FLJ22329 (Accession NM_024656) is another VGAM1971 host target gene. FLJ22329 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22329, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22329 BINDING SITE, designated SEQ ID:23958, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69620] Another function of VGAM1971 is therefore inhibition of FLJ22329 (Accession NM_024656). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22329. IKKE (Accession NM_014002) is another VGAM1971 host target gene. IKKE BINDING SITE is HOST

TARGET binding site found in the 5` untranslated region of mRNA encoded by IKKE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IKKE BINDING SITE, designated SEQ ID:15202, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69621] Another function of VGAM1971 is therefore inhibition of IKKE (Accession NM_014002). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IKKE. KIAA1344 (Accession XM_051699) is another VGAM1971 host target gene. KIAA1344 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1344, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1344 BINDING SITE, designated SEQ ID:35874, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69622] Another function of VGAM1971 is therefore inhibition of

KIAA1344 (Accession XM_051699). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1344. MAP (Accession NM_022818) is another VGAM1971 host target gene. MAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP BINDING SITE, designated SEQ ID:23097, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69623] Another function of VGAM1971 is therefore inhibition of MAP (Accession NM_022818). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP. MGC13061 (Accession NM_032322) is another VGAM1971 host target gene. MGC13061 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC13061, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of MGC13061 BINDING SITE, designated SEQ ID:26130, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69624] Another function of VGAM1971 is therefore inhibition of MGC13061 (Accession NM_032322). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13061. MGC1842 (Accession XM_037797) is another VGAM1971 host target gene. MGC1842 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC1842, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC1842 BINDING SITE, designated SEQ ID:32688, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69625] Another function of VGAM1971 is therefore inhibition of MGC1842 (Accession XM_037797). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC1842. PRO0943 (Accession NM_018568) is another

VGAM1971 host target gene. PRO0943 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0943, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0943 BINDING SITE, designated SEQ ID:20651, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69626] Another function of VGAM1971 is therefore inhibition of PRO0943 (Accession NM_018568). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0943. SEC14-like 1 (S. cerevisiae) (SEC14L1, Accession NM_003003) is another VGAM1971 host target gene. SEC14L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC14L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC14L1 BINDING SITE, designated SEQ ID:8903, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ

ID:4682.

[69627] Another function of VGAM1971 is therefore inhibition of SEC14-like 1 (S. cerevisiae) (SEC14L1, Accession NM_003003). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC14L1. Solute Carrier Family 26, Member 9 (SLC26A9, Accession NM_052934) is another VGAM1971 host target gene. SLC26A9 BINDING SITE1 and SLC26A9 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SLC26A9, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC26A9 BINDING SITE1 and SLC26A9 BINDING SITE2, designated SEQ ID:27494 and SEQ ID:28632 respectively, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69628] Another function of VGAM1971 is therefore inhibition of Solute Carrier Family 26, Member 9 (SLC26A9, Accession NM_052934). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC26A9. Zinc Finger Pro-

tein 387 (ZNF387, Accession NM_014682) is another VGAM1971 host target gene. ZNF387 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF387, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF387 BINDING SITE, designated SEQ ID:16180, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69629] Another function of VGAM1971 is therefore inhibition of Zinc Finger Protein 387 (ZNF387, Accession NM_014682). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF387. LOC153688 (Accession XM_098416) is another VGAM1971 host target gene. LOC153688 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153688, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153688 BINDING SITE, designated SEQ ID:41660, to the nucleotide sequence of

VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69630] Another function of VGAM1971 is therefore inhibition of LOC153688 (Accession XM_098416). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153688. LOC154428 (Accession XM_098528) is another VGAM1971 host target gene. LOC154428 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154428, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154428 BINDING SITE, designated SEQ ID:41703, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69631] Another function of VGAM1971 is therefore inhibition of LOC154428 (Accession XM_098528). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154428. LOC157273 (Accession XM_098743) is another VGAM1971 host target gene. LOC157273 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC157273, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157273 BINDING SITE, designated SEQ ID:41786, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69632] Another function of VGAM1971 is therefore inhibition of LOC157273 (Accession XM_098743). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157273. LOC163255 (Accession XM_092121) is another VGAM1971 host target gene. LOC163255 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC163255, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163255 BINDING SITE, designated SEQ ID:40109, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69633] Another function of VGAM1971 is therefore inhibition of LOC163255 (Accession XM_092121). Accordingly, utilities

of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163255. LOC220020 (Accession XM_167821) is another VGAM1971 host target gene. LOC220020 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220020, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220020 BINDING SITE, designated SEQ ID:44867, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69634] Another function of VGAM1971 is therefore inhibition of LOC220020 (Accession XM_167821). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220020. LOC91266 (Accession XM_037268) is another VGAM1971 host target gene. LOC91266 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC91266 BINDING SITE, designated SEQ ID:32604, to the nucleotide sequence of VGAM1971 RNA, herein designated VGAM RNA, also designated SEQ ID:4682.

[69635] Another function of VGAM1971 is therefore inhibition of LOC91266 (Accession XM_037268). Accordingly, utilities of VGAM1971 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91266. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1972 (VGAM1972) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69636] VGAM1972 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1972 was detected is described hereinabove with reference to Figs. 1-8.

[69637] VGAM1972 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine Herpesvirus 4. VGAM1972 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69638] VGAM1972 gene encodes a VGAM1972 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1972 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1972 precursor RNA is designated SEQ ID:1958, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1958 is located at position 10062 relative to the genome of Bovine Herpesvirus 4.

[69639] VGAM1972 precursor RNA folds onto itself, forming VGAM1972 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69640] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1972 folded precursor RNA into VGAM1972 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM1972 RNA is designated SEQ ID:4683, and is provided hereinbelow with reference to the sequence listing part.

[69641] VGAM1972 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1972 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1972 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69642] VGAM1972 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1972 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1972 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1972 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1972 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69643] The complementary binding of VGAM1972 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1972 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1972 host target RNA into VGAM1972 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69644] It is appreciated that VGAM1972 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1972 host target genes. The mRNA of each one of this plurality of VGAM1972 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1972 RNA, herein designated VGAM RNA, and which when bound by VGAM1972 RNA causes inhibition of translation of respective one or more VGAM1972 host target proteins.

[69645] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1972 gene, herein designated VGAM GENE, on one or more VGAM1972 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69646] It is yet further appreciated that a function of VGAM1972 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1972 include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1972 correlate with, and may be deduced from, the identity of the host target genes which VGAM1972 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69647] Nucleotide sequences of the VGAM1972 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1972 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1972 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1972 are further described hereinbelow with reference to Table 1.

[69648] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1972 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM1972 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69649] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1972 gene, herein designated VGAM is inhibition of expression of VGAM1972 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1972 correlate with, and may be deduced from, the identity of the target genes which VGAM1972 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69650] B-cell CLL/lymphoma 10 (BCL10, Accession NM_003921) is a VGAM1972 host target gene. BCL10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL10 BINDING SITE, designated SEQ ID:10009, to the nucleotide sequence of VGAM1972 RNA, herein designated VGAM RNA, also designated SEQ ID:4683.

[69651] A function of VGAM1972 is therefore inhibition of B-cell

CLL/lymphoma 10 (BCL10, Accession NM_003921), a gene which is a positive regulator of lymphocyte proliferation, NF-kappaB activator. Accordingly, utilities of VGAM1972 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL10. The function of BCL10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Golgi Complex Associated Protein 1, 60kDa (GOCAP1, Accession NM_022735) is another VGAM1972 host target gene. GOCAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GOCAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GOCAP1 BINDING SITE, designated SEQ ID:22939, to the nucleotide sequence of VGAM1972 RNA, herein designated VGAM RNA, also designated SEQ ID:4683.

[69652] Another function of VGAM1972 is therefore inhibition of Golgi Complex Associated Protein 1, 60kDa (GOCAP1, Accession NM_022735). Accordingly, utilities of VGAM1972 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with GOCAP1. G Protein-coupled Receptor 86 (GPR86, Accession NM_023914) is another VGAM1972 host target gene. GPR86 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPR86, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR86 BINDING SITE, designated SEQ ID:23387, to the nucleotide sequence of VGAM1972 RNA, herein designated VGAM RNA, also designated SEQ ID:4683.

[69653] Another function of VGAM1972 is therefore inhibition of G Protein-coupled Receptor 86 (GPR86, Accession NM_023914), a gene which plays a role in cell communication. Accordingly, utilities of VGAM1972 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR86. The function of GPR86 has been established by previous studies. By batch EST database searching, Wittenberger et al. (2001) identified a cDNA encoding GPR86. The deduced 333-amino acid protein lacks a leader peptide but possesses a DRF motif. Northern blot analysis revealed wide expression of a 2.9-kb GPR86 transcript in spleen, with weaker expres-

sion in placenta, leukocytes, and brain. In brain, expression was strongest in substantia nigra, thalamus, and medulla. Communi et al. (2001) determined that GPR86 shows a high affinity for ADP through pharmacologic characterization of GPR86-transfected human astrocytoma cells and CHO cells. Stimulation of GPR86 by ADP in stably expressing CHO cells resulted in inhibition of adenylyl cyclase and the phosphorylation of the MAP kinases Erk1 (OMIM Ref. No. 601795) and Erk2 (OMIM Ref. No. 176948). Communi et al. (2001) noted that inhibition of adenylyl cyclase and phosphorylation of the MAP kinases are transduction mechanisms that involve Gi proteins (see OMIM Ref. No. 139310).

[69654] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69655] Communi, D.; Gonzalez, N. S.; Detheux, M.; Brezillon, S.; Lannoy, V.; Parmentier, M.; Boeynaems, J.-M. : Identification of a novel human ADP receptor coupled to G(i). J. Biol. Chem. 276: 41479-41485, 2001. ; and

[69656] Wittenberger, T.; Schaller, H. C.; Hellebrand, S. : An expressed sequence tag (EST) data mining strategy succeeding in the discovery of new G-protein coupled receptors. J.

Molec. Biol.

[69657] Further studies establishing the function and utilities of GPR86 are found in John Hopkins OMIM database record ID 606380, and in sited publications numbered 647 and 10637 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Nuclear Receptor Subfamily 3, Group C, Member 1 (glucocorticoid receptor) (NR3C1, Accession NM_000176) is another VGAM1972 host target gene. NR3C1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NR3C1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR3C1 BINDING SITE, designated SEQ ID:5685, to the nucleotide sequence of VGAM1972 RNA, herein designated VGAM RNA, also designated SEQ ID:4683.

[69658] Another function of VGAM1972 is therefore inhibition of Nuclear Receptor Subfamily 3, Group C, Member 1 (glucocorticoid receptor) (NR3C1, Accession NM_000176). Accordingly, utilities of VGAM1972 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR3C1. Calneuron 1 (CALN1, Acces-

sion NM_031468) is another VGAM1972 host target gene. CALN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CALN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CALN1 BINDING SITE, designated SEQ ID:25515, to the nucleotide sequence of VGAM1972 RNA, herein designated VGAM RNA, also designated SEQ ID:4683.

[69659] Another function of VGAM1972 is therefore inhibition of Calneuron 1 (CALN1, Accession NM_031468). Accordingly, utilities of VGAM1972 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CALN1. Isopentenyl-diphosphate Delta Isomerase (IDI1, Accession XM_040272) is another VGAM1972 host target gene. IDI1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IDI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IDI1 BINDING SITE, designated SEQ ID:33285, to the nucleotide sequence of VGAM1972 RNA,

herein designated VGAM RNA, also designated SEQ ID:4683.

[69660] Another function of VGAM1972 is therefore inhibition of Isopentenyl-diphosphate Delta Isomerase (IDI1, Accession XM_040272). Accordingly, utilities of VGAM1972 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IDI1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1973 (VGAM1973) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69661] VGAM1973 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1973 was detected is described hereinabove with reference to Figs. 1-8.

[69662] VGAM1973 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine Herpesvirus 4. VGAM1973 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69663] VGAM1973 gene encodes a VGAM1973 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1973 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1973 precursor RNA is designated SEQ ID:1959, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1959 is located at position 5233 relative to the genome of Bovine Herpesvirus 4.

[69664] VGAM1973 precursor RNA folds onto itself, forming VGAM1973 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69665] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1973 folded precursor RNA into VGAM1973 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1973 RNA is designated SEQ ID:4684, and is provided hereinbelow with reference to the sequence listing part.

[69666] VGAM1973 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1973 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1973 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69667] VGAM1973 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1973 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1973 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1973 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1973 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69668] The complementary binding of VGAM1973 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1973 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1973 host target RNA into VGAM1973 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69669] It is appreciated that VGAM1973 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1973 host target genes. The mRNA of each one of this plurality of VGAM1973 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1973 RNA, herein designated VGAM RNA, and which when bound by VGAM1973 RNA causes inhibition of translation of respective one or more VGAM1973 host target proteins.

[69670] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1973 gene, herein designated VGAM GENE, on one or more VGAM1973 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69671] It is yet further appreciated that a function of VGAM1973 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1973 include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1973 correlate with, and may be deduced from, the identity of the host target genes which VGAM1973 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69672] Nucleotide sequences of the VGAM1973 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1973 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1973 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1973 are further described hereinbelow with reference to Table 1.

[69673] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1973 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM1973 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69674] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1973 gene, herein designated VGAM is inhibition of expression of VGAM1973 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1973 correlate with, and may be deduced from, the identity of the target genes which VGAM1973 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69675] V-abl Abelson Murine Leukemia Viral Oncogene Homolog 1 (ABL1, Accession NM_005157) is a VGAM1973 host target gene. ABL1 BINDING SITE1 and ABL1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ABL1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABL1 BINDING SITE1 and ABL1 BINDING SITE2, designated SEQ ID:11638 and SEQ ID:14227 respectively, to the nucleotide sequence of VGAM1973 RNA, herein designated VGAM RNA, also designated SEQ ID:4684.

[69676] A function of VGAM1973 is therefore inhibition of V-abl Abelson Murine Leukemia Viral Oncogene Homolog 1 (ABL1, Accession NM_005157). Accordingly, utilities of VGAM1973 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABL1. Kinesin-like 3 (KNSL3, Accession NM_005355) is another VGAM1973 host target gene. KNSL3 BINDING SITE1 and KNSL3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KNSL3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KNSL3 BINDING SITE1 and KNSL3 BINDING SITE2, designated SEQ ID:11823 and SEQ ID:24961 respectively, to the nucleotide sequence of VGAM1973 RNA, herein designated VGAM RNA, also designated SEQ ID:4684.

[69677] Another function of VGAM1973 is therefore inhibition of Kinesin-like 3 (KNSL3, Accession NM_005355), a gene which may function in intracellular transport and mitosis. Accordingly, utilities of VGAM1973 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KNSL3. The function of KNSL3 and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Cellular Repressor of E1A-stimulated Genes (CREG, Accession NM_003851) is another VGAM1973 host target gene. CREG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CREG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CREG BINDING SITE, designated SEQ ID:9947, to the nucleotide sequence of VGAM1973 RNA, herein designated VGAM RNA, also designated SEQ ID:4684.

[69678] Another function of VGAM1973 is therefore inhibition of Cellular Repressor of E1A-stimulated Genes (CREG, Accession NM_003851). Accordingly, utilities of VGAM1973 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CREG. FLJ22794 (Accession XM_166220) is another VGAM1973 host target gene. FLJ22794 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22794 BINDING SITE, designated SEQ ID:44027, to the nucleotide sequence of VGAM1973 RNA, herein designated VGAM RNA, also designated SEQ ID:4684.

[69679] Another function of VGAM1973 is therefore inhibition of FLJ22794 (Accession XM_166220). Accordingly, utilities of VGAM1973 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22794. KIAA0522 (Accession XM_050404) is another VGAM1973 host target gene. KIAA0522 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0522, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0522 BINDING SITE, designated SEQ ID:35622, to the nucleotide sequence of VGAM1973 RNA, herein designated VGAM RNA, also designated SEQ ID:4684.

[69680] Another function of VGAM1973 is therefore inhibition of KIAA0522 (Accession XM_050404). Accordingly, utilities of VGAM1973 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0522. KIAA0532 (Accession XM_047659) is another VGAM1973 host target gene. KIAA0532 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0532, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0532 BINDING SITE, designated SEQ ID:35023, to the nucleotide sequence of VGAM1973 RNA, herein designated VGAM RNA, also designated SEQ ID:4684.

[69681] Another function of VGAM1973 is therefore inhibition of KIAA0532 (Accession XM_047659). Accordingly, utilities of VGAM1973 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0532. MIL1 (Accession NM_015367) is another VGAM1973 host target gene. MIL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MIL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MIL1 BINDING SITE, designated SEQ ID:17666, to the nucleotide sequence of VGAM1973 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4684.

[69682] Another function of VGAM1973 is therefore inhibition of MIL1 (Accession NM_015367). Accordingly, utilities of VGAM1973 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIL1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1974 (VGAM1974) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69683] VGAM1974 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1974 was detected is described hereinabove with reference to Figs. 1-8.

[69684] VGAM1974 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine Herpesvirus 4. VGAM1974 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69685] VGAM1974 gene encodes a VGAM1974 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM1974 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1974 precursor RNA is designated SEQ ID:1960, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1960 is located at position 14078 relative to the genome of Bovine Herpesvirus 4.

[69686] VGAM1974 precursor RNA folds onto itself, forming VGAM1974 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69687] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1974 folded precursor RNA into VGAM1974 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 44%) nucleotide sequence of VGAM1974 RNA is designated SEQ ID:4685, and is provided hereinbelow with reference to the sequence listing part.

[69688] VGAM1974 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1974 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1974 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69689] VGAM1974 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1974 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1974 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1974 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1974 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69690] The complementary binding of VGAM1974 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1974 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1974 host target RNA into VGAM1974 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69691] It is appreciated that VGAM1974 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1974 host target genes. The mRNA of each one of this plurality of VGAM1974 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1974 RNA, herein designated VGAM RNA, and which when bound by VGAM1974 RNA causes inhibition of translation of respective one or more VGAM1974 host target proteins.

[69692] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1974 gene, herein designated VGAM GENE, on one or more VGAM1974 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69693] It is yet further appreciated that a function of VGAM1974 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1974 include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1974 correlate with, and may be deduced from, the identity of the host target genes which VGAM1974 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69694] Nucleotide sequences of the VGAM1974 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1974 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1974 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1974 are further described hereinbelow with reference to Table 1.

[69695] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1974 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1974 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[69696] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1974 gene, herein designated VGAM is inhibition of expression of VGAM1974 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1974 correlate with, and may be deduced from, the identity of the target genes which VGAM1974 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69697] Frizzled Homolog 10 (Drosophila) (FZD10, Accession NM_007197) is a VGAM1974 host target gene. FZD10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FZD10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FZD10 BINDING SITE, designated SEQ ID:14050, to the nucleotide sequence of VGAM1974 RNA, herein designated VGAM RNA, also designated SEQ ID:4685.

[69698] A function of VGAM1974 is therefore inhibition of Frizzled Homolog 10 (Drosophila) (FZD10, Accession NM_007197). Accordingly, utilities of VGAM1974 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with FZD10. FLJ13621 (Accession NM_025009) is another VGAM1974 host target gene. FLJ13621 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13621, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13621 BINDING SITE, designated SEQ ID:24580, to the nucleotide sequence of VGAM1974 RNA, herein designated VGAM RNA, also designated SEQ ID:4685.

[69699] Another function of VGAM1974 is therefore inhibition of FLJ13621 (Accession NM_025009). Accordingly, utilities of VGAM1974 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13621. KIAA0781 (Accession XM_041314) is another VGAM1974 host target gene. KIAA0781 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0781, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0781 BINDING SITE, designated SEQ ID:33497, to the

nucleotide sequence of VGAM1974 RNA, herein designated VGAM RNA, also designated SEQ ID:4685.

[69700] Another function of VGAM1974 is therefore inhibition of KIAA0781 (Accession XM_041314). Accordingly, utilities of VGAM1974 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0781. Kruppel-like Factor 5 (intestinal) (KLF5, Accession NM_001730) is another VGAM1974 host target gene. KLF5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLF5 BINDING SITE, designated SEQ ID:7460, to the nucleotide sequence of VGAM1974 RNA, herein designated VGAM RNA, also designated SEQ ID:4685.

[69701] Another function of VGAM1974 is therefore inhibition of Kruppel-like Factor 5 (intestinal) (KLF5, Accession NM_001730). Accordingly, utilities of VGAM1974 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF5. N-acetylated Alpha-linked Acidic Dipeptidase 2 (NAALAD2, Accession NM_005467) is another VGAM1974 host target gene.

NAALAD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NAALAD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAALAD2 BINDING SITE, designated SEQ ID:11962, to the nucleotide sequence of VGAM1974 RNA, herein designated VGAM RNA, also designated SEQ ID:4685.

[69702] Another function of VGAM1974 is therefore inhibition of N-acetylated Alpha-linked Acidic Dipeptidase 2 (NAALAD2, Accession NM_005467). Accordingly, utilities of VGAM1974 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAALAD2. LOC148266 (Accession XM_086128) is another VGAM1974 host target gene. LOC148266 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148266 BINDING SITE, designated SEQ ID:38515, to the nucleotide sequence of VGAM1974 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4685.

[69703] Another function of VGAM1974 is therefore inhibition of LOC148266 (Accession XM_086128). Accordingly, utilities of VGAM1974 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148266. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1975 (VGAM1975) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69704] VGAM1975 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1975 was detected is described hereinabove with reference to Figs. 1-8.

[69705] VGAM1975 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine Herpesvirus 4. VGAM1975 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69706] VGAM1975 gene encodes a VGAM1975 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM1975 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1975 precursor RNA is designated SEQ ID:1961, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1961 is located at position 9804 relative to the genome of Bovine Herpesvirus 4.

[69707] VGAM1975 precursor RNA folds onto itself, forming VGAM1975 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69708] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1975 folded precursor RNA into VGAM1975 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1975 RNA is designated SEQ ID:4686, and is provided hereinbelow with reference to the sequence listing part.

[69709] VGAM1975 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1975 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1975 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69710] VGAM1975 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1975 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1975 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1975 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1975 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69711] The complementary binding of VGAM1975 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1975 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1975 host target RNA into VGAM1975 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69712] It is appreciated that VGAM1975 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1975 host target genes. The mRNA of

each one of this plurality of VGAM1975 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1975 RNA, herein designated VGAM RNA, and which when bound by VGAM1975 RNA causes inhibition of translation of respective one or more VGAM1975 host target proteins.

[69713] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1975 gene, herein designated VGAM GENE, on one or more VGAM1975 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[69714] It is yet further appreciated that a function of VGAM1975 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1975 correlate with, and may be deduced from, the identity of the host target genes which VGAM1975 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69715] Nucleotide sequences of the VGAM1975 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1975 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1975 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1975 are further described hereinbelow with reference to Table 1.

[69716] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1975 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1975 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69717] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1975 gene, herein designated VGAM is inhibition of expression of VGAM1975 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1975 correlate with, and may be deduced from, the identity of the target genes which VGAM1975 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69718] Fibroblast Growth Factor 7 (keratinocyte growth factor) (FGF7, Accession NM_002009) is a VGAM1975 host target gene. FGF7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGF7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF7 BINDING SITE, designated SEQ ID:7748, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69719] A function of VGAM1975 is therefore inhibition of Fibroblast Growth Factor 7 (keratinocyte growth factor) (FGF7, Accession NM_002009), a gene which growth factor active

on keratinocytes. Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF7. The function of FGF7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM678.Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_001879) is another VGAM1975 host target gene. MASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MASP1 BINDING SITE, designated SEQ ID:7604, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69720] Another function of VGAM1975 is therefore inhibition of Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_001879), a gene which a complement-dependent bactericidal factor . Accordingly, utilities of VGAM1975 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with MASP1. The function of MASP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM566.Methyltransferase-like 1 (METTL1, Accession NM_023032) is another VGAM1975 host target gene. METTL1 BINDING SITE1 and METTL1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by METTL1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of METTL1 BINDING SITE1 and METTL1 BINDING SITE2, designated SEQ ID:23308 and SEQ ID:23313 respectively, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69721] Another function of VGAM1975 is therefore inhibition of Methyltransferase-like 1 (METTL1, Accession NM_023032). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with METTL1. Myosin, Heavy Polypeptide 11, Smooth Muscle (MYH11, Accession

NM_002474) is another VGAM1975 host target gene. MYH11 BINDING SITE1 and MYH11 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MYH11, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYH11 BINDING SITE1 and MYH11 BINDING SITE2, designated SEQ ID:8298 and SEQ ID:8334 respectively, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69722] Another function of VGAM1975 is therefore inhibition of Myosin, Heavy Polypeptide 11, Smooth Muscle (MYH11, Accession NM_002474), a gene which is involved in muscle contraction. Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYH11. The function of MYH11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM178.Paired Mesoderm Homeo Box 1 (PMX1, Accession NM_006902) is another VGAM1975 host target gene. PMX1 BINDING SITE1 and PMX1 BINDING SITE2 are HOST

TARGET binding sites found in untranslated regions of mRNA encoded by PMX1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMX1 BINDING SITE1 and PMX1 BINDING SITE2, designated SEQ ID:13777 and SEQ ID:22912 respectively, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69723] Another function of VGAM1975 is therefore inhibition of Paired Mesoderm Homeo Box 1 (PMX1, Accession NM_006902), a gene which acts as a transcriptional regulator of muscle creatine kinase. Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMX1. The function of PMX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Contactin Associated Protein 1 (CNTNAP1, Accession NM_003632) is another VGAM1975 host target gene. CNTNAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNTNAP1, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNTNAP1 BINDING SITE, designated SEQ ID:9694, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69724] Another function of VGAM1975 is therefore inhibition of Contactin Associated Protein 1 (CNTNAP1, Accession NM_003632). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNTNAP1. DKFZP434P1750 (Accession NM_015527) is another VGAM1975 host target gene. DKFZP434P1750 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434P1750, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434P1750 BINDING SITE, designated SEQ ID:17792, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69725] Another function of VGAM1975 is therefore inhibition of DKFZP434P1750 (Accession NM_015527). Accordingly,

utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434P1750. FLJ10687 (Accession NM_018178) is another VGAM1975 host target gene. FLJ10687 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10687, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10687 BINDING SITE, designated SEQ ID:20006, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69726] Another function of VGAM1975 is therefore inhibition of FLJ10687 (Accession NM_018178). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10687. FLJ11286 (Accession NM_018381) is another VGAM1975 host target gene. FLJ11286 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11286, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11286

BINDING SITE, designated SEQ ID:20412, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69727] Another function of VGAM1975 is therefore inhibition of FLJ11286 (Accession NM_018381). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11286. FLJ14154 (Accession NM_024845) is another VGAM1975 host target gene. FLJ14154 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14154, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14154 BINDING SITE, designated SEQ ID:24272, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69728] Another function of VGAM1975 is therefore inhibition of FLJ14154 (Accession NM_024845). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14154. FLJ20619 (Accession NM_017904) is another VGAM1975 host target gene. FLJ20619 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20619, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20619 BINDING SITE, designated SEQ ID:19570, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69729] Another function of VGAM1975 is therefore inhibition of FLJ20619 (Accession NM_017904). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20619. HN1L (Accession NM_144570) is another VGAM1975 host target gene. HN1L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HN1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HN1L BINDING SITE, designated SEQ ID:29377, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69730] Another function of VGAM1975 is therefore inhibition of

HN1L (Accession NM_144570). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HN1L. Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 1 (KCNS1, Accession NM_002251) is another VGAM1975 host target gene. KCNS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNS1 BINDING SITE, designated SEQ ID:8040, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69731] Another function of VGAM1975 is therefore inhibition of Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 1 (KCNS1, Accession NM_002251). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNS1. KIAA0435 (Accession NM_014801) is another VGAM1975 host target gene. KIAA0435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0435, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0435 BINDING SITE, designated SEQ ID:16720, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69732] Another function of VGAM1975 is therefore inhibition of KIAA0435 (Accession NM_014801). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0435. KIAA0544 (Accession XM_048119) is another VGAM1975 host target gene. KIAA0544 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0544, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0544 BINDING SITE, designated SEQ ID:35112, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69733] Another function of VGAM1975 is therefore inhibition of KIAA0544 (Accession XM_048119). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0544. KIAA0556 (Accession XM_044632) is another VGAM1975 host target gene. KIAA0556 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0556, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0556 BINDING SITE, designated SEQ ID:34251, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69734] Another function of VGAM1975 is therefore inhibition of KIAA0556 (Accession XM_044632). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0556. KIAA0848 (Accession NM_014926) is another VGAM1975 host target gene. KIAA0848 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0848, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0848 BINDING SITE, designated SEQ ID:17212, to the

nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69735] Another function of VGAM1975 is therefore inhibition of KIAA0848 (Accession NM_014926). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0848. MGC2574 (Accession NM_024098) is another VGAM1975 host target gene. MGC2574 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2574, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2574 BINDING SITE, designated SEQ ID:23539, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69736] Another function of VGAM1975 is therefore inhibition of MGC2574 (Accession NM_024098). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2574. N4BP3 (Accession XM_038920) is another VGAM1975 host target gene. N4BP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by N4BP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of N4BP3 BINDING SITE, designated SEQ ID:32936, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69737] Another function of VGAM1975 is therefore inhibition of N4BP3 (Accession XM_038920). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with N4BP3. SARM (Accession NM_015077) is another VGAM1975 host target gene. SARM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SARM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SARM BINDING SITE, designated SEQ ID:17450, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69738] Another function of VGAM1975 is therefore inhibition of SARM (Accession NM_015077). Accordingly, utilities of

VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SARM. SCYA16 (Accession NM_004590) is another VGAM1975 host target gene. SCYA16 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCYA16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCYA16 BINDING SITE, designated SEQ ID:10933, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69739] Another function of VGAM1975 is therefore inhibition of SCYA16 (Accession NM_004590). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCYA16. Synaptotagmin-like 2 (SYTL2, Accession NM_032943) is another VGAM1975 host target gene. SYTL2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SYTL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of SYTL2 BINDING SITE, designated SEQ ID:26757, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69740] Another function of VGAM1975 is therefore inhibition of Synaptotagmin-like 2 (SYTL2, Accession NM_032943). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYTL2. XT2 (Accession NM_022167) is another VGAM1975 host target gene. XT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XT2 BINDING SITE, designated SEQ ID:22721, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69741] Another function of VGAM1975 is therefore inhibition of XT2 (Accession NM_022167). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XT2. LOC145195 (Accession XM_096731) is another

VGAM1975 host target gene. LOC145195 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145195 BINDING SITE, designated SEQ ID:40511, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69742] Another function of VGAM1975 is therefore inhibition of LOC145195 (Accession XM_096731). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145195. LOC148137 (Accession NM_144692) is another VGAM1975 host target gene. LOC148137 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148137, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148137 BINDING SITE, designated SEQ ID:29512, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69743] Another function of VGAM1975 is therefore inhibition of LOC148137 (Accession NM_144692). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148137. LOC158116 (Accession XM_016240) is another VGAM1975 host target gene. LOC158116 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158116, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158116 BINDING SITE, designated SEQ ID:30251, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69744] Another function of VGAM1975 is therefore inhibition of LOC158116 (Accession XM_016240). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158116. LOC160646 (Accession XM_090413) is another VGAM1975 host target gene. LOC160646 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC160646, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC160646 BINDING SITE, designated SEQ ID:40003, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69745] Another function of VGAM1975 is therefore inhibition of LOC160646 (Accession XM_090413). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC160646. LOC51200 (Accession NM_016352) is another VGAM1975 host target gene. LOC51200 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51200, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51200 BINDING SITE, designated SEQ ID:18479, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69746] Another function of VGAM1975 is therefore inhibition of LOC51200 (Accession NM_016352). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC51200. LOC51267 (Accession NM_016511) is another VGAM1975 host target gene. LOC51267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51267 BINDING SITE, designated SEQ ID:18590, to the nucleotide sequence of VGAM1975 RNA, herein designated VGAM RNA, also designated SEQ ID:4686.

[69747] Another function of VGAM1975 is therefore inhibition of LOC51267 (Accession NM_016511). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51267. LOC81558 (Accession NM_030802) is another VGAM1975 host target gene. LOC81558 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC81558, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC81558 BINDING SITE, designated SEQ ID:25110, to the nucleotide sequence of VGAM1975 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4686.

[69748] Another function of VGAM1975 is therefore inhibition of LOC81558 (Accession NM_030802). Accordingly, utilities of VGAM1975 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC81558. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1976 (VGAM1976) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69749] VGAM1976 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1976 was detected is described hereinabove with reference to Figs. 1-8.

[69750] VGAM1976 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine Herpesvirus 4. VGAM1976 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69751] VGAM1976 gene encodes a VGAM1976 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM1976 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1976 precursor RNA is designated SEQ ID:1962, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1962 is located at position 13694 relative to the genome of Bovine Herpesvirus 4.

[69752] VGAM1976 precursor RNA folds onto itself, forming VGAM1976 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69753] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1976 folded precursor RNA into VGAM1976 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1976 RNA is designated SEQ ID:4687, and is provided hereinbelow with reference to the sequence listing part.

[69754] VGAM1976 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1976 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1976 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69755] VGAM1976 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1976 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1976 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1976 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1976 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69756] The complementary binding of VGAM1976 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1976 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1976 host target RNA into VGAM1976 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69757] It is appreciated that VGAM1976 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1976 host target genes. The mRNA of

each one of this plurality of VGAM1976 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1976 RNA, herein designated VGAM RNA, and which when bound by VGAM1976 RNA causes inhibition of translation of respective one or more VGAM1976 host target proteins.

[69758] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1976 gene, herein designated VGAM GENE, on one or more VGAM1976 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[69759] It is yet further appreciated that a function of VGAM1976 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1976 correlate with, and may be deduced from, the identity of the host target genes which VGAM1976 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69760] Nucleotide sequences of the VGAM1976 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1976 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1976 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1976 are further described hereinbelow with reference to Table 1.

[69761] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1976 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1976 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69762] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1976 gene, herein designated VGAM is inhibition of expression of VGAM1976 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1976 correlate with, and may be deduced from, the identity of the target genes which VGAM1976 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69763] Dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD, Accession NM_000109) is a VGAM1976 host target gene. DMD BINDING SITE1 through DMD BINDING SITE13 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DMD, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DMD BINDING SITE1 through DMD BINDING SITE13, designated SEQ ID:5574, SEQ ID:10157, SEQ ID:10164, SEQ ID:10170, SEQ ID:10178, SEQ ID:10183, SEQ ID:10188, SEQ ID:10199, SEQ ID:10205, SEQ ID:10210, SEQ ID:10215, SEQ ID:10226 and SEQ ID:10238 respectively, to the nu-

cleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69764] A function of VGAM1976 is therefore inhibition of Dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD, Accession NM_000109), a gene which muscular dystrophy . Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMD. The function of DMD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM218.Protocadherin 11 X-linked (PCDH11X, Accession NM_032968) is another VGAM1976 host target gene. PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDH11X, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2, designated SEQ ID:26792 and SEQ ID:26807 respectively, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69765] Another function of VGAM1976 is therefore inhibition of Protocadherin 11 X-linked (PCDH11X, Accession NM_032968), a gene which is thought to play a fundamental role in cell-cell recognition essential for the segmental development and function of the central nervous system. Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11X. The function of PCDH11X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.PDGFA Associated Protein 1 (PDAP1, Accession XM_166484) is another VGAM1976 host target gene. PDAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDAP1 BINDING SITE, designated SEQ ID:44422, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69766] Another function of VGAM1976 is therefore inhibition of

PDGFA Associated Protein 1 (PDAP1, Accession XM_166484). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDAP1. Phosphatidylinositol Glycan, Class A (paroxysmal nocturnal hemoglobinuria) (PIGA, Accession NM_020472) is another VGAM1976 host target gene. PIGA BINDING SITE1 through PIGA BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PIGA, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIGA BINDING SITE1 through PIGA BINDING SITE3, designated SEQ ID:21714, SEQ ID:21721 and SEQ ID:8501 respectively, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69767] Another function of VGAM1976 is therefore inhibition of Phosphatidylinositol Glycan, Class A (paroxysmal nocturnal hemoglobinuria) (PIGA, Accession NM_020472). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGA. SWI/SNF Related, Matrix Associated, Actin Dependent Regulator of Chromatin, Subfamily A,

Member 1 (SMARCA1, Accession NM_139035) is another VGAM1976 host target gene. SMARCA1 BINDING SITE1 and SMARCA1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SMARCA1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMARCA1 BINDING SITE1 and SMARCA1 BINDING SITE2, designated SEQ ID:29132 and SEQ ID:15723 respectively, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69768] Another function of VGAM1976 is therefore inhibition of SWI/SNF Related, Matrix Associated, Actin Dependent Regulator of Chromatin, Subfamily A, Member 1 (SMARCA1, Accession NM_139035), a gene which regulates transcription via it effects on chromatin structure. Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMARCA1. The function of SMARCA1 has been established by previous studies. In the course of positional cloning of genes carried on YACs that span the breakpoint in a t(X;3) translocation in a female with Lowe

syndrome (OMIM Ref. No. 309000), Okabe et al. (1992) isolated by chance a human gene with strong homology to SNF2 in S. cerevisiae. Despite strong homology at the amino acid level, the SNF2L1 gene in the human was not capable of complementing the yeast mutation. Furthermore, in contrast to SNF2 itself, a fusion protein consisting of the DNA binding domain of LexA and the human gene did not transactivate a reporter gene downstream of LexA binding sites in a yeast expression system. The similarity between SNF2L1 and the yeast gene suggested that the mammalian gene is part of an evolutionarily conserved family that has been implicated as a global activator of transcription in yeast, but its function in mammals remains unknown. See also SNF2L2 (OMIM Ref. No. 600014) and ATRX (OMIM Ref. No. 300032). Lazzaro and Picketts (2001) cloned the murine homologs of the Drosophila 'imitation switch' (ISWI) protein, Snf2h (SMARCA5; 603375) and Snf2l. In situ hybridization of mouse adult tissues and embryos showed that Snf2h expression correlated with cell proliferation, while Snf2l expression correlated with differentiation. Snf2l was expressed in terminally differentiated neurons after birth and in adult mice, as well as in adult ovaries and testes

[69769] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69770] Lazzaro, M. A.; Picketts, D. J. : Cloning and characterization of the murine Imitation Switch (ISWI) genes: differential expression patterns suggest distinct developmental roles for Snf2h and Snf2l. J. Neurochem. 77: 1145-1156, 2001. ; and

[69771] Okabe, I.; Bailey, L. C.; Attree, O.; Srinivasan, S.; Perkel, J. M.; Laurent, B. C.; Carlson, M.; Nelson, D. L.; Nussbaum, R. L. : Cloning of human and bovine homologs of SNF2/SWI2: a g.

[69772] Further studies establishing the function and utilities of SMARCA1 are found in John Hopkins OMIM database record ID 300012, and in sited publications numbered 7226-7227 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.FLJ14117 (Accession NM_022777) is another VGAM1976 host target gene. FLJ14117 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14117, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of FLJ14117 BINDING SITE, designated SEQ ID:23050, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69773] Another function of VGAM1976 is therefore inhibition of FLJ14117 (Accession NM_022777). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14117. FLJ14751 (Accession NM_032834) is another VGAM1976 host target gene. FLJ14751 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14751, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14751 BINDING SITE, designated SEQ ID:26613, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69774] Another function of VGAM1976 is therefore inhibition of FLJ14751 (Accession NM_032834). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14751. FLJ23153 (Accession NM_024636) is another

VGAM1976 host target gene. FLJ23153 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23153, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23153 BINDING SITE, designated SEQ ID:23909, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69775] Another function of VGAM1976 is therefore inhibition of FLJ23153 (Accession NM_024636). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23153. HSPC195 (Accession XM_087785) is another VGAM1976 host target gene. HSPC195 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HSPC195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPC195 BINDING SITE, designated SEQ ID:39425, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69776] Another function of VGAM1976 is therefore inhibition of HSPC195 (Accession XM_087785). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC195. KIAA0562 (Accession NM_014704) is another VGAM1976 host target gene. KIAA0562 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0562, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0562 BINDING SITE, designated SEQ ID:16239, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69777] Another function of VGAM1976 is therefore inhibition of KIAA0562 (Accession NM_014704). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0562. KIAA0923 (Accession NM_014021) is another VGAM1976 host target gene. KIAA0923 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0923, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0923 BINDING SITE, designated SEQ ID:15242, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69778] Another function of VGAM1976 is therefore inhibition of KIAA0923 (Accession NM_014021). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0923. KIAA1327 (Accession XM_051146) is another VGAM1976 host target gene. KIAA1327 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1327, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1327 BINDING SITE, designated SEQ ID:35763, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69779] Another function of VGAM1976 is therefore inhibition of KIAA1327 (Accession XM_051146). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1327. Mitochondrial Ribosomal Protein L20 (MRPL20, Accession NM_017971) is another VGAM1976 host target gene. MRPL20 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPL20, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPL20 BINDING SITE, designated SEQ ID:19694, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69780] Another function of VGAM1976 is therefore inhibition of Mitochondrial Ribosomal Protein L20 (MRPL20, Accession NM_017971). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL20. Prefoldin 4 (PFDN4, Accession NM_002623) is another VGAM1976 host target gene. PFDN4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PFDN4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PFDN4 BINDING SITE, des-

ignated SEQ ID:8486, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69781] Another function of VGAM1976 is therefore inhibition of Prefoldin 4 (PFDN4, Accession NM_002623). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PFDN4. RAB14, Member RAS Oncogene Family (RAB14, Accession NM_016322) is another VGAM1976 host target gene. RAB14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB14 BINDING SITE, designated SEQ ID:18449, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69782] Another function of VGAM1976 is therefore inhibition of RAB14, Member RAS Oncogene Family (RAB14, Accession NM_016322). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB14. RYK Receptor-like

Tyrosine Kinase (RYK, Accession XM_093692) is another VGAM1976 host target gene. RYK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RYK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RYK BINDING SITE, designated SEQ ID:40203, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69783] Another function of VGAM1976 is therefore inhibition of RYK Receptor-like Tyrosine Kinase (RYK, Accession XM_093692). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RYK. Wingless-type MMTV Integration Site Family, Member 16 (WNT16, Accession NM_057168) is another VGAM1976 host target gene. WNT16 BINDING SITE1 and WNT16 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WNT16, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT16 BINDING

SITE1 and WNT16 BINDING SITE2, designated SEQ ID:27675 and SEQ ID:18171 respectively, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69784] Another function of VGAM1976 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 16 (WNT16, Accession NM_057168). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WNT16. LOC144245 (Accession XM_047770) is another VGAM1976 host target gene. LOC144245 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144245, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144245 BINDING SITE, designated SEQ ID:35052, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69785] Another function of VGAM1976 is therefore inhibition of LOC144245 (Accession XM_047770). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC144245. LOC148697 (Accession XM_086276) is another VGAM1976 host target gene. LOC148697 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148697, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148697 BINDING SITE, designated SEQ ID:38576, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69786] Another function of VGAM1976 is therefore inhibition of LOC148697 (Accession XM_086276). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148697. LOC150933 (Accession XM_097971) is another VGAM1976 host target gene. LOC150933 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150933, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150933 BINDING SITE, designated SEQ ID:41273, to the nucleotide sequence of VGAM1976 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4687.

[69787] Another function of VGAM1976 is therefore inhibition of LOC150933 (Accession XM_097971). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150933. LOC152580 (Accession XM_098240) is another VGAM1976 host target gene. LOC152580 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152580, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152580 BINDING SITE, designated SEQ ID:41524, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69788] Another function of VGAM1976 is therefore inhibition of LOC152580 (Accession XM_098240). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152580. LOC152925 (Accession XM_087559) is another VGAM1976 host target gene. LOC152925 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152925, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152925 BINDING SITE, designated SEQ ID:39334, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69789] Another function of VGAM1976 is therefore inhibition of LOC152925 (Accession XM_087559). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152925. LOC219404 (Accession XM_167909) is another VGAM1976 host target gene. LOC219404 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219404, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219404 BINDING SITE, designated SEQ ID:44909, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69790] Another function of VGAM1976 is therefore inhibition of LOC219404 (Accession XM_167909). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC219404. LOC221738 (Accession XM_168097) is another VGAM1976 host target gene. LOC221738 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221738, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221738 BINDING SITE, designated SEQ ID:45027, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69791] Another function of VGAM1976 is therefore inhibition of LOC221738 (Accession XM_168097). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221738. LOC51068 (Accession NM_015938) is another VGAM1976 host target gene. LOC51068 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51068, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51068 BINDING SITE, designated SEQ ID:18060, to the

nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69792] Another function of VGAM1976 is therefore inhibition of LOC51068 (Accession NM_015938). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51068. LOC93380 (Accession XM_051020) is another VGAM1976 host target gene. LOC93380 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93380, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93380 BINDING SITE, designated SEQ ID:35729, to the nucleotide sequence of VGAM1976 RNA, herein designated VGAM RNA, also designated SEQ ID:4687.

[69793] Another function of VGAM1976 is therefore inhibition of LOC93380 (Accession XM_051020). Accordingly, utilities of VGAM1976 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93380. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 1977 (VGAM1977) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69794] VGAM1977 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1977 was detected is described hereinabove with reference to Figs. 1-8.

[69795] VGAM1977 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine Herpesvirus 4. VGAM1977 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69796] VGAM1977 gene encodes a VGAM1977 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1977 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1977 precursor RNA is designated SEQ ID:1963, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1963 is located at position 5340 relative to the genome of Bovine Herpesvirus 4.

[69797] VGAM1977 precursor RNA folds onto itself, forming VGAM1977 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69798] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1977 folded precursor RNA into VGAM1977 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM1977 RNA is designated SEQ ID:4688, and is provided hereinbelow with reference to the sequence listing part.

[69799] VGAM1977 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1977 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1977 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69800] VGAM1977 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1977 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1977 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1977 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1977 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69801] The complementary binding of VGAM1977 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1977 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1977 host target RNA into VGAM1977 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69802] It is appreciated that VGAM1977 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1977 host target genes. The mRNA of each one of this plurality of VGAM1977 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1977 RNA, herein designated VGAM RNA, and which when bound by VGAM1977 RNA causes inhibition of translation of respective one or more VGAM1977 host target proteins.

[69803] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1977 gene, herein designated VGAM GENE, on one or more VGAM1977 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69804] It is yet further appreciated that a function of VGAM1977 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1977 include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1977 correlate with, and may be deduced from, the identity of

the host target genes which VGAM1977 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69805] Nucleotide sequences of the VGAM1977 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1977 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1977 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1977 are further described hereinbelow with reference to Table 1.

[69806] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1977 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1977 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69807] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1977 gene, herein designated VGAM is inhibition of expression of VGAM1977 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1977 correlate with, and may be deduced from, the identity of the target genes which VGAM1977

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69808] Archain 1 (ARCN1, Accession NM_001655) is a VGAM1977 host target gene. ARCN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARCN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARCN1 BINDING SITE, designated SEQ ID:7363, to the nucleotide sequence of VGAM1977 RNA, herein designated VGAM RNA, also designated SEQ ID:4688.

[69809] A function of VGAM1977 is therefore inhibition of Archain 1 (ARCN1, Accession NM_001655), a gene which plays a fundamental role in eukaryotic cell biology. Accordingly, utilities of VGAM1977 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARCN1. The function of ARCN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1226.FLJ12888 (Accession NM_024945) is another VGAM1977 host target gene. FLJ12888 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by FLJ12888, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12888 BINDING SITE, designated SEQ ID:24494, to the nucleotide sequence of VGAM1977 RNA, herein designated VGAM RNA, also designated SEQ ID:4688.

[69810] Another function of VGAM1977 is therefore inhibition of FLJ12888 (Accession NM_024945). Accordingly, utilities of VGAM1977 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12888. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1978 (VGAM1978) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69811] VGAM1978 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1978 was detected is described hereinabove with reference to Figs. 1-8.

[69812] VGAM1978 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine Herpesvirus 4. VGAM1978 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69813] VGAM1978 gene encodes a VGAM1978 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1978 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1978 precursor RNA is designated SEQ ID:1964, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1964 is located at position 2128 relative to the genome of Bovine Herpesvirus 4.

[69814] VGAM1978 precursor RNA folds onto itself, forming VGAM1978 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[69815] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1978 folded precursor RNA into VGAM1978 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM1978 RNA is designated SEQ ID:4689, and is provided hereinbelow with reference to the sequence listing part.

[69816] VGAM1978 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1978 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1978 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69817] VGAM1978 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1978 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1978 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1978 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1978 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69818] The complementary binding of VGAM1978 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1978 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1978 host target RNA into VGAM1978 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69819] It is appreciated that VGAM1978 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1978 host target genes. The mRNA of each one of this plurality of VGAM1978 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1978 RNA, herein designated VGAM RNA, and which when bound by VGAM1978 RNA causes inhibition of translation of respective one or more VGAM1978 host target proteins.

[69820] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1978 gene, herein designated VGAM GENE, on one or more VGAM1978 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69821] It is yet further appreciated that a function of VGAM1978 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1978 correlate with, and may be deduced from, the identity of the host target genes which VGAM1978 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69822] Nucleotide sequences of the VGAM1978 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1978 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1978 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1978 are further described hereinbelow with reference to Table 1.

[69823] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1978 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1978 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69824] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1978 gene, herein designated VGAM is inhibition of expression of VGAM1978 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1978 correlate with, and may be deduced from, the identity of the target genes which VGAM1978 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69825] BLTR2 (Accession NM_019839) is a VGAM1978 host target gene. BLTR2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BLTR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of BLTR2 BINDING SITE, designated SEQ ID:21245, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69826] A function of VGAM1978 is therefore inhibition of BLTR2 (Accession NM_019839). Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BLTR2. CERD4 (Accession NM_012074) is another VGAM1978 host target gene. CERD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CERD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CERD4 BINDING SITE, designated SEQ ID:14354, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69827] Another function of VGAM1978 is therefore inhibition of CERD4 (Accession NM_012074). Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CERD4. Cytochrome P450, Subfamily I (dioxin-inducible),

Polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1, Accession NM_000104) is another VGAM1978 host target gene. CYP1B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP1B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP1B1 BINDING SITE, designated SEQ ID:5567, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69828] Another function of VGAM1978 is therefore inhibition of Cytochrome P450, Subfamily I (dioxin-inducible), Polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1, Accession NM_000104), a gene which participates in the metabolism of a molecule that is a participant in eye development. Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP1B1. The function of CYP1B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM894.Gap Junction Protein, Alpha 1, 43kDa (connexin 43) (GJA1, Ac-

cession NM_000165) is another VGAM1978 host target gene. GJA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GJA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GJA1 BINDING SITE, designated SEQ ID:5678, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69829] Another function of VGAM1978 is therefore inhibition of Gap Junction Protein, Alpha 1, 43kDa (connexin 43) (GJA1, Accession NM_000165), a gene which may act in synchronizing heart contraction and embryonic development. Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GJA1. The function of GJA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM341.5-hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868) is another VGAM1978 host target gene. HTR2C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HTR2C, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HTR2C BINDING SITE, designated SEQ ID:6536, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69830] Another function of VGAM1978 is therefore inhibition of 5-hydroxytryptamine (serotonin) Receptor 2C (HTR2C, Accession NM_000868), a gene which activates phospholipase C and regulates intracellular calcium flux. Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR2C. The function of HTR2C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1052.Platelet-activating Factor Acetylhydrolase, Isoform Ib, Gamma Subunit 29kDa (PAFAH1B3, Accession NM_002573) is another VGAM1978 host target gene. PAFAH1B3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PAFAH1B3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of PAFAH1B3 BINDING SITE, designated SEQ ID:8433, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69831] Another function of VGAM1978 is therefore inhibition of Platelet-activating Factor Acetylhydrolase, Isoform Ib, Gamma Subunit 29kDa (PAFAH1B3, Accession NM_002573), a gene which plays a role during the development of brain. Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAFAH1B3. The function of PAFAH1B3 has been established by previous studies. Platelet-activating factor acetylhydrolase (PAFAH) catalyzes the removal of the acetyl group at the sn-2 position of the glycerol backbone of platelet-activating factor (PAF), producing biologically inactive lyso-PAF. Isoform 1B of PAFAH consists of 3 subunits: alpha (PAFAH1B1; 601545), beta (PAFAH1B2; 602508), and gamma. The catalytic activity of the enzyme resides in the beta and gamma subunits, whereas the alpha subunit has regulatory activity. PAFAH1B1 has been identified as a causative gene of Miller-Dieker lissencephaly (OMIM Ref. No. 247200). By screening a human fetal liver cDNA library

with oligonucleotides based on the cDNA sequence of the bovine PAFAH-gamma subunit, Adachi et al. (1995) cloned a cDNA encoding PAFAH1B3. The deduced 231-amino acid human protein has 97.8% identity with the bovine PAFAH-gamma subunit. The authors found that the PAFAH1B3 gene spans approximately 5.6 kb and contains 5 exons. Southern blot analysis showed that PAFAH1B3 is a single-copy gene in the human genome. Northern blot analysis detected a 1.0-kb PAFAH1B3 transcript in several human adult and fetal tissues, with the highest expression in fetal brain. Adachi et al. (1995) expressed the PAFAH1B3 cDNA in E. coli and found that the resulting protein was catalytically active, demonstrating that trimer formation is not essential for PAFAH1B3 activity. Nothwang et al. (2001) reported a translocation t(1;19)(q21.3;q13.2) in a female with mental retardation, ataxia, and atrophy of the brain. Sequence analysis of the breakpoints revealed an Alu repeat-mediated mechanism of recombination that led to truncation of PAFAH1B3 and the kinase CLK2 (OMIM Ref. No. 602989). One expressed fusion gene encoded the first 136 amino acids of PAFAH1B3, followed by the complete CLK2 protein. Truncated PAFAH1B3 protein lost its potential to interact with

LIS1 (OMIM Ref. No. 601545), whereas CLK2 activity was conserved within the fusion protein. These data emphasized the importance of PAFAH1B in brain development and function.

[69832] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69833] Adachi, H.; Tsujimoto, M.; Hattori, M.; Arai, H.; Inoue, K. : cDNA cloning of human cytosolic platelet-activating factor acetylhydrolase gamma-subunit and its mRNA expression in human tissues. Biochem. Biophys. Res. Commun. 214: 180-187, 1995. ; and

[69834] Nothwang, H. G.; Kim, H. G.; Aoki, J.; Geisterfer, M.; Kubart, S.; Wegner, R. D.; van Moers, A.; Ashworth, L. K.; Haaf, T.; Bell, J.; Arai, H.; Tommerup, N.; Ropers, H. H.; Wirth, J. : F.

[69835] Further studies establishing the function and utilities of PAFAH1B3 are found in John Hopkins OMIM database record ID 603074, and in sited publications numbered 885 and 9036 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Platelet-derived Growth Factor Receptor, Alpha Polypeptide (PDGFRA, Accession NM_006206) is another

VGAM1978 host target gene. PDGFRA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDGFRA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDGFRA BINDING SITE, designated SEQ ID:12887, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69836] Another function of VGAM1978 is therefore inhibition of Platelet-derived Growth Factor Receptor, Alpha Polypeptide (PDGFRA, Accession NM_006206), a gene which this receptor binds platelet-derived growth factor and has a tyrosine-protein kinase activity. Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFRA. The function of PDGFRA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM117.Protein Phosphatase 1, Catalytic Subunit, Beta Isoform (PPP1CB, Accession NM_002709) is another VGAM1978 host target gene. PPP1CB BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by PPP1CB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1CB BINDING SITE, designated SEQ ID:8561, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69837] Another function of VGAM1978 is therefore inhibition of Protein Phosphatase 1, Catalytic Subunit, Beta Isoform (PPP1CB, Accession NM_002709), a gene which is the catalytic subunit of protein phosphatase 1. Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1CB. The function of PPP1CB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM46.TRIP15 (Accession NM_004236) is another VGAM1978 host target gene. TRIP15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIP15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

TRIP15 BINDING SITE, designated SEQ ID:10431, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69838] Another function of VGAM1978 is therefore inhibition of TRIP15 (Accession NM_004236), a gene which is a subunit of the COP9 signalosome complex. Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIP15. The function of TRIP15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM452.HSPC065 (Accession NM_014157) is another VGAM1978 host target gene. HSPC065 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSPC065, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPC065 BINDING SITE, designated SEQ ID:15457, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69839] Another function of VGAM1978 is therefore inhibition of HSPC065 (Accession NM_014157). Accordingly, utilities of

VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC065. KIAA0153 (Accession NM_015140) is another VGAM1978 host target gene. KIAA0153 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0153, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0153 BINDING SITE, designated SEQ ID:17500, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69840] Another function of VGAM1978 is therefore inhibition of KIAA0153 (Accession NM_015140). Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0153. MGC10870 (Accession NM_032301) is another VGAM1978 host target gene. MGC10870 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC10870, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

MGC10870 BINDING SITE, designated SEQ ID:26082, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69841] Another function of VGAM1978 is therefore inhibition of MGC10870 (Accession NM_032301). Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10870. LOC144231 (Accession XM_096561) is another VGAM1978 host target gene. LOC144231 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144231 BINDING SITE, designated SEQ ID:40396, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69842] Another function of VGAM1978 is therefore inhibition of LOC144231 (Accession XM_096561). Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144231. LOC163231 (Accession XM_092094) is another VGAM1978 host target gene. LOC163231 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC163231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163231 BINDING SITE, designated SEQ ID:40103, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69843] Another function of VGAM1978 is therefore inhibition of LOC163231 (Accession XM_092094). Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163231. LOC205313 (Accession XM_119628) is another VGAM1978 host target gene. LOC205313 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC205313, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC205313 BINDING SITE, designated SEQ ID:43595, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69844] Another function of VGAM1978 is therefore inhibition of

LOC205313 (Accession XM_119628). Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC205313. LOC58525 (Accession XM_086045) is another VGAM1978 host target gene. LOC58525 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC58525, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC58525 BINDING SITE, designated SEQ ID:38456, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69845] Another function of VGAM1978 is therefore inhibition of LOC58525 (Accession XM_086045). Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC58525. LOC91650 (Accession XM_039853) is another VGAM1978 host target gene. LOC91650 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91650, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC91650 BINDING SITE, designated SEQ ID:33201, to the nucleotide sequence of VGAM1978 RNA, herein designated VGAM RNA, also designated SEQ ID:4689.

[69846] Another function of VGAM1978 is therefore inhibition of LOC91650 (Accession XM_039853). Accordingly, utilities of VGAM1978 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91650. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1979 (VGAM1979) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69847] VGAM1979 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1979 was detected is described hereinabove with reference to Figs. 1-8.

[69848] VGAM1979 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine Herpesvirus 4. VGAM1979 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[69849] VGAM1979 gene encodes a VGAM1979 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1979 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1979 precursor RNA is designated SEQ ID:1965, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1965 is located at position 11708 relative to the genome of Bovine Herpesvirus 4.

[69850] VGAM1979 precursor RNA folds onto itself, forming VGAM1979 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69851] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1979 folded precursor RNA into VGAM1979 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM1979 RNA is designated SEQ ID:4690, and is provided hereinbelow with reference to the sequence listing part.

[69852] VGAM1979 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1979 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1979 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69853] VGAM1979 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1979 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1979 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1979 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1979 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69854] The complementary binding of VGAM1979 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1979 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1979 host target RNA into VGAM1979 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69855] It is appreciated that VGAM1979 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1979 host target genes. The mRNA of each one of this plurality of VGAM1979 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1979 RNA, herein designated VGAM RNA, and which when bound by VGAM1979 RNA causes inhibition of translation of respective one or more VGAM1979 host target proteins.

[69856] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1979 gene, herein designated VGAM GENE, on one or more VGAM1979 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69857] It is yet further appreciated that a function of VGAM1979 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1979 correlate with, and may be deduced from, the identity of the host target genes which VGAM1979 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69858] Nucleotide sequences of the VGAM1979 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1979 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1979 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1979 are further described hereinbelow with reference to Table 1.

[69859] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM1979 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1979 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69860] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1979 gene, herein designated VGAM is inhibition of expression of VGAM1979 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1979 correlate with, and may be deduced from, the identity of the target genes which VGAM1979 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69861] Protein Phosphatase 2, Regulatory Subunit B (B56), Epsilon Isoform (PPP2R5E, Accession NM_006246) is a VGAM1979 host target gene. PPP2R5E BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP2R5E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP2R5E BINDING SITE, designated SEQ ID:12921, to the nucleotide sequence of VGAM1979 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4690.

[69862] A function of VGAM1979 is therefore inhibition of Protein Phosphatase 2, Regulatory Subunit B (B56), Epsilon Isoform (PPP2R5E, Accession NM_006246), a gene which is a regulatory subunit of protein phosphatase 2A. Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP2R5E. The function of PPP2R5E and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM302.Pyrroline-5-carboxylate Reductase 1 (PYCR1, Accession XM_046472) is another VGAM1979 host target gene. PYCR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PYCR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PYCR1 BINDING SITE, designated SEQ ID:34730, to the nucleotide sequence of VGAM1979 RNA, herein designated VGAM RNA, also designated SEQ ID:4690.

[69863] Another function of VGAM1979 is therefore inhibition of

Pyrroline-5-carboxylate Reductase 1 (PYCR1, Accession XM_046472), a gene which catalyzes the NAD(P)H-dependent conversion of pyrroline-5-carboxylate to proline. Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PYCR1. The function of PYCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM178.Tetratricopeptide Repeat Domain 3 (TTC3, Accession NM_003316) is another VGAM1979 host target gene. TTC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TTC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTC3 BINDING SITE, designated SEQ ID:9314, to the nucleotide sequence of VGAM1979 RNA, herein designated VGAM RNA, also designated SEQ ID:4690.

[69864] Another function of VGAM1979 is therefore inhibition of Tetratricopeptide Repeat Domain 3 (TTC3, Accession NM_003316), a gene which contains tetratricopeptide repeat (TPR) motifs. Accordingly, utilities of VGAM1979 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with TTC3. The function of TTC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM699.CASPR3 (Accession NM_024879) is another VGAM1979 host target gene. CASPR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CASPR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASPR3 BINDING SITE, designated SEQ ID:24316, to the nucleotide sequence of VGAM1979 RNA, herein designated VGAM RNA, also designated SEQ ID:4690.

[69865] Another function of VGAM1979 is therefore inhibition of CASPR3 (Accession NM_024879). Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASPR3. Cell Adhesion Molecule with Homology to L1CAM (close homolog of L1) (CHL1, Accession NM_006614) is another VGAM1979 host target gene. CHL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by CHL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHL1 BINDING SITE, designated SEQ ID:13397, to the nucleotide sequence of VGAM1979 RNA, herein designated VGAM RNA, also designated SEQ ID:4690.

[69866] Another function of VGAM1979 is therefore inhibition of Cell Adhesion Molecule with Homology to L1CAM (close homolog of L1) (CHL1, Accession NM_006614). Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHL1. FLJ20060 (Accession NM_017645) is another VGAM1979 host target gene. FLJ20060 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20060, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20060 BINDING SITE, designated SEQ ID:19149, to the nucleotide sequence of VGAM1979 RNA, herein designated VGAM RNA, also designated SEQ ID:4690.

[69867] Another function of VGAM1979 is therefore inhibition of

FLJ20060 (Accession NM_017645). Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20060. FLJ22569 (Accession NM_023925) is another VGAM1979 host target gene. FLJ22569 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22569, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22569 BINDING SITE, designated SEQ ID:23402, to the nucleotide sequence of VGAM1979 RNA, herein designated VGAM RNA, also designated SEQ ID:4690.

[69868] Another function of VGAM1979 is therefore inhibition of FLJ22569 (Accession NM_023925). Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22569. KIAA0367 (Accession XM_041018) is another VGAM1979 host target gene. KIAA0367 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0367, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0367 BINDING SITE, designated SEQ ID:33426, to the nucleotide sequence of VGAM1979 RNA, herein designated VGAM RNA, also designated SEQ ID:4690.

[69869] Another function of VGAM1979 is therefore inhibition of KIAA0367 (Accession XM_041018). Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0367. MGC10200 (Accession NM_145060) is another VGAM1979 host target gene. MGC10200 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC10200, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10200 BINDING SITE, designated SEQ ID:29695, to the nucleotide sequence of VGAM1979 RNA, herein designated VGAM RNA, also designated SEQ ID:4690.

[69870] Another function of VGAM1979 is therefore inhibition of MGC10200 (Accession NM_145060). Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10200. TERF1 (TRF1)-interacting Nuclear Factor 2

(TINF2, Accession NM_012461) is another VGAM1979 host target gene. TINF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TINF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TINF2 BINDING SITE, designated SEQ ID:14835, to the nucleotide sequence of VGAM1979 RNA, herein designated VGAM RNA, also designated SEQ ID:4690.

[69871] Another function of VGAM1979 is therefore inhibition of TERF1 (TRF1)-interacting Nuclear Factor 2 (TINF2, Accession NM_012461). Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TINF2. LOC162333 (Accession XM_102591) is another VGAM1979 host target gene. LOC162333 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC162333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162333 BINDING SITE, designated SEQ ID:42125, to the nucleotide sequence of

VGAM1979 RNA, herein designated VGAM RNA, also designated SEQ ID:4690.

[69872] Another function of VGAM1979 is therefore inhibition of LOC162333 (Accession XM_102591). Accordingly, utilities of VGAM1979 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162333. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1980 (VGAM1980) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69873] VGAM1980 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1980 was detected is described hereinabove with reference to Figs. 1-8.

[69874] VGAM1980 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Bovine Herpesvirus 4. VGAM1980 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69875] VGAM1980 gene encodes a VGAM1980 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1980 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1980 precursor RNA is designated SEQ ID:1966, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1966 is located at position 9455 relative to the genome of Bovine Herpesvirus 4.

[69876] VGAM1980 precursor RNA folds onto itself, forming VGAM1980 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69877] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1980 folded precursor RNA into VGAM1980 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM1980 RNA is designated SEQ ID:4691, and is provided hereinbelow with reference to the sequence listing part.

[69878] VGAM1980 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1980 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1980 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69879] VGAM1980 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1980 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1980 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1980 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1980 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69880] The complementary binding of VGAM1980 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1980 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1980 host target RNA into VGAM1980 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69881] It is appreciated that VGAM1980 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM1980 host target genes. The mRNA of each one of this plurality of VGAM1980 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1980 RNA, herein designated VGAM RNA, and which when bound by VGAM1980 RNA causes inhibition of translation of respective one or more VGAM1980 host target proteins.

[69882] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1980 gene, herein designated VGAM GENE, on one or more VGAM1980 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69883] It is yet further appreciated that a function of VGAM1980 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1980 include diagnosis, prevention and treatment of viral infection by Bovine Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM1980 correlate with, and may be deduced from, the identity of the host target genes which VGAM1980 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69884] Nucleotide sequences of the VGAM1980 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1980 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1980 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1980 are further described hereinbelow with reference to Table 1.

[69885] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1980 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM1980 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69886] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1980 gene, herein designated VGAM is inhibition of expression of VGAM1980 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1980 correlate with, and may be deduced from, the identity of the target genes which VGAM1980 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69887] Lipin 1 (LPIN1, Accession XM_041136) is a VGAM1980 host target gene. LPIN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LPIN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LPIN1 BINDING SITE, designated SEQ ID:33466, to the nucleotide sequence of VGAM1980 RNA, herein designated VGAM RNA, also designated SEQ ID:4691.

[69888] A function of VGAM1980 is therefore inhibition of Lipin 1 (LPIN1, Accession XM_041136), a gene which is involved

in adipocyte differenciation (by similarity). Accordingly, utilities of VGAM1980 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPIN1. The function of LPIN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM35.Presenilin 1 (Alzheimer disease 3) (PSEN1, Accession NM_000021) is another VGAM1980 host target gene. PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PSEN1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2, designated SEQ ID:5455 and SEQ ID:14233 respectively, to the nucleotide sequence of VGAM1980 RNA, herein designated VGAM RNA, also designated SEQ ID:4691.

[69889] Another function of VGAM1980 is therefore inhibition of Presenilin 1 (Alzheimer disease 3) (PSEN1, Accession NM_000021). Accordingly, utilities of VGAM1980 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSEN1. KIAA1203

(Accession XM_049683) is another VGAM1980 host target gene. KIAA1203 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1203, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1203 BINDING SITE, designated SEQ ID:35465, to the nucleotide sequence of VGAM1980 RNA, herein designated VGAM RNA, also designated SEQ ID:4691.

[69890] Another function of VGAM1980 is therefore inhibition of KIAA1203 (Accession XM_049683). Accordingly, utilities of VGAM1980 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1203. PIPPIN (Accession XM_086825) is another VGAM1980 host target gene. PIPPIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIPPIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIPPIN BINDING SITE, designated SEQ ID:38908, to the nucleotide sequence of VGAM1980 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4691.

[69891] Another function of VGAM1980 is therefore inhibition of PIPPIN (Accession XM_086825). Accordingly, utilities of VGAM1980 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIPPIN. PRO0529 (Accession NM_014074) is another VGAM1980 host target gene. PRO0529 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0529, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0529 BINDING SITE, designated SEQ ID:15302, to the nucleotide sequence of VGAM1980 RNA, herein designated VGAM RNA, also designated SEQ ID:4691.

[69892] Another function of VGAM1980 is therefore inhibition of PRO0529 (Accession NM_014074). Accordingly, utilities of VGAM1980 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0529. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1981 (VGAM1981) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69893] VGAM1981 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1981 was detected is described hereinabove with reference to Figs. 1-8.

[69894] VGAM1981 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra Virus. VGAM1981 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69895] VGAM1981 gene encodes a VGAM1981 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1981 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1981 precursor RNA is designated SEQ ID:1967, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1967 is located at position 10871 relative to the genome of Hendra Virus.

[69896] VGAM1981 precursor RNA folds onto itself, forming

VGAM1981 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69897] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1981 folded precursor RNA into VGAM1981 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM1981 RNA is designated SEQ ID:4692, and is provided hereinbelow with reference to the sequence listing part.

[69898] VGAM1981 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1981 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1981 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69899] VGAM1981 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1981 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1981 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1981 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1981 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69900] The complementary binding of VGAM1981 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1981 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1981 host target RNA into VGAM1981 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69901] It is appreciated that VGAM1981 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1981 host target genes. The mRNA of each one of this plurality of VGAM1981 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1981 RNA, herein designated VGAM RNA, and which when bound by VGAM1981 RNA causes inhibition of translation of respective one or more VGAM1981 host target proteins.

[69902] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1981 gene, herein designated VGAM GENE, on one or more VGAM1981 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69903] It is yet further appreciated that a function of VGAM1981 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of viral infection by Hendra Virus. Specific functions, and accordingly utilities, of VGAM1981 correlate with, and may be deduced from, the identity of the host target genes which VGAM1981 binds and inhibits, and the

function of these host target genes, as elaborated herein-below.

[69904] Nucleotide sequences of the VGAM1981 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1981 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1981 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1981 are further described hereinbelow with reference to Table 1.

[69905] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1981 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1981 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69906] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1981 gene, herein designated VGAM is inhibition of expression of VGAM1981 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1981 correlate with, and may be deduced from, the identity of the target genes which VGAM1981 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[69907] Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411) is a VGAM1981 host target gene. HLCS BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HLCS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HLCS BINDING SITE, designated SEQ ID:5987, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69908] A function of VGAM1981 is therefore inhibition of Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411). Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLCS. Ligase IV, DNA, ATP-dependent (LIG4, Accession NM_002312) is another VGAM1981 host target gene. LIG4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LIG4, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIG4 BINDING SITE, designated SEQ ID:8107, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69909] Another function of VGAM1981 is therefore inhibition of Ligase IV, DNA, ATP-dependent (LIG4, Accession NM_002312), a gene which functions in DNA nonhomologous end-joining and V(D)J recombination. Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIG4. The function of LIG4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM258.Microtubule-associated Protein, RP/EB Family, Member 2 (MAPRE2, Accession NM_014268) is another VGAM1981 host target gene. MAPRE2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAPRE2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

MAPRE2 BINDING SITE, designated SEQ ID:15543, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69910] Another function of VGAM1981 is therefore inhibition of Microtubule-associated Protein, RP/EB Family, Member 2 (MAPRE2, Accession NM_014268), a gene which The functional inactivation of the APC gene product is a key event in colorectal tumorigenesis. Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPRE2. The function of MAPRE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM178.Phospholipase A2, Group X (PLA2G10, Accession NM_003561) is another VGAM1981 host target gene. PLA2G10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PLA2G10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLA2G10 BINDING SITE, designated SEQ ID:9617, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4692.

[69911] Another function of VGAM1981 is therefore inhibition of Phospholipase A2, Group X (PLA2G10, Accession NM_003561). Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLA2G10. Pleiomorphic Adenoma Gene 1 (PLAG1, Accession NM_002655) is another VGAM1981 host target gene. PLAG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLAG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLAG1 BINDING SITE, designated SEQ ID:8514, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69912] Another function of VGAM1981 is therefore inhibition of Pleiomorphic Adenoma Gene 1 (PLAG1, Accession NM_002655), a gene which contains a zinc finger domain. Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAG1. The function of PLAG1 and its association with various diseases and clinical condi-

tions, has been established by previous studies, as described hereinabove with reference to VGAM29.Staufen, RNA Binding Protein (Drosophila) (STAU, Accession NM_004602) is another VGAM1981 host target gene. STAU BINDING SITE1 through STAU BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by STAU, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAU BINDING SITE1 through STAU BINDING SITE4, designated SEQ ID:10939, SEQ ID:18924, SEQ ID:18912 and SEQ ID:18918 respectively, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69913] Another function of VGAM1981 is therefore inhibition of Staufen, RNA Binding Protein (Drosophila) (STAU, Accession NM_004602), a gene which may play a role in specific positioning of mrnas at given sites in the cell and in stimulating their translation at the site. Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAU. The function of STAU and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM916.FLJ13910 (Accession NM_022780) is another VGAM1981 host target gene. FLJ13910 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13910, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13910 BINDING SITE, designated SEQ ID:23053, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69914] Another function of VGAM1981 is therefore inhibition of FLJ13910 (Accession NM_022780). Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13910. FLJ20086 (Accession NM_017661) is another VGAM1981 host target gene. FLJ20086 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20086, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20086

BINDING SITE, designated SEQ ID:19189, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69915] Another function of VGAM1981 is therefore inhibition of FLJ20086 (Accession NM_017661). Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20086. KIAA0931 (Accession XM_041191) is another VGAM1981 host target gene. KIAA0931 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0931, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0931 BINDING SITE, designated SEQ ID:33480, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69916] Another function of VGAM1981 is therefore inhibition of KIAA0931 (Accession XM_041191). Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0931. KIAA0953 (Accession XM_039733) is another VGAM1981 host target gene. KIAA0953 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0953, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0953 BINDING SITE, designated SEQ ID:33166, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69917] Another function of VGAM1981 is therefore inhibition of KIAA0953 (Accession XM_039733). Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0953. KIAA1323 (Accession XM_032146) is another VGAM1981 host target gene. KIAA1323 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1323 BINDING SITE, designated SEQ ID:31560, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69918] Another function of VGAM1981 is therefore inhibition of

KIAA1323 (Accession XM_032146). Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1323. Retinoic Acid Induced 17 (RAI17, Accession XM_166091) is another VGAM1981 host target gene. RAI17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAI17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAI17 BINDING SITE, designated SEQ ID:43855, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69919] Another function of VGAM1981 is therefore inhibition of Retinoic Acid Induced 17 (RAI17, Accession XM_166091). Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI17. SEC24 Related Gene Family, Member B (S. cerevisiae) (SEC24B, Accession NM_006323) is another VGAM1981 host target gene. SEC24B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC24B, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC24B BINDING SITE, designated SEQ ID:13015, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69920] Another function of VGAM1981 is therefore inhibition of SEC24 Related Gene Family, Member B (S. cerevisiae) (SEC24B, Accession NM_006323). Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC24B. Sialyltransferase 4A (beta-galactoside alpha-2,3-sialytransferase) (SIAT4A, Accession NM_003033) is another VGAM1981 host target gene. SIAT4A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SIAT4A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIAT4A BINDING SITE, designated SEQ ID:8977, to the nucleotide sequence of VGAM1981 RNA, herein designated VGAM RNA, also designated SEQ ID:4692.

[69921] Another function of VGAM1981 is therefore inhibition of Sialyltransferase 4A (beta-galactoside alpha-

2,3-sialytransferase) (SIAT4A, Accession NM_003033). Accordingly, utilities of VGAM1981 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIAT4A. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1982 (VGAM1982) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69922] VGAM1982 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1982 was detected is described hereinabove with reference to Figs. 1-8.

[69923] VGAM1982 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra Virus. VGAM1982 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69924] VGAM1982 gene encodes a VGAM1982 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1982 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1982 precursor RNA is designated SEQ ID:1968, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1968 is located at position 3780 relative to the genome of Hendra Virus.

[69925] VGAM1982 precursor RNA folds onto itself, forming VGAM1982 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69926] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1982 folded precursor RNA into VGAM1982 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM1982 RNA is designated SEQ ID:4693, and is provided hereinbelow with reference to the sequence listing part.

[69927] VGAM1982 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1982 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1982 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69928] VGAM1982 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1982 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1982 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM1982 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1982 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69929] The complementary binding of VGAM1982 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1982 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1982 host target RNA into VGAM1982 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69930] It is appreciated that VGAM1982 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1982 host target genes. The mRNA of each one of this plurality of VGAM1982 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM1982 RNA, herein designated VGAM RNA, and which when bound by VGAM1982 RNA causes inhibition of translation of respective one or more VGAM1982 host target proteins.

[69931] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1982 gene, herein designated VGAM GENE, on one or more VGAM1982 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69932] It is yet further appreciated that a function of VGAM1982

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1982 include diagnosis, prevention and treatment of viral infection by Hendra Virus. Specific functions, and accordingly utilities, of VGAM1982 correlate with, and may be deduced from, the identity of the host target genes which VGAM1982 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69933] Nucleotide sequences of the VGAM1982 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1982 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1982 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1982 are further described hereinbelow with reference to Table 1.

[69934] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1982 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1982 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69935] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1982 gene, herein designated VGAM is inhibition of expression of VGAM1982 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1982 correlate with, and may be deduced from, the identity of the target genes which VGAM1982 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69936] KIAA0553 (Accession XM_045981) is a VGAM1982 host target gene. KIAA0553 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0553, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0553 BINDING SITE, designated SEQ ID:34636, to the nucleotide sequence of VGAM1982 RNA, herein designated VGAM RNA, also designated SEQ ID:4693.

[69937] A function of VGAM1982 is therefore inhibition of KIAA0553 (Accession XM_045981). Accordingly, utilities of VGAM1982 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0553. MST4 (Accession NM_016542) is another

VGAM1982 host target gene. MST4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MST4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MST4 BINDING SITE, designated SEQ ID:18607, to the nucleotide sequence of VGAM1982 RNA, herein designated VGAM RNA, also designated SEQ ID:4693.

[69938] Another function of VGAM1982 is therefore inhibition of MST4 (Accession NM_016542). Accordingly, utilities of VGAM1982 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MST4. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1983 (VGAM1983) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69939] VGAM1983 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1983 was detected is described hereinabove with reference to Figs. 1-8.

[69940] VGAM1983 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra Virus. VGAM1983 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69941] VGAM1983 gene encodes a VGAM1983 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1983 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1983 precursor RNA is designated SEQ ID:1969, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1969 is located at position 5639 relative to the genome of Hendra Virus.

[69942] VGAM1983 precursor RNA folds onto itself, forming VGAM1983 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[69943] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1983 folded precursor RNA into VGAM1983 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM1983 RNA is designated SEQ ID:4694, and is provided hereinbelow with reference to the sequence listing part.

[69944] VGAM1983 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1983 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1983 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69945] VGAM1983 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1983 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1983 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1983 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1983 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69946] The complementary binding of VGAM1983 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1983 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1983 host target RNA into VGAM1983 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69947] It is appreciated that VGAM1983 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1983 host target genes. The mRNA of each one of this plurality of VGAM1983 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1983 RNA, herein designated VGAM RNA, and which when bound by VGAM1983 RNA causes inhibition of translation of respective one or more VGAM1983 host target proteins.

[69948] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1983 gene, herein designated VGAM GENE, on one or more VGAM1983 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69949] It is yet further appreciated that a function of VGAM1983 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1983 include diagnosis, prevention and treatment of viral infection by Hendra Virus. Specific functions, and accordingly utilities, of VGAM1983 correlate with, and may be deduced from, the identity of the host target genes which VGAM1983 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69950] Nucleotide sequences of the VGAM1983 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1983 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1983 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1983 are further described hereinbelow with reference to Table 1.

[69951] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1983 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1983 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69952] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1983 gene, herein designated VGAM is inhibition of expression of VGAM1983 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1983 correlate with, and may be deduced from, the identity of the target genes which VGAM1983 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69953] Arginine Vasopressin Receptor 2 (nephrogenic diabetes insipidus) (AVPR2, Accession NM_000054) is a VGAM1983 host target gene. AVPR2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AVPR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AVPR2 BINDING SITE, designated SEQ ID:5511, to the nucleotide sequence of VGAM1983 RNA, herein designated VGAM RNA, also designated SEQ ID:4694.

[69954] A function of VGAM1983 is therefore inhibition of Arginine Vasopressin Receptor 2 (nephrogenic diabetes insipidus) (AVPR2, Accession NM_000054). Accordingly, utilities of VGAM1983 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AVPR2. High Mobility Group AT-hook 2 (HMGA2, Accession NM_003483) is another VGAM1983 host target gene. HMGA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HMGA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMGA2 BINDING SITE, designated SEQ ID:9563, to the nucleotide sequence of VGAM1983 RNA, herein designated VGAM RNA, also designated SEQ ID:4694.

[69955] Another function of VGAM1983 is therefore inhibition of High Mobility Group AT-hook 2 (HMGA2, Accession

NM_003483), a gene which may affect transcription and cell differentiation; shares common DNA-binding motif with other HMG HMG I/Y family members. Accordingly, utilities of VGAM1983 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMGA2. The function of HMGA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM552.Myotubularin Related Protein 2 (MTMR2, Accession NM_016156) is another VGAM1983 host target gene. MTMR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTMR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTMR2 BINDING SITE, designated SEQ ID:18244, to the nucleotide sequence of VGAM1983 RNA, herein designated VGAM RNA, also designated SEQ ID:4694.

[69956] Another function of VGAM1983 is therefore inhibition of Myotubularin Related Protein 2 (MTMR2, Accession NM_016156). Accordingly, utilities of VGAM1983 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with MTMR2. Vascular Cell Adhesion Molecule 1 (VCAM1, Accession NM_080682) is another VGAM1983 host target gene. VCAM1 BINDING SITE1 and VCAM1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by VCAM1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VCAM1 BINDING SITE1 and VCAM1 BINDING SITE2, designated SEQ ID:27984 and SEQ ID:6738 respectively, to the nucleotide sequence of VGAM1983 RNA, herein designated VGAM RNA, also designated SEQ ID:4694.

[69957] Another function of VGAM1983 is therefore inhibition of Vascular Cell Adhesion Molecule 1 (VCAM1, Accession NM_080682). Accordingly, utilities of VGAM1983 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VCAM1. SPEC1 (Accession NM_020239) is another VGAM1983 host target gene. SPEC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPEC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of SPEC1 BINDING SITE, designated SEQ ID:21514, to the nucleotide sequence of VGAM1983 RNA, herein designated VGAM RNA, also designated SEQ ID:4694.

[69958] Another function of VGAM1983 is therefore inhibition of SPEC1 (Accession NM_020239). Accordingly, utilities of VGAM1983 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPEC1. LOC89932 (Accession XM_027341) is another VGAM1983 host target gene. LOC89932 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC89932, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC89932 BINDING SITE, designated SEQ ID:30492, to the nucleotide sequence of VGAM1983 RNA, herein designated VGAM RNA, also designated SEQ ID:4694.

[69959] Another function of VGAM1983 is therefore inhibition of LOC89932 (Accession XM_027341). Accordingly, utilities of VGAM1983 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC89932. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1984 (VGAM1984) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69960] VGAM1984 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1984 was detected is described hereinabove with reference to Figs. 1-8.

[69961] VGAM1984 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra Virus.
VGAM1984 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69962] VGAM1984 gene encodes a VGAM1984 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1984 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1984 precursor RNA is designated SEQ ID:1970, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:1970 is located at position 7867 relative to the genome of Hendra Virus.

[69963] VGAM1984 precursor RNA folds onto itself, forming VGAM1984 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69964] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1984 folded precursor RNA into VGAM1984 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1984 RNA is designated SEQ ID:4695, and is provided hereinbelow with reference to the sequence listing part.

[69965] VGAM1984 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1984 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1984 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69966] VGAM1984 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1984 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1984 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1984 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM1984 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69967] The complementary binding of VGAM1984 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1984 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1984 host target RNA into VGAM1984 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69968] It is appreciated that VGAM1984 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1984 host target genes. The mRNA of each one of this plurality of VGAM1984 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1984 RNA, herein designated VGAM RNA, and which when bound by VGAM1984 RNA causes

inhibition of translation of respective one or more VGAM1984 host target proteins.

[69969] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1984 gene, herein designated VGAM GENE, on one or more VGAM1984 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69970] It is yet further appreciated that a function of VGAM1984 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1984 include diagnosis, prevention and

treatment of viral infection by Hendra Virus. Specific functions, and accordingly utilities, of VGAM1984 correlate with, and may be deduced from, the identity of the host target genes which VGAM1984 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[69971] Nucleotide sequences of the VGAM1984 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1984 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1984 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1984 are further described hereinbelow with reference to Table 1.

[69972] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1984 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1984 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69973] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1984 gene, herein designated VGAM is inhibition of expression of VGAM1984 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM1984 correlate with, and may be deduced from, the identity of the target genes which VGAM1984 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[69974] Secretogranin III (SCG3, Accession NM_013243) is a VGAM1984 host target gene. SCG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCG3 BINDING SITE, designated SEQ ID:14904, to the nucleotide sequence of VGAM1984 RNA, herein designated VGAM RNA, also designated SEQ ID:4695.

[69975] A function of VGAM1984 is therefore inhibition of Secretogranin III (SCG3, Accession NM_013243). Accordingly, utilities of VGAM1984 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCG3. FLJ20086 (Accession NM_017661) is another VGAM1984 host target gene. FLJ20086 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20086, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20086 BINDING SITE, designated SEQ ID:19192, to the nucleotide sequence of VGAM1984 RNA, herein designated VGAM RNA, also designated SEQ ID:4695.

[69976] Another function of VGAM1984 is therefore inhibition of FLJ20086 (Accession NM_017661). Accordingly, utilities of VGAM1984 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20086. Junctional Adhesion Molecule 1 (JAM1, Accession NM_144501) is another VGAM1984 host target gene. JAM1 BINDING SITE1 through JAM1 BINDING SITE5 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by JAM1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JAM1 BINDING SITE1 through JAM1 BINDING SITE5, designated SEQ ID:29321, SEQ ID:29328, SEQ ID:18861, SEQ ID:29337 and SEQ ID:29348 respectively, to the nucleotide sequence of VGAM1984 RNA, herein designated VGAM RNA, also designated SEQ ID:4695.

[69977] Another function of VGAM1984 is therefore inhibition of Junctional Adhesion Molecule 1 (JAM1, Accession NM_144501). Accordingly, utilities of VGAM1984 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAM1. Yes-associated Protein 1, 65kDa (YAP1, Accession NM_006106) is another VGAM1984 host target gene. YAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by YAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YAP1 BINDING SITE, designated SEQ ID:12750, to the nucleotide sequence of VGAM1984 RNA, herein designated VGAM RNA, also designated SEQ ID:4695.

[69978] Another function of VGAM1984 is therefore inhibition of Yes-associated Protein 1, 65kDa (YAP1, Accession NM_006106). Accordingly, utilities of VGAM1984 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YAP1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1985

(VGAM1985) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[69979] VGAM1985 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1985 was detected is described hereinabove with reference to Figs. 1-8.

[69980] VGAM1985 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra Virus. VGAM1985 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[69981] VGAM1985 gene encodes a VGAM1985 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1985 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1985 precursor RNA is designated SEQ ID:1971, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1971 is located at position 3920 relative to the genome of Hendra Virus.

[69982] VGAM1985 precursor RNA folds onto itself, forming

VGAM1985 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[69983] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1985 folded precursor RNA into VGAM1985 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM1985 RNA is designated SEQ ID:4696, and is provided hereinbelow with reference to the sequence listing part.

[69984] VGAM1985 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1985 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1985 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[69985] VGAM1985 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1985 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1985 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1985 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1985 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[69986] The complementary binding of VGAM1985 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1985 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1985 host target RNA into VGAM1985 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[69987] It is appreciated that VGAM1985 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1985 host target genes. The mRNA of each one of this plurality of VGAM1985 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1985 RNA, herein designated VGAM RNA, and which when bound by VGAM1985 RNA causes inhibition of translation of respective one or more VGAM1985 host target proteins.

[69988] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1985 gene, herein designated VGAM GENE, on one or more VGAM1985 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[69989] It is yet further appreciated that a function of VGAM1985 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of viral infection by Hendra Virus. Specific functions, and accordingly utilities, of VGAM1985 correlate with, and may be deduced from, the identity of the host target genes which VGAM1985 binds and inhibits, and the

function of these host target genes, as elaborated herein-below.

[69990] Nucleotide sequences of the VGAM1985 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1985 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1985 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1985 are further described hereinbelow with reference to Table 1.

[69991] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1985 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1985 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[69992] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1985 gene, herein designated VGAM is inhibition of expression of VGAM1985 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1985 correlate with, and may be deduced from, the identity of the target genes which VGAM1985 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[69993] Cyclin-dependent Kinase Inhibitor 2A (melanoma, p16, inhibits CDK4) (CDKN2A, Accession NM_058197) is a VGAM1985 host target gene. CDKN2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDKN2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDKN2A BINDING SITE, designated SEQ ID:27757, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[69994] A function of VGAM1985 is therefore inhibition of Cyclin-dependent Kinase Inhibitor 2A (melanoma, p16, inhibits CDK4) (CDKN2A, Accession NM_058197). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKN2A. Cysteine Knot Superfamily 1, BMP Antagonist 1 (CKTSF1B1, Accession NM_013372) is another VGAM1985 host target gene. CKTSF1B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CKTSF1B1, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CK-TSF1B1 BINDING SITE, designated SEQ ID:15023, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[69995] Another function of VGAM1985 is therefore inhibition of Cysteine Knot Superfamily 1, BMP Antagonist 1 (CKTSF1B1, Accession NM_013372), a gene which blocks signaling of bone morphogenetic protein (BMP) . Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CKTSF1B1. The function of CKTSF1B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM28.HLA Class II Region Expressed Gene KE4 (HKE4, Accession NM_006979) is another VGAM1985 host target gene. HKE4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HKE4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HKE4 BINDING SITE, designated SEQ ID:13841, to the nucleotide se-

quence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[69996] Another function of VGAM1985 is therefore inhibition of HLA Class II Region Expressed Gene KE4 (HKE4, Accession NM_006979), a gene which Contains histidine-rich charge clusters. Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HKE4. The function of HKE4 has been established by previous studies. Among the many non-HLA genes that have been identified in the region of the major histocompatibility complex (OMIM Ref. No. 6p21.3) in mouse and human are the genes symbolized Ke4 and Ke6 in the mouse. Ando et al. (1996) stated that the function of these genes is unknown, although Ke6 may be involved in the manifestation of polycystic kidney disease (PKD; 173900) because of its aberrant expression in 2 different murine models of PKD (Aziz et al., 1993; Aziz et al., 1994). Ando et al. (1996) isolated cDNA clones corresponding to the human Ke4 and Ke6 (OMIM Ref. No. 601417) genes (designated HKE4 and HKE6 by them) and located at the centromeric end of the HLA region on human 6p21.3. The predicted amino acid sequences of HKE4 and HKE6 exhibited 81.5 and 85.6% identity to the mouse

homologs, respectively. Ando et al. (1996) speculated that HKE4 may encode a membrane protein with histidine-rich charge clusters. Kikuti et al. (1997) examined YAC clone Y42, which contains the MHC class II region of chromosome 6q21.3. This region has a relatively high gene density. They identified the following human genes (in order from centromere toward telomere): HSET (OMIM Ref. No. 603763)--HKE1.5--HKE2--HKE3--RING1--(OMIM Ref. No. 602045)--HKE6 (OMIM Ref. No. 601417)--HKE4--RXRB (OMIM Ref. No. 180246)--COL11A2 (OMIM Ref. No. 120290)--DPB2.

[69997] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[69998] Ando, A.; Kikuti, Y. Y.; Shigenari, A.; Kawata, H.; Okamoto, N.; Shiina, T.; Chen, L.; Ikemura, T.; Abe, K.; Kimura, M.; Inoko, H. : cDNA cloning of the human homologues of the mouse Ke4 and Ke6 genes at the centromeric end of the human MHC region. Genomics 35: 600-602, 1996. ; and

[69999] Kikuti, Y. Y.; Tamiya, G.; Ando, A.; Chen, L.; Kimura, M.; Ferreira, E.; Tsuji, K.; Trowsdale, J.; Inoko, H. : Physical mapping 220 kb centromeric of the human MHC and DNA sequence analy.

[70000] Further studies establishing the function and utilities of HKE4 are found in John Hopkins OMIM database record ID 601416, and in sited publications numbered 9390-9393 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.LFG (Accession XM_084780) is another VGAM1985 host target gene. LFG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LFG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LFG BINDING SITE, designated SEQ ID:37695, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70001] Another function of VGAM1985 is therefore inhibition of LFG (Accession XM_084780). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LFG. Polycystic Kidney Disease 1 (autosomal dominant) (PKD1, Accession NM_000296) is another VGAM1985 host target gene. PKD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PKD1, corresponding to a HOST TARGET binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PKD1 BINDING SITE, designated SEQ ID:5840, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70002] Another function of VGAM1985 is therefore inhibition of Polycystic Kidney Disease 1 (autosomal dominant) (PKD1, Accession NM_000296). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKD1. RAB27A, Member RAS Oncogene Family (RAB27A, Accession NM_004580) is another VGAM1985 host target gene. RAB27A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB27A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB27A BINDING SITE, designated SEQ ID:10927, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70003] Another function of VGAM1985 is therefore inhibition of RAB27A, Member RAS Oncogene Family (RAB27A, Acces-

sion NM_004580). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB27A. RB1-inducible Coiled-coil 1 (RB1CC1, Accession NM_014781) is another VGAM1985 host target gene. RB1CC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RB1CC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RB1CC1 BINDING SITE, designated SEQ ID:16633, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70004] Another function of VGAM1985 is therefore inhibition of RB1-inducible Coiled-coil 1 (RB1CC1, Accession NM_014781), a gene which is likely to participate in nuclear architecture by connecting chromatin with the nuclear matrix or envelope. Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RB1CC1. The function of RB1CC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to VGAM18.Adaptor-related Protein Complex 3, Mu 2 Subunit (AP3M2, Accession NM_006803) is another VGAM1985 host target gene. AP3M2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP3M2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP3M2 BINDING SITE, designated SEQ ID:13676, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70005] Another function of VGAM1985 is therefore inhibition of Adaptor-related Protein Complex 3, Mu 2 Subunit (AP3M2, Accession NM_006803). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP3M2. Chromosome 17 Open Reading Frame 26 (C17orf26, Accession NM_139177) is another VGAM1985 host target gene. C17orf26 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C17orf26, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of C17orf26 BINDING SITE, designated SEQ ID:29186, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70006] Another function of VGAM1985 is therefore inhibition of Chromosome 17 Open Reading Frame 26 (C17orf26, Accession NM_139177). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C17orf26. FLJ20584 (Accession NM_017891) is another VGAM1985 host target gene. FLJ20584 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20584, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20584 BINDING SITE, designated SEQ ID:19563, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70007] Another function of VGAM1985 is therefore inhibition of FLJ20584 (Accession NM_017891). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20584. TRIAD3 (Accession XM_170517) is another VGAM1985 host target gene. TRIAD3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIAD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIAD3 BINDING SITE, designated SEQ ID:45348, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70008] Another function of VGAM1985 is therefore inhibition of TRIAD3 (Accession XM_170517). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIAD3. LOC126267 (Accession XM_065012) is another VGAM1985 host target gene. LOC126267 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC126267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126267 BINDING SITE, designated SEQ ID:37271, to the nucleotide sequence of VGAM1985 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4696.

[70009] Another function of VGAM1985 is therefore inhibition of LOC126267 (Accession XM_065012). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126267. LOC147229 (Accession XM_085742) is another VGAM1985 host target gene. LOC147229 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147229 BINDING SITE, designated SEQ ID:38320, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70010] Another function of VGAM1985 is therefore inhibition of LOC147229 (Accession XM_085742). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147229. LOC163081 (Accession XM_091987) is another VGAM1985 host target gene. LOC163081 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC163081, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163081 BINDING SITE, designated SEQ ID:40087, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70011] Another function of VGAM1985 is therefore inhibition of LOC163081 (Accession XM_091987). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163081. LOC166424 (Accession XM_105867) is another VGAM1985 host target gene. LOC166424 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC166424, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC166424 BINDING SITE, designated SEQ ID:42194, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70012] Another function of VGAM1985 is therefore inhibition of LOC166424 (Accession XM_105867). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC166424. LOC255242 (Accession XM_171095) is another VGAM1985 host target gene. LOC255242 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255242, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255242 BINDING SITE, designated SEQ ID:45905, to the nucleotide sequence of VGAM1985 RNA, herein designated VGAM RNA, also designated SEQ ID:4696.

[70013] Another function of VGAM1985 is therefore inhibition of LOC255242 (Accession XM_171095). Accordingly, utilities of VGAM1985 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255242. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1986 (VGAM1986) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70014] VGAM1986 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1986 was detected is described hereinabove with reference to Figs. 1-8.

[70015] VGAM1986 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra Virus. VGAM1986 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70016] VGAM1986 gene encodes a VGAM1986 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1986 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1986 precursor RNA is designated SEQ ID:1972, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1972 is located at position 4500 relative to the genome of Hendra Virus.

[70017] VGAM1986 precursor RNA folds onto itself, forming VGAM1986 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70018] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1986 folded precursor RNA into VGAM1986 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM1986 RNA is designated SEQ ID:4697, and is provided hereinbelow with reference to the sequence listing part.

[70019] VGAM1986 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1986 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1986 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70020] VGAM1986 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1986 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1986 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1986 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1986 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70021] The complementary binding of VGAM1986 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM1986 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1986 host target RNA into VGAM1986 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70022] It is appreciated that VGAM1986 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1986 host target genes. The mRNA of each one of this plurality of VGAM1986 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1986 RNA, herein designated VGAM RNA, and which when bound by VGAM1986 RNA causes inhibition of translation of respective one or more VGAM1986 host target proteins.

[70023] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1986 gene, herein designated VGAM GENE, on one or more VGAM1986 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70024] It is yet further appreciated that a function of VGAM1986 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1986 include diagnosis, prevention and treatment of viral infection by Hendra Virus. Specific functions, and accordingly utilities, of VGAM1986 correlate with, and may be deduced from, the identity of the host target genes which VGAM1986 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70025] Nucleotide sequences of the VGAM1986 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM1986 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1986 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1986 are further described hereinbelow with reference to Table 1.

[70026] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1986 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1986 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70027] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1986 gene, herein designated VGAM is inhibition of expression of VGAM1986 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1986 correlate with, and may be deduced from, the identity of the target genes which VGAM1986 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70028] X-ray Repair Complementing Defective Repair In Chinese Hamster Cells 3 (XRCC3, Accession NM_005432) is a VGAM1986 host target gene. XRCC3 BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by XRCC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XRCC3 BINDING SITE, designated SEQ ID:11905, to the nucleotide sequence of VGAM1986 RNA, herein designated VGAM RNA, also designated SEQ ID:4697.

[70029] A function of VGAM1986 is therefore inhibition of X-ray Repair Complementing Defective Repair In Chinese Hamster Cells 3 (XRCC3, Accession NM_005432), a gene which is required for meiotic recombination, synaptonemal complex formation and cell cycle progression. Accordingly, utilities of VGAM1986 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XRCC3. The function of XRCC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1290.HEMK (Accession NM_016173) is another VGAM1986 host target gene. HEMK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HEMK, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HEMK BINDING SITE, designated SEQ ID:18264, to the nucleotide sequence of VGAM1986 RNA, herein designated VGAM RNA, also designated SEQ ID:4697.

[70030] Another function of VGAM1986 is therefore inhibition of HEMK (Accession NM_016173). Accordingly, utilities of VGAM1986 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEMK. Lectin, Galactoside-binding, Soluble, 8 (galectin 8) (LGALS8, Accession NM_006499) is another VGAM1986 host target gene. LGALS8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LGALS8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LGALS8 BINDING SITE, designated SEQ ID:13243, to the nucleotide sequence of VGAM1986 RNA, herein designated VGAM RNA, also designated SEQ ID:4697.

[70031] Another function of VGAM1986 is therefore inhibition of Lectin, Galactoside-binding, Soluble, 8 (galectin 8) (LGALS8, Accession NM_006499). Accordingly, utilities of

VGAM1986 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LGALS8. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 3B (PPP1R3B, Accession NM_024607) is another VGAM1986 host target gene. PPP1R3B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R3B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R3B BINDING SITE, designated SEQ ID:23857, to the nucleotide sequence of VGAM1986 RNA, herein designated VGAM RNA, also designated SEQ ID:4697.

[70032] Another function of VGAM1986 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 3B (PPP1R3B, Accession NM_024607). Accordingly, utilities of VGAM1986 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R3B. SCAN Domain Containing 2 (SCAND2, Accession NM_033640) is another VGAM1986 host target gene. SCAND2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCAND2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAND2 BINDING SITE, designated SEQ ID:27355, to the nucleotide sequence of VGAM1986 RNA, herein designated VGAM RNA, also designated SEQ ID:4697.

[70033] Another function of VGAM1986 is therefore inhibition of SCAN Domain Containing 2 (SCAND2, Accession NM_033640). Accordingly, utilities of VGAM1986 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAND2. LOC113763 (Accession NM_138434) is another VGAM1986 host target gene. LOC113763 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC113763, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC113763 BINDING SITE, designated SEQ ID:28800, to the nucleotide sequence of VGAM1986 RNA, herein designated VGAM RNA, also designated SEQ ID:4697.

[70034] Another function of VGAM1986 is therefore inhibition of LOC113763 (Accession NM_138434). Accordingly, utilities

of VGAM1986 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113763. LOC137964 (Accession XM_059933) is another VGAM1986 host target gene. LOC137964 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC137964, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC137964 BINDING SITE, designated SEQ ID:37110, to the nucleotide sequence of VGAM1986 RNA, herein designated VGAM RNA, also designated SEQ ID:4697.

[70035] Another function of VGAM1986 is therefore inhibition of LOC137964 (Accession XM_059933). Accordingly, utilities of VGAM1986 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137964. LOC150577 (Accession XM_097918) is another VGAM1986 host target gene. LOC150577 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC150577 BINDING SITE, designated SEQ ID:41216, to the nucleotide sequence of VGAM1986 RNA, herein designated VGAM RNA, also designated SEQ ID:4697.

[70036] Another function of VGAM1986 is therefore inhibition of LOC150577 (Accession XM_097918). Accordingly, utilities of VGAM1986 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150577. LOC199863 (Accession XM_117147) is another VGAM1986 host target gene. LOC199863 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199863, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199863 BINDING SITE, designated SEQ ID:43254, to the nucleotide sequence of VGAM1986 RNA, herein designated VGAM RNA, also designated SEQ ID:4697.

[70037] Another function of VGAM1986 is therefore inhibition of LOC199863 (Accession XM_117147). Accordingly, utilities of VGAM1986 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199863. LOC253897 (Accession XM_171187) is another VGAM1986 host target gene. LOC253897 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253897, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253897 BINDING SITE, designated SEQ ID:45967, to the nucleotide sequence of VGAM1986 RNA, herein designated VGAM RNA, also designated SEQ ID:4697.

[70038] Another function of VGAM1986 is therefore inhibition of LOC253897 (Accession XM_171187). Accordingly, utilities of VGAM1986 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253897. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1987 (VGAM1987) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70039] VGAM1987 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1987 was detected is described hereinabove with reference to Figs. 1-8.

[70040] VGAM1987 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra Virus. VGAM1987 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70041] VGAM1987 gene encodes a VGAM1987 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1987 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1987 precursor RNA is designated SEQ ID:1973, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1973 is located at position 11388 relative to the genome of Hendra Virus.

[70042] VGAM1987 precursor RNA folds onto itself, forming VGAM1987 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[70043] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1987 folded precursor RNA into VGAM1987 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM1987 RNA is designated SEQ ID:4698, and is provided hereinbelow with reference to the sequence listing part.

[70044] VGAM1987 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1987 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1987 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70045] VGAM1987 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1987 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1987 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1987 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1987 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70046] The complementary binding of VGAM1987 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1987 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1987 host target RNA into VGAM1987 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70047] It is appreciated that VGAM1987 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1987 host target genes. The mRNA of each one of this plurality of VGAM1987 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1987 RNA, herein designated VGAM RNA, and which when bound by VGAM1987 RNA causes inhibition of translation of respective one or more VGAM1987 host target proteins.

[70048] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1987 gene, herein designated VGAM GENE, on one or more VGAM1987 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70049] It is yet further appreciated that a function of VGAM1987 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1987 include diagnosis, prevention and treatment of viral infection by Hendra Virus. Specific functions, and accordingly utilities, of VGAM1987 correlate with, and may be deduced from, the identity of the host target genes which VGAM1987 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70050] Nucleotide sequences of the VGAM1987 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1987 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1987 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1987 are further described hereinbelow with reference to Table 1.

[70051] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1987 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1987 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70052] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1987 gene, herein designated VGAM is inhibition of expression of VGAM1987 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1987 correlate with, and may be deduced from, the identity of the target genes which VGAM1987 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70053] KIAA1467 (Accession XM_049605) is a VGAM1987 host target gene. KIAA1467 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1467, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of KIAA1467 BINDING SITE, designated SEQ ID:35455, to the nucleotide sequence of VGAM1987 RNA, herein designated VGAM RNA, also designated SEQ ID:4698.

[70054] A function of VGAM1987 is therefore inhibition of KIAA1467 (Accession XM_049605). Accordingly, utilities of VGAM1987 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1467. MGC11061 (Accession NM_032312) is another VGAM1987 host target gene. MGC11061 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC11061, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11061 BINDING SITE, designated SEQ ID:26116, to the nucleotide sequence of VGAM1987 RNA, herein designated VGAM RNA, also designated SEQ ID:4698.

[70055] Another function of VGAM1987 is therefore inhibition of MGC11061 (Accession NM_032312). Accordingly, utilities of VGAM1987 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11061. Synaptosomal-associated Protein, 91kDa Ho-

molog (mouse) (SNAP91, Accession NM_014841) is another VGAM1987 host target gene. SNAP91 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNAP91, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNAP91 BINDING SITE, designated SEQ ID:16869, to the nucleotide sequence of VGAM1987 RNA, herein designated VGAM RNA, also designated SEQ ID:4698.

[70056] Another function of VGAM1987 is therefore inhibition of Synaptosomal-associated Protein, 91kDa Homolog (mouse) (SNAP91, Accession NM_014841). Accordingly, utilities of VGAM1987 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP91. LOC120406 (Accession XM_061976) is another VGAM1987 host target gene. LOC120406 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120406, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120406 BINDING SITE, designated SEQ ID:37220, to

the nucleotide sequence of VGAM1987 RNA, herein designated VGAM RNA, also designated SEQ ID:4698.

[70057] Another function of VGAM1987 is therefore inhibition of LOC120406 (Accession XM_061976). Accordingly, utilities of VGAM1987 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120406. LOC93349 (Accession NM_138402) is another VGAM1987 host target gene. LOC93349 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93349, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93349 BINDING SITE, designated SEQ ID:28769, to the nucleotide sequence of VGAM1987 RNA, herein designated VGAM RNA, also designated SEQ ID:4698.

[70058] Another function of VGAM1987 is therefore inhibition of LOC93349 (Accession NM_138402). Accordingly, utilities of VGAM1987 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93349. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 1988 (VGAM1988) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70059] VGAM1988 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1988 was detected is described hereinabove with reference to Figs. 1-8.

[70060] VGAM1988 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra Virus. VGAM1988 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70061] VGAM1988 gene encodes a VGAM1988 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1988 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1988 precursor RNA is designated SEQ ID:1974, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1974 is located at position 15383 relative to the genome of Hendra Virus.

[70062] VGAM1988 precursor RNA folds onto itself, forming VGAM1988 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70063] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1988 folded precursor RNA into VGAM1988 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM1988 RNA is designated SEQ ID:4699, and is provided hereinbelow with reference to the sequence listing part.

[70064] VGAM1988 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1988 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM1988 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70065] VGAM1988 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1988 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1988 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1988 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1988 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70066] The complementary binding of VGAM1988 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1988 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1988 host target RNA into VGAM1988 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70067] It is appreciated that VGAM1988 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1988 host target genes. The mRNA of each one of this plurality of VGAM1988 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1988 RNA, herein designated VGAM RNA, and which when bound by VGAM1988 RNA causes inhibition of translation of respective one or more VGAM1988 host target proteins.

[70068] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1988 gene, herein designated VGAM GENE, on one or more VGAM1988 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70069] It is yet further appreciated that a function of VGAM1988 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of viral infection by Hendra Virus. Specific functions, and accordingly utilities, of VGAM1988 correlate with, and may be deduced from, the identity of the host

target genes which VGAM1988 binds and inhibits, and the function of these host target genes, as elaborated herein-below.

[70070] Nucleotide sequences of the VGAM1988 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1988 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1988 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1988 are further described hereinbelow with reference to Table 1.

[70071] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1988 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1988 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70072] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1988 gene, herein designated VGAM is inhibition of expression of VGAM1988 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1988 correlate with, and may be deduced from, the identity of the target genes which VGAM1988

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70073] Adenomatosis Polyposis Coli (APC, Accession NM_000038) is a VGAM1988 host target gene. APC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APC BINDING SITE, designated SEQ ID:5481, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70074] A function of VGAM1988 is therefore inhibition of Adenomatosis Polyposis Coli (APC, Accession NM_000038). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APC. Protein Kinase (cAMP-dependent, catalytic) Inhibitor Beta (PKIB, Accession NM_032471) is another VGAM1988 host target gene. PKIB BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PKIB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PKIB BINDING SITE, designated SEQ ID:26229, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70075] Another function of VGAM1988 is therefore inhibition of Protein Kinase (cAMP-dependent, catalytic) Inhibitor Beta (PKIB, Accession NM_032471). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKIB. Sodium Channel, Nonvoltage-gated 1, Gamma (SCNN1G, Accession NM_001039) is another VGAM1988 host target gene. SCNN1G BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCNN1G, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCNN1G BINDING SITE, designated SEQ ID:6704, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70076] Another function of VGAM1988 is therefore inhibition of Sodium Channel, Nonvoltage-gated 1, Gamma (SCNN1G, Accession NM_001039). Accordingly, utilities of

VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCNN1G. Transcription Factor 1, Hepatic; LF-B1, Hepatic Nuclear Factor (HNF1), Albumin Proximal Factor (TCF1, Accession NM_000545) is another VGAM1988 host target gene. TCF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF1 BINDING SITE, designated SEQ ID:6147, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70077] Another function of VGAM1988 is therefore inhibition of Transcription Factor 1, Hepatic; LF-B1, Hepatic Nuclear Factor (HNF1), Albumin Proximal Factor (TCF1, Accession NM_000545), a gene which is required for the expression of several liver specific genes. binds to the inverted palindrome 5'-gttaatnattaac-3'. Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF1. The function of TCF1 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to VGAM1189.BLOV1 (Accession XM_083866) is another VGAM1988 host target gene. BLOV1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BLOV1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BLOV1 BINDING SITE, designated SEQ ID:37520, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70078] Another function of VGAM1988 is therefore inhibition of BLOV1 (Accession XM_083866). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BLOV1. FLJ00058 (Accession XM_086123) is another VGAM1988 host target gene. FLJ00058 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ00058, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00058 BINDING SITE, designated SEQ ID:38508, to the nucleotide sequence of

VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70079] Another function of VGAM1988 is therefore inhibition of FLJ00058 (Accession XM_086123). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00058. FLJ10276 (Accession NM_018045) is another VGAM1988 host target gene. FLJ10276 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10276, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10276 BINDING SITE, designated SEQ ID:19790, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70080] Another function of VGAM1988 is therefore inhibition of FLJ10276 (Accession NM_018045). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10276. FLJ10803 (Accession NM_018224) is another VGAM1988 host target gene. FLJ10803 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ10803, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10803 BINDING SITE, designated SEQ ID:20153, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70081] Another function of VGAM1988 is therefore inhibition of FLJ10803 (Accession NM_018224). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10803. FLJ11142 (Accession NM_018338) is another VGAM1988 host target gene. FLJ11142 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11142, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11142 BINDING SITE, designated SEQ ID:20343, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70082] Another function of VGAM1988 is therefore inhibition of FLJ11142 (Accession NM_018338). Accordingly, utilities of

VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11142. KIAA0997 (Accession NM_014950) is another VGAM1988 host target gene. KIAA0997 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0997, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0997 BINDING SITE, designated SEQ ID:17280, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70083] Another function of VGAM1988 is therefore inhibition of KIAA0997 (Accession NM_014950). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0997. KIAA1069 (Accession XM_042635) is another VGAM1988 host target gene. KIAA1069 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1069, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1069 BINDING SITE, designated SEQ ID:33723, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70084] Another function of VGAM1988 is therefore inhibition of KIAA1069 (Accession XM_042635). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1069. NUDEL (Accession NM_030808) is another VGAM1988 host target gene. NUDEL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUDEL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUDEL BINDING SITE, designated SEQ ID:25122, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70085] Another function of VGAM1988 is therefore inhibition of NUDEL (Accession NM_030808). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUDEL. LOC151178 (Accession XM_087117) is another VGAM1988 host target gene. LOC151178 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151178 BINDING SITE, designated SEQ ID:39071, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70086] Another function of VGAM1988 is therefore inhibition of LOC151178 (Accession XM_087117). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151178. LOC199786 (Accession XM_114021) is another VGAM1988 host target gene. LOC199786 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199786 BINDING SITE, designated SEQ ID:42618, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70087] Another function of VGAM1988 is therefore inhibition of

LOC199786 (Accession XM_114021). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199786. LOC255975 (Accession XM_171083) is another VGAM1988 host target gene. LOC255975 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255975, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255975 BINDING SITE, designated SEQ ID:45890, to the nucleotide sequence of VGAM1988 RNA, herein designated VGAM RNA, also designated SEQ ID:4699.

[70088] Another function of VGAM1988 is therefore inhibition of LOC255975 (Accession XM_171083). Accordingly, utilities of VGAM1988 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255975. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1989 (VGAM1989) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[70089] VGAM1989 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1989 was detected is described hereinabove with reference to Figs. 1-8.

[70090] VGAM1989 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Hendra Virus. VGAM1989 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70091] VGAM1989 gene encodes a VGAM1989 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1989 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1989 precursor RNA is designated SEQ ID:1975, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1975 is located at position 1467 relative to the genome of Hendra Virus.

[70092] VGAM1989 precursor RNA folds onto itself, forming VGAM1989 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70093] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1989 folded precursor RNA into VGAM1989 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM1989 RNA is designated SEQ ID:4700, and is provided hereinbelow with reference to the sequence listing part.

[70094] VGAM1989 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1989 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1989 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70095] VGAM1989 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1989 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1989 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1989 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1989 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[70096] The complementary binding of VGAM1989 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1989 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1989 host target RNA into VGAM1989 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70097] It is appreciated that VGAM1989 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1989 host target genes. The mRNA of each one of this plurality of VGAM1989 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1989 RNA, herein designated VGAM RNA, and which when bound by VGAM1989 RNA causes inhibition of translation of respective one or more VGAM1989 host target proteins.

[70098] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1989 gene, herein designated VGAM GENE, on one

or more VGAM1989 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70099] It is yet further appreciated that a function of VGAM1989 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of viral infection by Hendra Virus. Specific functions, and accordingly utilities, of VGAM1989 correlate with, and may be deduced from, the identity of the host target genes which VGAM1989 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70100] Nucleotide sequences of the VGAM1989 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1989 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1989 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1989 are further described hereinbelow with reference to Table 1.

[70101] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1989 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1989 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70102] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1989 gene, herein designated VGAM is inhibition of expression of VGAM1989 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1989 correlate with, and may be deduced from, the identity of the target genes which VGAM1989 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70103] Diptheria Toxin Resistance Protein Required For Diph-

thamide Biosynthesis-like 1 (S. cerevisiae) (DPH2L1, Accession NM_001383) is a VGAM1989 host target gene. DPH2L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DPH2L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DPH2L1 BINDING SITE, designated SEQ ID:7053, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70104] A function of VGAM1989 is therefore inhibition of Diphtheria Toxin Resistance Protein Required For Diphthamide Biosynthesis-like 1 (S. cerevisiae) (DPH2L1, Accession NM_001383), a gene which may be involved in regulating global protein synthesis; has similarity to S. cerevisiae Dph2p. Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPH2L1. The function of DPH2L1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM608.RNA (guanine-7-) Methyltransferase (RNMT,

Accession NM_003799) is another VGAM1989 host target gene. RNMT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNMT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNMT BINDING SITE, designated SEQ ID:9882, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70105] Another function of VGAM1989 is therefore inhibition of RNA (guanine-7-) Methyltransferase (RNMT, Accession NM_003799), a gene which catalyzes the methylation of GpppN- at the guanine N7 position. Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNMT. The function of RNMT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM178.Transcription Factor 19 (SC1) (TCF19, Accession XM_175167) is another VGAM1989 host target gene. TCF19 BINDING SITE1 and TCF19 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TCF19, corresponding to HOST TAR-

GET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF19 BINDING SITE1 and TCF19 BINDING SITE2, designated SEQ ID:46658 and SEQ ID:46707 respectively, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70106] Another function of VGAM1989 is therefore inhibition of Transcription Factor 19 (SC1) (TCF19, Accession XM_175167), a gene which plays an important role in the transcription of genes required for the later stages of cell cycle progression. Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF19. The function of TCF19 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM299.FLJ20374 (Accession NM_017793) is another VGAM1989 host target gene. FLJ20374 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20374, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ20374 BINDING SITE, designated SEQ ID:19429, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70107] Another function of VGAM1989 is therefore inhibition of FLJ20374 (Accession NM_017793). Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20374. FLJ25415 (Accession NM_144708) is another VGAM1989 host target gene. FLJ25415 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ25415, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ25415 BINDING SITE, designated SEQ ID:29533, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70108] Another function of VGAM1989 is therefore inhibition of FLJ25415 (Accession NM_144708). Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25415. KIAA0798 (Accession NM_014650) is another

VGAM1989 host target gene. KIAA0798 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0798, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0798 BINDING SITE, designated SEQ ID:16068, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70109] Another function of VGAM1989 is therefore inhibition of KIAA0798 (Accession NM_014650). Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0798. KIAA1281 (Accession XM_114432) is another VGAM1989 host target gene. KIAA1281 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1281, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1281 BINDING SITE, designated SEQ ID:42961, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70110] Another function of VGAM1989 is therefore inhibition of KIAA1281 (Accession XM_114432). Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1281. MACMARCKS (Accession NM_023009) is another VGAM1989 host target gene. MACMARCKS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MACMARCKS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MACMARCKS BINDING SITE, designated SEQ ID:23273, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70111] Another function of VGAM1989 is therefore inhibition of MACMARCKS (Accession NM_023009). Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MACMARCKS. MGC10812 (Accession NM_031425) is another VGAM1989 host target gene. MGC10812 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC10812, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10812 BINDING SITE, designated SEQ ID:25412, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70112] Another function of VGAM1989 is therefore inhibition of MGC10812 (Accession NM_031425). Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10812. MGC2628 (Accession NM_024076) is another VGAM1989 host target gene. MGC2628 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2628, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2628 BINDING SITE, designated SEQ ID:23509, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70113] Another function of VGAM1989 is therefore inhibition of MGC2628 (Accession NM_024076). Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC2628. Synaptophysin-like Protein (SYPL, Accession XM_167511) is another VGAM1989 host target gene. SYPL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYPL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYPL BINDING SITE, designated SEQ ID:44645, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70114] Another function of VGAM1989 is therefore inhibition of Synaptophysin-like Protein (SYPL, Accession XM_167511). Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYPL. LOC143310 (Accession XM_084485) is another VGAM1989 host target gene. LOC143310 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143310, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143310 BINDING SITE, designated SEQ ID:37605, to the nucleotide sequence of

VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70115] Another function of VGAM1989 is therefore inhibition of LOC143310 (Accession XM_084485). Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143310. LOC169577 (Accession XM_095785) is another VGAM1989 host target gene. LOC169577 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC169577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169577 BINDING SITE, designated SEQ ID:40283, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70116] Another function of VGAM1989 is therefore inhibition of LOC169577 (Accession XM_095785). Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169577. LOC219920 (Accession XM_167787) is another VGAM1989 host target gene. LOC219920 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC219920, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219920 BINDING SITE, designated SEQ ID:44803, to the nucleotide sequence of VGAM1989 RNA, herein designated VGAM RNA, also designated SEQ ID:4700.

[70117] Another function of VGAM1989 is therefore inhibition of LOC219920 (Accession XM_167787). Accordingly, utilities of VGAM1989 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219920. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1990 (VGAM1990) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70118] VGAM1990 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1990 was detected is described hereinabove with reference to Figs. 1-8.

[70119] VGAM1990 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Nipah Virus. VGAM1990 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70120] VGAM1990 gene encodes a VGAM1990 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1990 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1990 precursor RNA is designated SEQ ID:1976, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1976 is located at position 7327 relative to the genome of Nipah Virus.

[70121] VGAM1990 precursor RNA folds onto itself, forming VGAM1990 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70122] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM1990 folded precursor RNA into VGAM1990 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM1990 RNA is designated SEQ ID:4701, and is provided hereinbelow with reference to the sequence listing part.

[70123] VGAM1990 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1990 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1990 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70124] VGAM1990 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1990 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1990 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1990 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1990 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70125] The complementary binding of VGAM1990 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1990 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1990 host target RNA into VGAM1990 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70126] It is appreciated that VGAM1990 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1990 host target genes. The mRNA of each one of this plurality of VGAM1990 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1990 RNA, herein designated VGAM RNA, and which when bound by VGAM1990 RNA causes inhibition of translation of respective one or more VGAM1990 host target proteins.

[70127] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1990 gene, herein designated VGAM GENE, on one or more VGAM1990 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70128] It is yet further appreciated that a function of VGAM1990 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1990 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM1990 correlate with, and may be deduced from, the identity of the host target genes which VGAM1990 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70129] Nucleotide sequences of the VGAM1990 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1990 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1990 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1990 are further described hereinbelow with reference to Table 1.

[70130] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1990 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1990 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70131] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1990 gene, herein designated VGAM is inhibition of expression of VGAM1990 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1990 correlate with, and may be deduced from, the identity of the target genes which VGAM1990 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70132] Tumor Necrosis Factor Receptor Superfamily, Member 6 (TNFRSF6, Accession NM_000043) is a VGAM1990 host target gene. TNFRSF6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFRSF6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFRSF6 BINDING SITE,

designated SEQ ID:5484, to the nucleotide sequence of VGAM1990 RNA, herein designated VGAM RNA, also designated SEQ ID:4701.

[70133] A function of VGAM1990 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 6 (TNFRSF6, Accession NM_000043). Accordingly, utilities of VGAM1990 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF6. Preimplantation Protein 3 (PREI3, Accession XM_038960) is another VGAM1990 host target gene. PREI3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PREI3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PREI3 BINDING SITE, designated SEQ ID:32965, to the nucleotide sequence of VGAM1990 RNA, herein designated VGAM RNA, also designated SEQ ID:4701.

[70134] Another function of VGAM1990 is therefore inhibition of Preimplantation Protein 3 (PREI3, Accession XM_038960). Accordingly, utilities of VGAM1990 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PREI3. Ubiquitin Specific Protease 25

(USP25, Accession NM_013396) is another VGAM1990 host target gene. USP25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP25 BINDING SITE, designated SEQ ID:15046, to the nucleotide sequence of VGAM1990 RNA, herein designated VGAM RNA, also designated SEQ ID:4701.

[70135] Another function of VGAM1990 is therefore inhibition of Ubiquitin Specific Protease 25 (USP25, Accession NM_013396). Accordingly, utilities of VGAM1990 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP25. LOC146092 (Accession XM_096927) is another VGAM1990 host target gene. LOC146092 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146092 BINDING SITE, designated SEQ ID:40652, to the nucleotide sequence of

VGAM1990 RNA, herein designated VGAM RNA, also designated SEQ ID:4701.

[70136] Another function of VGAM1990 is therefore inhibition of LOC146092 (Accession XM_096927). Accordingly, utilities of VGAM1990 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146092. LOC92181 (Accession XM_043394) is another VGAM1990 host target gene. LOC92181 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92181, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92181 BINDING SITE, designated SEQ ID:33941, to the nucleotide sequence of VGAM1990 RNA, herein designated VGAM RNA, also designated SEQ ID:4701.

[70137] Another function of VGAM1990 is therefore inhibition of LOC92181 (Accession XM_043394). Accordingly, utilities of VGAM1990 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92181. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 1991 (VGAM1991) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70138] VGAM1991 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1991 was detected is described hereinabove with reference to Figs. 1-8.

[70139] VGAM1991 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah Virus. VGAM1991 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70140] VGAM1991 gene encodes a VGAM1991 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1991 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1991 precursor RNA is designated SEQ ID:1977, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1977 is located at position 2776 relative to the genome of Nipah Virus.

[70141] VGAM1991 precursor RNA folds onto itself, forming

VGAM1991 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70142] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1991 folded precursor RNA into VGAM1991 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1991 RNA is designated SEQ ID:4702, and is provided hereinbelow with reference to the sequence listing part.

[70143] VGAM1991 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1991 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1991 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70144] VGAM1991 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1991 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1991 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1991 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1991 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70145] The complementary binding of VGAM1991 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1991 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1991 host target RNA into VGAM1991 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70146] It is appreciated that VGAM1991 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1991 host target genes. The mRNA of each one of this plurality of VGAM1991 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1991 RNA, herein designated VGAM RNA, and which when bound by VGAM1991 RNA causes inhibition of translation of respective one or more VGAM1991 host target proteins.

[70147] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM1991 gene, herein designated VGAM GENE, on one or more VGAM1991 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70148] It is yet further appreciated that a function of VGAM1991 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM1991 correlate with, and may be deduced from, the identity of the host target genes which VGAM1991 binds and inhibits, and the

function of these host target genes, as elaborated herein-below.

[70149] Nucleotide sequences of the VGAM1991 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1991 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1991 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1991 are further described hereinbelow with reference to Table 1.

[70150] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1991 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1991 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70151] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1991 gene, herein designated VGAM is inhibition of expression of VGAM1991 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1991 correlate with, and may be deduced from, the identity of the target genes which VGAM1991 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[70152] Methyltransferase-like 1 (METTL1, Accession NM_023032) is a VGAM1991 host target gene. METTL1 BINDING SITE1 and METTL1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by METTL1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of METTL1 BINDING SITE1 and METTL1 BINDING SITE2, designated SEQ ID:23306 and SEQ ID:23311 respectively, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70153] A function of VGAM1991 is therefore inhibition of Methyltransferase-like 1 (METTL1, Accession NM_023032). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with METTL1. Solute Carrier Family 21 (organic anion transporter), Member 3 (SLC21A3, Accession NM_134431) is another VGAM1991 host target gene. SLC21A3 BINDING SITE1 and SLC21A3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SLC21A3, corresponding to HOST

TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC21A3 BINDING SITE1 and SLC21A3 BINDING SITE2, designated SEQ ID:28673 and SEQ ID:18250 respectively, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70154] Another function of VGAM1991 is therefore inhibition of Solute Carrier Family 21 (organic anion transporter), Member 3 (SLC21A3, Accession NM_134431), a gene which mediates the na(+)-independent transport of organic anions such as bsp and conjugated (taurocholate) and unconjugated (cholate) bile acids. Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC21A3. The function of SLC21A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1965.Chromosome 5 Open Reading Frame 4 (C5orf4, Accession NM_032385) is another VGAM1991 host target gene. C5orf4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C5orf4, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5orf4 BINDING SITE, designated SEQ ID:26181, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70155] Another function of VGAM1991 is therefore inhibition of Chromosome 5 Open Reading Frame 4 (C5orf4, Accession NM_032385). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf4. DJ122O8.2 (Accession NM_020466) is another VGAM1991 host target gene. DJ122O8.2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DJ122O8.2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DJ122O8.2 BINDING SITE, designated SEQ ID:21702, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70156] Another function of VGAM1991 is therefore inhibition of DJ122O8.2 (Accession NM_020466). Accordingly, utilities

of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DJ122O8.2. DKFZp547I224 (Accession NM_020221) is another VGAM1991 host target gene. DKFZp547I224 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp547I224, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547I224 BINDING SITE, designated SEQ ID:21479, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70157] Another function of VGAM1991 is therefore inhibition of DKFZp547I224 (Accession NM_020221). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547I224. FLJ10759 (Accession NM_018207) is another VGAM1991 host target gene. FLJ10759 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10759, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of FLJ10759 BINDING SITE, designated SEQ ID:20100, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70158] Another function of VGAM1991 is therefore inhibition of FLJ10759 (Accession NM_018207). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10759. FLJ21432 (Accession NM_024551) is another VGAM1991 host target gene. FLJ21432 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21432, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21432 BINDING SITE, designated SEQ ID:23764, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70159] Another function of VGAM1991 is therefore inhibition of FLJ21432 (Accession NM_024551). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21432. KIAA1034 (Accession XM_031223) is another

VGAM1991 host target gene. KIAA1034 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1034 BINDING SITE, designated SEQ ID:31311, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70160] Another function of VGAM1991 is therefore inhibition of KIAA1034 (Accession XM_031223). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1034. MGC3020 (Accession NM_024048) is another VGAM1991 host target gene. MGC3020 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC3020, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC3020 BINDING SITE, designated SEQ ID:23481, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70161] Another function of VGAM1991 is therefore inhibition of MGC3020 (Accession NM_024048). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3020. PRO2435 (Accession NM_018527) is another VGAM1991 host target gene. PRO2435 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2435 BINDING SITE, designated SEQ ID:20599, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70162] Another function of VGAM1991 is therefore inhibition of PRO2435 (Accession NM_018527). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2435. LOC143310 (Accession XM_084485) is another VGAM1991 host target gene. LOC143310 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143310, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143310 BINDING SITE, designated SEQ ID:37604, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70163] Another function of VGAM1991 is therefore inhibition of LOC143310 (Accession XM_084485). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143310. LOC143465 (Accession XM_096430) is another VGAM1991 host target gene. LOC143465 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143465, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143465 BINDING SITE, designated SEQ ID:40360, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70164] Another function of VGAM1991 is therefore inhibition of LOC143465 (Accession XM_096430). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC143465. LOC154877 (Accession XM_098626) is another VGAM1991 host target gene. LOC154877 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154877, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE, designated SEQ ID:41738, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70165] Another function of VGAM1991 is therefore inhibition of LOC154877 (Accession XM_098626). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154877. LOC196527 (Accession XM_113743) is another VGAM1991 host target gene. LOC196527 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196527, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196527 BINDING SITE, designated SEQ ID:42398, to the nucleotide sequence of VGAM1991 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4702.

[70166] Another function of VGAM1991 is therefore inhibition of LOC196527 (Accession XM_113743). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196527. LOC221738 (Accession XM_168097) is another VGAM1991 host target gene. LOC221738 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221738, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221738 BINDING SITE, designated SEQ ID:45026, to the nucleotide sequence of VGAM1991 RNA, herein designated VGAM RNA, also designated SEQ ID:4702.

[70167] Another function of VGAM1991 is therefore inhibition of LOC221738 (Accession XM_168097). Accordingly, utilities of VGAM1991 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221738. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1992 (VGAM1992) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70168] VGAM1992 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1992 was detected is described hereinabove with reference to Figs. 1-8.

[70169] VGAM1992 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah Virus. VGAM1992 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70170] VGAM1992 gene encodes a VGAM1992 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1992 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1992 precursor RNA is designated SEQ ID:1978, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1978 is located at position 12009 relative to the genome of Nipah Virus.

[70171] VGAM1992 precursor RNA folds onto itself, forming VGAM1992 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70172] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1992 folded precursor RNA into VGAM1992 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM1992 RNA is designated SEQ ID:4703, and is provided hereinbelow with reference to the sequence listing part.

[70173] VGAM1992 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1992 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1992 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70174] VGAM1992 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1992 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1992 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1992 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1992 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70175] The complementary binding of VGAM1992 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1992 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1992 host target RNA into VGAM1992 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70176] It is appreciated that VGAM1992 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1992 host target genes. The mRNA of each one of this plurality of VGAM1992 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1992 RNA, herein designated VGAM RNA, and which when bound by VGAM1992 RNA causes inhibition of translation of respective one or more VGAM1992 host target proteins.

[70177] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM1992 gene, herein designated VGAM GENE, on one or more VGAM1992 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70178] It is yet further appreciated that a function of VGAM1992 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1992 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM1992 correlate with, and may be deduced from, the identity of the host target genes which VGAM1992 binds and inhibits, and the function of these host target genes, as elaborated herein-

below.

[70179] Nucleotide sequences of the VGAM1992 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1992 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1992 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1992 are further described hereinbelow with reference to Table 1.

[70180] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1992 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1992 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70181] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1992 gene, herein designated VGAM is inhibition of expression of VGAM1992 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1992 correlate with, and may be deduced from, the identity of the target genes which VGAM1992 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70182] Transcription Elongation Factor A (SII), 1 (TCEA1, Accession XM_087370) is a VGAM1992 host target gene. TCEA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCEA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCEA1 BINDING SITE, designated SEQ ID:39201, to the nucleotide sequence of VGAM1992 RNA, herein designated VGAM RNA, also designated SEQ ID:4703.

[70183] A function of VGAM1992 is therefore inhibition of Transcription Elongation Factor A (SII), 1 (TCEA1, Accession XM_087370), a gene which helps RNA polymerase II to transcribe past blockages. Accordingly, utilities of VGAM1992 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCEA1. The function of TCEA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM211.LOC203084 (Accession XM_113540) is another VGAM1992 host target gene. LOC203084 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203084, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203084 BINDING SITE, designated SEQ ID:42279, to the nucleotide sequence of VGAM1992 RNA, herein designated VGAM RNA, also designated SEQ ID:4703.

[70184] Another function of VGAM1992 is therefore inhibition of LOC203084 (Accession XM_113540). Accordingly, utilities of VGAM1992 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203084. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1993 (VGAM1993) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70185] VGAM1993 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1993 was detected is described hereinabove with reference to Figs. 1-8.

[70186] VGAM1993 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah Virus. VGAM1993

host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70187] VGAM1993 gene encodes a VGAM1993 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1993 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1993 precursor RNA is designated SEQ ID:1979, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1979 is located at position 17946 relative to the genome of Nipah Virus.

[70188] VGAM1993 precursor RNA folds onto itself, forming VGAM1993 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70189] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1993 folded precursor RNA into VGAM1993

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM1993 RNA is designated SEQ ID:4704, and is provided hereinbelow with reference to the sequence listing part.

[70190] VGAM1993 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1993 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1993 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70191] VGAM1993 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1993 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1993 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1993 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1993 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70192] The complementary binding of VGAM1993 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1993 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1993 host target RNA into VGAM1993 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[70193] It is appreciated that VGAM1993 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1993 host target genes. The mRNA of each one of this plurality of VGAM1993 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1993 RNA, herein designated VGAM RNA, and which when bound by VGAM1993 RNA causes inhibition of translation of respective one or more VGAM1993 host target proteins.

[70194] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1993 gene, herein designated VGAM GENE, on one or more VGAM1993 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70195] It is yet further appreciated that a function of VGAM1993 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1993 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM1993 correlate with, and may be deduced from, the identity of the host target genes which VGAM1993 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70196] Nucleotide sequences of the VGAM1993 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1993 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1993 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1993 are further described hereinbelow with reference to Table 1.

[70197] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1993 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1993 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70198] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1993 gene, herein designated VGAM is inhibition of expression of VGAM1993 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1993 correlate with, and may be deduced from, the identity of the target genes which VGAM1993 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70199] ZNF333 (Accession NM_032433) is a VGAM1993 host target gene. ZNF333 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF333 BINDING SITE, designated SEQ ID:26202, to the nucleotide sequence of VGAM1993 RNA, herein designated VGAM RNA, also designated SEQ

ID:4704.

[70200] A function of VGAM1993 is therefore inhibition of ZNF333 (Accession NM_032433). Accordingly, utilities of VGAM1993 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF333. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1994 (VGAM1994) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70201] VGAM1994 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1994 was detected is described hereinabove with reference to Figs. 1-8.

[70202] VGAM1994 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah Virus. VGAM1994 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70203] VGAM1994 gene encodes a VGAM1994 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM1994 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1994 precursor RNA is designated SEQ ID:1980, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1980 is located at position 17237 relative to the genome of Nipah Virus.

[70204] VGAM1994 precursor RNA folds onto itself, forming VGAM1994 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70205] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1994 folded precursor RNA into VGAM1994 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 67%) nucleotide sequence of VGAM1994 RNA is designated SEQ ID:4705, and is provided hereinbelow with reference to the sequence listing part.

[70206] VGAM1994 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1994 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1994 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70207] VGAM1994 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1994 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1994 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1994 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1994 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70208] The complementary binding of VGAM1994 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1994 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1994 host target RNA into VGAM1994 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70209] It is appreciated that VGAM1994 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1994 host target genes. The mRNA of each one of this plurality of VGAM1994 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1994 RNA, herein designated VGAM RNA, and which when bound by VGAM1994 RNA causes inhibition of translation of respective one or more VGAM1994 host target proteins.

[70210] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1994 gene, herein designated VGAM GENE, on one or more VGAM1994 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70211] It is yet further appreciated that a function of VGAM1994 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1994 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM1994 correlate with, and may be deduced from, the identity of the host target genes which VGAM1994 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70212] Nucleotide sequences of the VGAM1994 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1994 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1994 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1994 are further described hereinbelow with reference to Table 1.

[70213] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1994 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1994 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[70214] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1994 gene, herein designated VGAM is inhibition of expression of VGAM1994 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1994 correlate with, and may be deduced from, the identity of the target genes which VGAM1994 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70215] Heat Shock 70kDa Protein 5 (glucose-regulated protein, 78kDa) (HSPA5, Accession NM_005347) is a VGAM1994 host target gene. HSPA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSPA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPA5 BINDING SITE, designated SEQ ID:11821, to the nucleotide sequence of VGAM1994 RNA, herein designated VGAM RNA, also designated SEQ ID:4705.

[70216] A function of VGAM1994 is therefore inhibition of Heat Shock 70kDa Protein 5 (glucose-regulated protein, 78kDa) (HSPA5, Accession NM_005347), a gene which is involved

in the folding and assembly of proteins in the endoplasmic reticulum (ER). Accordingly, utilities of VGAM1994 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPA5. The function of HSPA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1782.Calsenilin, Presenilin Binding Protein, EF Hand Transcription Factor (CSEN, Accession NM_013434) is another VGAM1994 host target gene. CSEN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSEN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSEN BINDING SITE, designated SEQ ID:15092, to the nucleotide sequence of VGAM1994 RNA, herein designated VGAM RNA, also designated SEQ ID:4705.

[70217] Another function of VGAM1994 is therefore inhibition of Calsenilin, Presenilin Binding Protein, EF Hand Transcription Factor (CSEN, Accession NM_013434). Accordingly, utilities of VGAM1994 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with CSEN. KIAA1509 (Accession XM_029353) is another VGAM1994 host target gene. KIAA1509 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1509, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1509 BINDING SITE, designated SEQ ID:30872, to the nucleotide sequence of VGAM1994 RNA, herein designated VGAM RNA, also designated SEQ ID:4705.

[70218] Another function of VGAM1994 is therefore inhibition of KIAA1509 (Accession XM_029353). Accordingly, utilities of VGAM1994 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1509. LOC148760 (Accession XM_097514) is another VGAM1994 host target gene. LOC148760 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148760, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148760 BINDING SITE, designated SEQ ID:40897, to the nucleotide sequence of VGAM1994 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4705.

[70219] Another function of VGAM1994 is therefore inhibition of LOC148760 (Accession XM_097514). Accordingly, utilities of VGAM1994 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148760. LOC168667 (Accession XM_166592) is another VGAM1994 host target gene. LOC168667 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC168667, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC168667 BINDING SITE, designated SEQ ID:44566, to the nucleotide sequence of VGAM1994 RNA, herein designated VGAM RNA, also designated SEQ ID:4705.

[70220] Another function of VGAM1994 is therefore inhibition of LOC168667 (Accession XM_166592). Accordingly, utilities of VGAM1994 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168667. LOC253842 (Accession XM_173230) is another VGAM1994 host target gene. LOC253842 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253842, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253842 BINDING SITE, designated SEQ ID:46503, to the nucleotide sequence of VGAM1994 RNA, herein designated VGAM RNA, also designated SEQ ID:4705.

[70221] Another function of VGAM1994 is therefore inhibition of LOC253842 (Accession XM_173230). Accordingly, utilities of VGAM1994 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253842. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1995 (VGAM1995) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70222] VGAM1995 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1995 was detected is described hereinabove with reference to Figs. 1-8.

[70223] VGAM1995 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah Virus. VGAM1995

host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70224] VGAM1995 gene encodes a VGAM1995 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1995 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1995 precursor RNA is designated SEQ ID:1981, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1981 is located at position 9693 relative to the genome of Nipah Virus.

[70225] VGAM1995 precursor RNA folds onto itself, forming VGAM1995 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70226] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1995 folded precursor RNA into VGAM1995

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1995 RNA is designated SEQ ID:4706, and is provided hereinbelow with reference to the sequence listing part.

[70227] VGAM1995 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1995 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1995 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70228] VGAM1995 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1995 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1995 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1995 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1995 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70229] The complementary binding of VGAM1995 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1995 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1995 host target RNA into VGAM1995 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[70230] It is appreciated that VGAM1995 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1995 host target genes. The mRNA of each one of this plurality of VGAM1995 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1995 RNA, herein designated VGAM RNA, and which when bound by VGAM1995 RNA causes inhibition of translation of respective one or more VGAM1995 host target proteins.

[70231] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1995 gene, herein designated VGAM GENE, on one or more VGAM1995 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70232] It is yet further appreciated that a function of VGAM1995 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM1995 correlate with, and may be deduced from, the identity of the host target genes which VGAM1995 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70233] Nucleotide sequences of the VGAM1995 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1995 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1995 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1995 are further described hereinbelow with reference to Table 1.

[70234] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1995 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1995 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70235] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1995 gene, herein designated VGAM is inhibition of expression of VGAM1995 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1995 correlate with, and may be deduced from, the identity of the target genes which VGAM1995 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70236] Ankyrin 1, Erythrocytic (ANK1, Accession XM_016774) is a VGAM1995 host target gene. ANK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANK1 BINDING SITE, designated SEQ ID:30279, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4706.

[70237] A function of VGAM1995 is therefore inhibition of Ankyrin 1, Erythrocytic (ANK1, Accession XM_016774). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANK1. APM1 (Accession NM_004797) is another VGAM1995 host target gene. APM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APM1 BINDING SITE, designated SEQ ID:11211, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70238] Another function of VGAM1995 is therefore inhibition of APM1 (Accession NM_004797). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APM1. Collagen, Type I, Alpha 2 (COL1A2, Accession NM_000089) is another VGAM1995 host target gene. COL1A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

COL1A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL1A2 BINDING SITE, designated SEQ ID:5541, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70239] Another function of VGAM1995 is therefore inhibition of Collagen, Type I, Alpha 2 (COL1A2, Accession NM_000089). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL1A2. Coagulation Factor VII (serum prothrombin conversion accelerator) (F7, Accession NM_000131) is another VGAM1995 host target gene. F7 BINDING SITE1 and F7 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by F7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of F7 BINDING SITE1 and F7 BINDING SITE2, designated SEQ ID:5607 and SEQ ID:21236 respectively, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ

ID:4706.

[70240] Another function of VGAM1995 is therefore inhibition of Coagulation Factor VII (serum prothrombin conversion accelerator) (F7, Accession NM_000131). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F7. Potassium Inwardly-rectifying Channel, Subfamily J, Member 8 (KCNJ8, Accession NM_004982) is another VGAM1995 host target gene. KCNJ8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCNJ8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNJ8 BINDING SITE, designated SEQ ID:11429, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70241] Another function of VGAM1995 is therefore inhibition of Potassium Inwardly-rectifying Channel, Subfamily J, Member 8 (KCNJ8, Accession NM_004982), a gene which is a potassium inwardly-rectifying channel. Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with KCNJ8. The function of KCNJ8 has been established by previous studies. Inagaki et al. (1995) isolated a cDNA from a rat pancreatic islet cell library that encodes a member of the inward rectifier potassium channel family. The predicted 424-amino acid protein, which they designated uKATP-1, has 2 transmembrane domains and shares 43 to 46% identity with other inward rectifier potassium channels, including ROMK1 (OMIM Ref. No. 600359), IRK1 (OMIM Ref. No. 600681), GIRK1 (OMIM Ref. No. 601534), and cKATP-1 (OMIM Ref. No. 600734). When the protein was expressed in Xenopus oocytes, a weak rectifier activity was demonstrated that was blocked with Ba(+2) and activated by diazoxide. Northern blots showed that the mRNA is widely expressed in various tissues of the rat. Inagaki et al. (1995) cloned the human gene, designated KCNJ8. The predicted human protein is 98% identical to that of the rat. Animal model experiments lend further support to the function of KCNJ8. ANIMAL MODEL Miki et al. (2002) found that mice lacking the Kir6.1 gene had a high rate of sudden death associated with spontaneous ST elevation followed by atrioventricular block, as seen on the electrocardiogram. The potassium channel opener pinacidil did not induce potassium channels in

vascular smooth muscle cells of Kir6.1 null mice, and there was no vasodilation response to pinacidil. Administration of methylergometrine, a vasoconstrictive agent, elicited ST elevation followed by cardiac death in Kir6.1 null mice but not in wildtype mice, indicating a phenotype characterized by hypercontractility of coronary arteries and resembling Prinzmetal (or variant) angina in humans (Prinzmetal et al., 1959). Prinzmetal angina occurs exclusively at rest and is associated with elevation of ST segments on EKG during the attack. Although the attack disappears spontaneously in most cases, it can lead to myocardial infarction, severe AV block, life-threatening ventricular tachycardia, and sudden death if the coronary vasospasm is prolonged (MacAlpin, 1993). The elevated ST segments on EKG during the attack are diagnostic, as is induction of coronary spasm by ergot alkaloids or acetylcholine. Vasospastic angina is more common in Japanese than in Caucasians (Beltrame et al., 1999; Pristipino et al., 2000). Miki et al. (2002) concluded that the Kir6.1-containing potassium channel is critical in the regulation of vascular tone, especially in the coronary arteries, and its disruption may cause Prinzmetal angina. They suggested that it will be important to learn whether ge-

netic differences in the KIR6.1 gene are associated with Prinzmetal angina in various populations

[70242] It is appreciated that the abovementioned animal model for KCNJ8 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[70243] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[70244] Miki, T.; Suzuki, M.; Shibasaki, T.; Uemura, H.; Sato, T.; Yamaguchi, K.; Koseki, H.; Iwanaga, T.; Nakaya, H.; Seino, S. : Mouse model of Prinzmetal angina by disruption of the inward rectifier Kir6.1. Nature Med. 8: 466-472, 2002. ; and

[70245] Inagaki, N.; Inazawa, J.; Seino, S. : cDNA sequence, gene structure, and chromosomal localization of the human ATP-sensitive potassium channel, uK(ATP)-1, gene (KCNJ8). Genomics 30: 102.

[70246] Further studies establishing the function and utilities of KCNJ8 are found in John Hopkins OMIM database record ID 600935, and in sited publications numbered 6865-686 and 7024-7026 listed in the bibliography section hereinbelow, which are also hereby incorporated by refer-

ence.5'-nucleotidase, Cytosolic II (NT5C2, Accession NM_012229) is another VGAM1995 host target gene. NT5C2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NT5C2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NT5C2 BINDING SITE, designated SEQ ID:14525, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70247] Another function of VGAM1995 is therefore inhibition of 5'-nucleotidase, Cytosolic II (NT5C2, Accession NM_012229). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NT5C2.

p21(CDKN1A)-activated Kinase 4 (PAK4, Accession NM_005884) is another VGAM1995 host target gene. PAK4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAK4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of PAK4 BINDING SITE, designated SEQ ID:12507, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70248] Another function of VGAM1995 is therefore inhibition of p21(CDKN1A)-activated Kinase 4 (PAK4, Accession NM_005884). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAK4. Pumilio Homolog 2 (Drosophila) (PUM2, Accession NM_015317) is another VGAM1995 host target gene. PUM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PUM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PUM2 BINDING SITE, designated SEQ ID:17633, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70249] Another function of VGAM1995 is therefore inhibition of Pumilio Homolog 2 (Drosophila) (PUM2, Accession NM_015317). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PUM2. Retinaldehyde Bind-

ing Protein 1 (RLBP1, Accession NM_000326) is another VGAM1995 host target gene. RLBP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RLBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RLBP1 BINDING SITE, designated SEQ ID:5869, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70250] Another function of VGAM1995 is therefore inhibition of Retinaldehyde Binding Protein 1 (RLBP1, Accession NM_000326). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RLBP1. TIC (Accession NM_012455) is another VGAM1995 host target gene. TIC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIC BINDING SITE, designated SEQ ID:14828, to the nucleotide sequence of VGAM1995 RNA, herein designated

VGAM RNA, also designated SEQ ID:4706.

[70251] Another function of VGAM1995 is therefore inhibition of TIC (Accession NM_012455). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIC. Ubiquitin Specific Protease 9, Y Chromosome (fat facets-like Drosophila) (USP9Y, Accession XM_034147) is another VGAM1995 host target gene. USP9Y BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by USP9Y, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP9Y BINDING SITE, designated SEQ ID:32017, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70252] Another function of VGAM1995 is therefore inhibition of Ubiquitin Specific Protease 9, Y Chromosome (fat facets-like Drosophila) (USP9Y, Accession XM_034147), a gene which removes ubiquitin from ubiquitin-conjugated proteins and has a role in spermatogenesis. Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with USP9Y. The function of USP9Y and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM894.Chromosome 20 Open Reading Frame 54 (C20orf54, Accession NM_033409) is another VGAM1995 host target gene. C20orf54 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf54, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf54 BINDING SITE, designated SEQ ID:27229, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70253] Another function of VGAM1995 is therefore inhibition of Chromosome 20 Open Reading Frame 54 (C20orf54, Accession NM_033409). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf54. CDT1 (Accession XM_085327) is another VGAM1995 host target gene. CDT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDT1, corresponding to a HOST TARGET binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDT1 BINDING SITE, designated SEQ ID:38069, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70254] Another function of VGAM1995 is therefore inhibition of CDT1 (Accession XM_085327). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDT1. Cytosolic Ovarian Carcinoma Antigen 1 (COVA1, Accession XM_055323) is another VGAM1995 host target gene. COVA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COVA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COVA1 BINDING SITE, designated SEQ ID:36266, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70255] Another function of VGAM1995 is therefore inhibition of Cytosolic Ovarian Carcinoma Antigen 1 (COVA1, Accession XM_055323). Accordingly, utilities of VGAM1995 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with COVA1. CSR1 (Accession NM_016240) is another VGAM1995 host target gene. CSR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSR1 BINDING SITE, designated SEQ ID:18361, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70256] Another function of VGAM1995 is therefore inhibition of CSR1 (Accession NM_016240). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSR1. Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_013989) is another VGAM1995 host target gene. DIO2 BINDING SITE1 and DIO2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DIO2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DIO2 BINDING SITE1 and

DIO2 BINDING SITE2, designated SEQ ID:15164 and SEQ ID:6454 respectively, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70257] Another function of VGAM1995 is therefore inhibition of Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_013989). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIO2. Docking Protein 4 (DOK4, Accession NM_018110) is another VGAM1995 host target gene. DOK4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DOK4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DOK4 BINDING SITE, designated SEQ ID:19883, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70258] Another function of VGAM1995 is therefore inhibition of Docking Protein 4 (DOK4, Accession NM_018110). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with DOK4. FLJ10079 (Accession XM_012540) is another VGAM1995 host target gene. FLJ10079 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10079, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10079 BINDING SITE, designated SEQ ID:30215, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70259] Another function of VGAM1995 is therefore inhibition of FLJ10079 (Accession XM_012540). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10079. FLJ10300 (Accession NM_018051) is another VGAM1995 host target gene. FLJ10300 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10300, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10300 BINDING SITE, designated SEQ ID:19810, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM

RNA, also designated SEQ ID:4706.

[70260] Another function of VGAM1995 is therefore inhibition of FLJ10300 (Accession NM_018051). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10300. FLJ10904 (Accession NM_018268) is another VGAM1995 host target gene. FLJ10904 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10904, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10904 BINDING SITE, designated SEQ ID:20240, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70261] Another function of VGAM1995 is therefore inhibition of FLJ10904 (Accession NM_018268). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10904. FLJ10986 (Accession NM_018291) is another VGAM1995 host target gene. FLJ10986 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10986, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10986 BINDING SITE, designated SEQ ID:20281, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70262] Another function of VGAM1995 is therefore inhibition of FLJ10986 (Accession NM_018291). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10986. FLJ12969 (Accession NM_022838) is another VGAM1995 host target gene. FLJ12969 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12969, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12969 BINDING SITE, designated SEQ ID:23125, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70263] Another function of VGAM1995 is therefore inhibition of FLJ12969 (Accession NM_022838). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12969. FLJ32356 (Accession NM_144671) is another VGAM1995 host target gene. FLJ32356 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ32356, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32356 BINDING SITE, designated SEQ ID:29493, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70264] Another function of VGAM1995 is therefore inhibition of FLJ32356 (Accession NM_144671). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32356. Integrin, Alpha 10 (ITGA10, Accession XM_002097) is another VGAM1995 host target gene. ITGA10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ITGA10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA10 BINDING SITE, designated SEQ

ID:29864, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70265] Another function of VGAM1995 is therefore inhibition of Integrin, Alpha 10 (ITGA10, Accession XM_002097). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA10. KIAA0318 (Accession XM_044334) is another VGAM1995 host target gene. KIAA0318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0318 BINDING SITE, designated SEQ ID:34189, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70266] Another function of VGAM1995 is therefore inhibition of KIAA0318 (Accession XM_044334). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0318. KIAA0416 (Accession NM_015564) is another

VGAM1995 host target gene. KIAA0416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0416 BINDING SITE, designated SEQ ID:17830, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70267] Another function of VGAM1995 is therefore inhibition of KIAA0416 (Accession NM_015564). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0416. KIAA0426 (Accession NM_014724) is another VGAM1995 host target gene. KIAA0426 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0426 BINDING SITE, designated SEQ ID:16314, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70268] Another function of VGAM1995 is therefore inhibition of KIAA0426 (Accession NM_014724). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0426. KIAA0459 (Accession XM_027862) is another VGAM1995 host target gene. KIAA0459 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:30581, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70269] Another function of VGAM1995 is therefore inhibition of KIAA0459 (Accession XM_027862). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459. KIAA0711 (Accession NM_014867) is another VGAM1995 host target gene. KIAA0711 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0711, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0711 BINDING SITE, designated SEQ ID:16960, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70270] Another function of VGAM1995 is therefore inhibition of KIAA0711 (Accession NM_014867). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0711. KIAA1199 (Accession XM_051860) is another VGAM1995 host target gene. KIAA1199 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1199, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1199 BINDING SITE, designated SEQ ID:35901, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70271] Another function of VGAM1995 is therefore inhibition of KIAA1199 (Accession XM_051860). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1199. KIAA1950 (Accession XM_166532) is another VGAM1995 host target gene. KIAA1950 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1950, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1950 BINDING SITE, designated SEQ ID:44489, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70272] Another function of VGAM1995 is therefore inhibition of KIAA1950 (Accession XM_166532). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1950. LSR7 (Accession NM_018559) is another VGAM1995 host target gene. LSR7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LSR7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LSR7 BINDING SITE, designated SEQ ID:20642, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4706.

[70273] Another function of VGAM1995 is therefore inhibition of LSR7 (Accession NM_018559). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LSR7. Mitogen-activated Protein Kinase 8 Interacting Protein 3 (MAPK8IP3, Accession NM_033392) is another VGAM1995 host target gene. MAPK8IP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAPK8IP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPK8IP3 BINDING SITE, designated SEQ ID:27221, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70274] Another function of VGAM1995 is therefore inhibition of Mitogen-activated Protein Kinase 8 Interacting Protein 3 (MAPK8IP3, Accession NM_033392). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK8IP3. Phosphodiesterase 8A (PDE8A, Accession XM_031443) is another VGAM1995 host target gene.

PDE8A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE8A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE8A BINDING SITE, designated SEQ ID:31380, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70275] Another function of VGAM1995 is therefore inhibition of Phosphodiesterase 8A (PDE8A, Accession XM_031443). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE8A. PDZ Domain Containing 2 (PDZD2, Accession XM_087705) is another VGAM1995 host target gene. PDZD2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PDZD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDZD2 BINDING SITE, designated SEQ ID:39393, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4706.

[70276] Another function of VGAM1995 is therefore inhibition of PDZ Domain Containing 2 (PDZD2, Accession XM_087705). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDZD2. Paternally Expressed 10 (PEG10, Accession NM_015068) is another VGAM1995 host target gene. PEG10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PEG10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEG10 BINDING SITE, designated SEQ ID:17433, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70277] Another function of VGAM1995 is therefore inhibition of Paternally Expressed 10 (PEG10, Accession NM_015068). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEG10. PRO0233 (Accession NM_014121) is another VGAM1995 host target gene. PRO0233 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by PRO0233, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0233 BINDING SITE, designated SEQ ID:15374, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70278] Another function of VGAM1995 is therefore inhibition of PRO0233 (Accession NM_014121). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0233. SEC24 Related Gene Family, Member C (S. cerevisiae) (SEC24C, Accession NM_004922) is another VGAM1995 host target gene. SEC24C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC24C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC24C BINDING SITE, designated SEQ ID:11357, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70279] Another function of VGAM1995 is therefore inhibition of SEC24 Related Gene Family, Member C (S. cerevisiae) (SEC24C, Accession NM_004922). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC24C. SMC1 Structural Maintenance of Chromosomes 1-like 1 (yeast) (SMC1L1, Accession XM_050403) is another VGAM1995 host target gene. SMC1L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMC1L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMC1L1 BINDING SITE, designated SEQ ID:35620, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70280] Another function of VGAM1995 is therefore inhibition of SMC1 Structural Maintenance of Chromosomes 1-like 1 (yeast) (SMC1L1, Accession XM_050403). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMC1L1. Ubiquitin Specific Protease 24 (USP24, Accession XM_165973) is another VGAM1995 host target

gene. USP24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP24 BINDING SITE, designated SEQ ID:43813, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70281] Another function of VGAM1995 is therefore inhibition of Ubiquitin Specific Protease 24 (USP24, Accession XM_165973). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP24. WD Repeat Domain 9 (WDR9, Accession NM_018963) is another VGAM1995 host target gene. WDR9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WDR9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WDR9 BINDING SITE, designated SEQ ID:21033, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4706.

[70282] Another function of VGAM1995 is therefore inhibition of WD Repeat Domain 9 (WDR9, Accession NM_018963). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WDR9. LOC124470 (Accession XM_064152) is another VGAM1995 host target gene. LOC124470 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC124470, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124470 BINDING SITE, designated SEQ ID:37256, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70283] Another function of VGAM1995 is therefore inhibition of LOC124470 (Accession XM_064152). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124470. LOC146489 (Accession XM_047734) is another VGAM1995 host target gene. LOC146489 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC146489, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146489 BINDING SITE, designated SEQ ID:35038, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70284] Another function of VGAM1995 is therefore inhibition of LOC146489 (Accession XM_047734). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146489. LOC147650 (Accession XM_085824) is another VGAM1995 host target gene. LOC147650 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147650, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147650 BINDING SITE, designated SEQ ID:38348, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70285] Another function of VGAM1995 is therefore inhibition of LOC147650 (Accession XM_085824). Accordingly, utilities

of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147650. LOC162333 (Accession XM_102591) is another VGAM1995 host target gene. LOC162333 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC162333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162333 BINDING SITE, designated SEQ ID:42123, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70286] Another function of VGAM1995 is therefore inhibition of LOC162333 (Accession XM_102591). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162333. LOC167040 (Accession XM_106497) is another VGAM1995 host target gene. LOC167040 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC167040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC167040 BINDING SITE, designated SEQ ID:42201, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70287] Another function of VGAM1995 is therefore inhibition of LOC167040 (Accession XM_106497). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC167040. LOC201283 (Accession XM_017132) is another VGAM1995 host target gene. LOC201283 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201283, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201283 BINDING SITE, designated SEQ ID:30302, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70288] Another function of VGAM1995 is therefore inhibition of LOC201283 (Accession XM_017132). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201283. LOC202460 (Accession XM_114493) is another VGAM1995 host target gene. LOC202460 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202460, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202460 BINDING SITE, designated SEQ ID:42983, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70289] Another function of VGAM1995 is therefore inhibition of LOC202460 (Accession XM_114493). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202460. LOC206327 (Accession XM_121168) is another VGAM1995 host target gene. LOC206327 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC206327, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC206327 BINDING SITE, designated SEQ ID:43613, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70290] Another function of VGAM1995 is therefore inhibition of

LOC206327 (Accession XM_121168). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC206327. LOC221474 (Accession XM_166464) is another VGAM1995 host target gene. LOC221474 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221474, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221474 BINDING SITE, designated SEQ ID:44383, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70291] Another function of VGAM1995 is therefore inhibition of LOC221474 (Accession XM_166464). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221474. LOC51170 (Accession NM_016245) is another VGAM1995 host target gene. LOC51170 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51170, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of LOC51170 BINDING SITE, designated SEQ ID:18363, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70292] Another function of VGAM1995 is therefore inhibition of LOC51170 (Accession NM_016245). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51170. LOC90333 (Accession XM_030958) is another VGAM1995 host target gene. LOC90333 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90333 BINDING SITE, designated SEQ ID:31227, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70293] Another function of VGAM1995 is therefore inhibition of LOC90333 (Accession XM_030958). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90333. LOC92568 (Accession XM_045852) is another

VGAM1995 host target gene. LOC92568 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92568, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92568 BINDING SITE, designated SEQ ID:34574, to the nucleotide sequence of VGAM1995 RNA, herein designated VGAM RNA, also designated SEQ ID:4706.

[70294] Another function of VGAM1995 is therefore inhibition of LOC92568 (Accession XM_045852). Accordingly, utilities of VGAM1995 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92568. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1996 (VGAM1996) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70295] VGAM1996 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1996 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[70296] VGAM1996 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah Virus. VGAM1996 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70297] VGAM1996 gene encodes a VGAM1996 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1996 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1996 precursor RNA is designated SEQ ID:1982, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1982 is located at position 8558 relative to the genome of Nipah Virus.

[70298] VGAM1996 precursor RNA folds onto itself, forming VGAM1996 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[70299] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1996 folded precursor RNA into VGAM1996 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM1996 RNA is designated SEQ ID:4707, and is provided hereinbelow with reference to the sequence listing part.

[70300] VGAM1996 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1996 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1996 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70301] VGAM1996 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1996 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1996 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1996 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1996 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70302] The complementary binding of VGAM1996 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1996 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1996 host target RNA into VGAM1996 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70303] It is appreciated that VGAM1996 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1996 host target genes. The mRNA of each one of this plurality of VGAM1996 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1996 RNA, herein designated VGAM RNA, and which when bound by VGAM1996 RNA causes inhibition of translation of respective one or more VGAM1996 host target proteins.

[70304] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1996 gene, herein designated VGAM GENE, on one or more VGAM1996 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70305] It is yet further appreciated that a function of VGAM1996 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1996 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM1996 correlate with, and may be deduced from, the identity of the host target genes which VGAM1996 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70306] Nucleotide sequences of the VGAM1996 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1996 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1996 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1996 are further described hereinbelow with reference to Table 1.

[70307] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1996 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1996 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70308] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1996 gene, herein designated VGAM is inhibition of expression of VGAM1996 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1996 correlate with, and may be deduced from, the identity of the target genes which VGAM1996 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70309] AXL Receptor Tyrosine Kinase (AXL, Accession NM_001699) is a VGAM1996 host target gene. AXL BINDING SITE1 and AXL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AXL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE1 and AXL BINDING SITE2, designated SEQ ID:7417 and SEQ ID:22438 respectively, to the nucleotide sequence of VGAM1996 RNA, herein designated VGAM RNA, also designated SEQ ID:4707.

[70310] A function of VGAM1996 is therefore inhibition of AXL Receptor Tyrosine Kinase (AXL, Accession NM_001699). Accordingly, utilities of VGAM1996 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL. Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NM_003679) is another VGAM1996 host target gene. KMO BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KMO, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KMO BINDING SITE, designated SEQ ID:9778, to the nucleotide sequence of VGAM1996 RNA, herein designated VGAM RNA, also designated SEQ ID:4707.

[70311] Another function of VGAM1996 is therefore inhibition of Kynurenine 3-monooxygenase (kynurenine 3-hydroxylase) (KMO, Accession NM_003679), a gene

which may play a role in encephalic photoreception. Accordingly, utilities of VGAM1996 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KMO. The function of KMO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM162.G-rich RNA Sequence Binding Factor 1 (GRSF1, Accession NM_002092) is another VGAM1996 host target gene. GRSF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRSF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRSF1 BINDING SITE, designated SEQ ID:7880, to the nucleotide sequence of VGAM1996 RNA, herein designated VGAM RNA, also designated SEQ ID:4707.

[70312] Another function of VGAM1996 is therefore inhibition of G-rich RNA Sequence Binding Factor 1 (GRSF1, Accession NM_002092). Accordingly, utilities of VGAM1996 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRSF1. KIAA1467 (Accession XM_049605) is another VGAM1996 host target

gene. KIAA1467 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1467, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1467 BINDING SITE, designated SEQ ID:35450, to the nucleotide sequence of VGAM1996 RNA, herein designated VGAM RNA, also designated SEQ ID:4707.

[70313] Another function of VGAM1996 is therefore inhibition of KIAA1467 (Accession XM_049605). Accordingly, utilities of VGAM1996 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1467. RYK Receptor-like Tyrosine Kinase (RYK, Accession XM_093692) is another VGAM1996 host target gene. RYK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RYK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RYK BINDING SITE, designated SEQ ID:40202, to the nucleotide sequence of VGAM1996 RNA, herein designated VGAM RNA, also designated SEQ ID:4707.

[70314] Another function of VGAM1996 is therefore inhibition of RYK Receptor-like Tyrosine Kinase (RYK, Accession XM_093692). Accordingly, utilities of VGAM1996 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RYK. Solute Carrier Family 19, Member 3 (SLC19A3, Accession NM_025243) is another VGAM1996 host target gene. SLC19A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC19A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC19A3 BINDING SITE, designated SEQ ID:24925, to the nucleotide sequence of VGAM1996 RNA, herein designated VGAM RNA, also designated SEQ ID:4707.

[70315] Another function of VGAM1996 is therefore inhibition of Solute Carrier Family 19, Member 3 (SLC19A3, Accession NM_025243). Accordingly, utilities of VGAM1996 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC19A3. LOC256277 (Accession XM_170644) is another VGAM1996 host target gene. LOC256277 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded

by LOC256277, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256277 BINDING SITE, designated SEQ ID:45423, to the nucleotide sequence of VGAM1996 RNA, herein designated VGAM RNA, also designated SEQ ID:4707.

[70316] Another function of VGAM1996 is therefore inhibition of LOC256277 (Accession XM_170644). Accordingly, utilities of VGAM1996 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256277. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1997 (VGAM1997) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70317] VGAM1997 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1997 was detected is described hereinabove with reference to Figs. 1-8.

[70318] VGAM1997 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Nipah Virus. VGAM1997 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70319] VGAM1997 gene encodes a VGAM1997 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1997 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1997 precursor RNA is designated SEQ ID:1983, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1983 is located at position 1708 relative to the genome of Nipah Virus.

[70320] VGAM1997 precursor RNA folds onto itself, forming VGAM1997 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70321] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM1997 folded precursor RNA into VGAM1997 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1997 RNA is designated SEQ ID:4708, and is provided hereinbelow with reference to the sequence listing part.

[70322] VGAM1997 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1997 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1997 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70323] VGAM1997 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1997 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1997 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1997 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1997 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70324] The complementary binding of VGAM1997 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1997 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1997 host target RNA into VGAM1997 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70325] It is appreciated that VGAM1997 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1997 host target genes. The mRNA of each one of this plurality of VGAM1997 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1997 RNA, herein designated VGAM RNA, and which when bound by VGAM1997 RNA causes inhibition of translation of respective one or more VGAM1997 host target proteins.

[70326] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1997 gene, herein designated VGAM GENE, on one or more VGAM1997 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70327] It is yet further appreciated that a function of VGAM1997 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1997 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM1997 correlate with, and may be deduced from, the identity of the host target genes which VGAM1997 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70328] Nucleotide sequences of the VGAM1997 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1997 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1997 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1997 are further described hereinbelow with reference to Table 1.

[70329] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1997 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1997 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[70330] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1997 gene, herein designated VGAM is inhibition of expression of VGAM1997 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1997 correlate with, and may be deduced from, the identity of the target genes which VGAM1997 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70331] FLJ14547 (Accession NM_032804) is a VGAM1997 host target gene. FLJ14547 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14547, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14547 BINDING SITE, designated SEQ ID:26562, to the nucleotide sequence of VGAM1997 RNA, herein designated VGAM RNA, also designated SEQ ID:4708.

[70332] A function of VGAM1997 is therefore inhibition of FLJ14547 (Accession NM_032804). Accordingly, utilities of VGAM1997 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ14547. SMBP (Accession XM_050993) is another VGAM1997 host target gene. SMBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMBP BINDING SITE, designated SEQ ID:35705, to the nucleotide sequence of VGAM1997 RNA, herein designated VGAM RNA, also designated SEQ ID:4708.

[70333] Another function of VGAM1997 is therefore inhibition of SMBP (Accession XM_050993). Accordingly, utilities of VGAM1997 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMBP. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1998 (VGAM1998) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70334] VGAM1998 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1998 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[70335] VGAM1998 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah Virus. VGAM1998 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70336] VGAM1998 gene encodes a VGAM1998 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1998 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1998 precursor RNA is designated SEQ ID:1984, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1984 is located at position 15895 relative to the genome of Nipah Virus.

[70337] VGAM1998 precursor RNA folds onto itself, forming VGAM1998 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[70338] An enzyme complex designated DICER COMPLEX, `dices` the VGAM1998 folded precursor RNA into VGAM1998 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM1998 RNA is designated SEQ ID:4709, and is provided hereinbelow with reference to the sequence listing part.

[70339] VGAM1998 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1998 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1998 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70340] VGAM1998 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1998 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM1998 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1998 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1998 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70341] The complementary binding of VGAM1998 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1998 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM1998 host target RNA into VGAM1998 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70342] It is appreciated that VGAM1998 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1998 host target genes. The mRNA of each one of this plurality of VGAM1998 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1998 RNA, herein designated VGAM RNA, and which when bound by VGAM1998 RNA causes inhibition of translation of respective one or more VGAM1998 host target proteins.

[70343] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1998 gene, herein designated VGAM GENE, on one or more VGAM1998 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70344] It is yet further appreciated that a function of VGAM1998 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM1998 correlate with, and may be deduced from, the identity of the host target genes which VGAM1998 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70345] Nucleotide sequences of the VGAM1998 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1998 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1998 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM1998 are further described hereinbelow with reference to Table 1.

[70346] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1998 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1998 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70347] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1998 gene, herein designated VGAM is inhibition of expression of VGAM1998 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1998 correlate with, and may be deduced from, the identity of the target genes which VGAM1998 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70348] Angiopoietin 1 (ANGPT1, Accession NM_139290) is a VGAM1998 host target gene. ANGPT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANGPT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of ANGPT1 BINDING SITE, designated SEQ ID:29291, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70349] A function of VGAM1998 is therefore inhibition of Angiopoietin 1 (ANGPT1, Accession NM_139290), a gene which binds and activates tie2 receptor by inducing its tyrosine phosphorylation. Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANGPT1. The function of ANGPT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM291.B-cell Linker (BLNK, Accession NM_013314) is another VGAM1998 host target gene. BLNK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BLNK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BLNK BINDING SITE, designated SEQ ID:14963, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70350] Another function of VGAM1998 is therefore inhibition of B-cell Linker (BLNK, Accession NM_013314), a gene which is a component of the BCR transducer complex, promotes B-cell development. Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BLNK. The function of BLNK has been established by previous studies. In evaluating patients with absent B cells, Minegishi et al. (1999) identified a male with a homozygous splice defect in the gene encoding the cytoplasmic adaptor protein BLNK (604515.0001). Although this patient had normal numbers of pro-B cells, he had no pre-B cells or mature B cells, indicating that BLNK plays a critical role in orchestrating the pro-B cell to pre-B cell transition. The immune system and overall growth and development were otherwise normal in this patient, suggesting that BLNK function is highly specific. The patient had developed recurrent otitis at 8 months of age; after 2 episodes of pneumonia, he was evaluated for immunodeficiency at 16 months of age. At that time, he had no detectable serum IgG, IgM, or IgA, and he had less than 1% B cells in the peripheral circulation. He was started on gammaglobulin replacement, and between 2 and 20 years of age he did well except for

chronic otitis and sinusitis, hepatitis C acquired from intravenous gammaglobulin, and an episode of protein-losing enteropathy in adolescence. Animal model experiments lend further support to the function of BLNK. Pappu et al. (1999) generated mice deficient in BLNK by targeted disruption. B-cell development in BLNK -/- mice was blocked at the transition from B220+CD43+ progenitor B to B220+CD43- precursor B cells. Only a small percentage of IgM M++, but not mature IgM(lo)IgD(hi), B cells were detected in the periphery. Pappu et al. (1999) concluded that BLNK is an essential component of the B-cell receptor signaling pathways and is required to promote B-cell development.

[70351] It is appreciated that the abovementioned animal model for BLNK is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[70352] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[70353] Minegishi, Y.; Rohrer, J.; Coustan-Smith, E.; Lederman, H. M.; Pappu, R.; Campana, D.; Chan, A. C.; Conley, M. E. : An essential role for BLNK in human B cell development. Sci-

ence 286: 1954-1957, 1999. ; and

[70354] Pappu, R.; Cheng, A. M.; Li, B.; Gong, Q.; Chiu, C.; Griffin, N.; White, M.; Sleckman, B. P.; Chan, A. C. : Requirement for B cell linker protein (BLNK) in B cell development. Science.

[70355] Further studies establishing the function and utilities of BLNK are found in John Hopkins OMIM database record ID 604515, and in sited publications numbered 5446-544 and 4787-4788 listed in the bibliography section herein-below, which are also hereby incorporated by reference.Coagulation Factor VIII, Procoagulant Component (hemophilia A) (F8, Accession NM_000132) is another VGAM1998 host target gene. F8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by F8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of F8 BINDING SITE, designated SEQ ID:5619, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70356] Another function of VGAM1998 is therefore inhibition of Coagulation Factor VIII, Procoagulant Component

(hemophilia A) (F8, Accession NM_000132). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F8. F-box and Leucine-rich Repeat Protein 7 (FBXL7, Accession NM_012304) is another VGAM1998 host target gene. FBXL7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXL7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXL7 BINDING SITE, designated SEQ ID:14673, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70357] Another function of VGAM1998 is therefore inhibition of F-box and Leucine-rich Repeat Protein 7 (FBXL7, Accession NM_012304), a gene which may be involved in in phosphorylation-dependent ubiquitination. Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXL7. The function of FBXL7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to VGAM1924.Leucine-rich Repeat-containing 2 (LRRC2, Accession NM_024512) is another VGAM1998 host target gene. LRRC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LRRC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRRC2 BINDING SITE, designated SEQ ID:23705, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70358] Another function of VGAM1998 is therefore inhibition of Leucine-rich Repeat-containing 2 (LRRC2, Accession NM_024512). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRRC2. Nucleolar Protein 3 (apoptosis repressor with CARD domain) (NOL3, Accession NM_003946) is another VGAM1998 host target gene. NOL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NOL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of NOL3 BINDING SITE, designated SEQ ID:10063, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70359] Another function of VGAM1998 is therefore inhibition of Nucleolar Protein 3 (apoptosis repressor with CARD domain) (NOL3, Accession NM_003946), a gene which inhibits CASP2 and CASP8 and interacts with splicing factors. Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOL3. The function of NOL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM554.Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha-1 antiproteinase, antitrypsin), Member 5 (SERPINA5, Accession NM_000624) is another VGAM1998 host target gene. SERPINA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SERPINA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERPINA5 BINDING SITE, designated SEQ ID:6240, to the nucleotide sequence of VGAM1998 RNA,

herein designated VGAM RNA, also designated SEQ ID:4709.

[70360] Another function of VGAM1998 is therefore inhibition of Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha-1 antiproteinase, antitrypsin), Member 5 (SERPINA5, Accession NM_000624), a gene which inhibits activated protein c as well as plasminogen activators. Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINA5. The function of SERPINA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1233.DKFZP434N178 (Accession XM_050278) is another VGAM1998 host target gene. DKFZP434N178 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434N178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434N178 BINDING SITE, designated SEQ ID:35597, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70361] Another function of VGAM1998 is therefore inhibition of DKFZP434N178 (Accession XM_050278). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434N178. FLJ10458 (Accession NM_018096) is another VGAM1998 host target gene. FLJ10458 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10458, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10458 BINDING SITE, designated SEQ ID:19866, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70362] Another function of VGAM1998 is therefore inhibition of FLJ10458 (Accession NM_018096). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10458. KIAA0326 (Accession XM_034819) is another VGAM1998 host target gene. KIAA0326 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0326, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0326 BINDING SITE, designated SEQ ID:32157, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70363] Another function of VGAM1998 is therefore inhibition of KIAA0326 (Accession XM_034819). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0326. KIAA0420 (Accession XM_032693) is another VGAM1998 host target gene. KIAA0420 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0420, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0420 BINDING SITE, designated SEQ ID:31730, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70364] Another function of VGAM1998 is therefore inhibition of KIAA0420 (Accession XM_032693). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0420. KIAA0494 (Accession NM_014774) is another VGAM1998 host target gene. KIAA0494 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0494, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0494 BINDING SITE, designated SEQ ID:16589, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70365] Another function of VGAM1998 is therefore inhibition of KIAA0494 (Accession NM_014774). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0494. KIAA0552 (Accession NM_014731) is another VGAM1998 host target gene. KIAA0552 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0552, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0552 BINDING SITE, designated SEQ ID:16346, to the nucleotide sequence of VGAM1998 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4709.

[70366] Another function of VGAM1998 is therefore inhibition of KIAA0552 (Accession NM_014731). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0552. KIAA0970 (Accession NM_014923) is another VGAM1998 host target gene. KIAA0970 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0970, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0970 BINDING SITE, designated SEQ ID:17204, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70367] Another function of VGAM1998 is therefore inhibition of KIAA0970 (Accession NM_014923). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0970. LOC145453 (Accession XM_085120) is another VGAM1998 host target gene. LOC145453 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145453, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145453 BINDING SITE, designated SEQ ID:37838, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70368] Another function of VGAM1998 is therefore inhibition of LOC145453 (Accession XM_085120). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145453. LOC155064 (Accession XM_088128) is another VGAM1998 host target gene. LOC155064 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155064, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155064 BINDING SITE, designated SEQ ID:39532, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70369] Another function of VGAM1998 is therefore inhibition of LOC155064 (Accession XM_088128). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC155064. LOC221738 (Accession XM_168097) is another VGAM1998 host target gene. LOC221738 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221738, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221738 BINDING SITE, designated SEQ ID:45030, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70370] Another function of VGAM1998 is therefore inhibition of LOC221738 (Accession XM_168097). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221738. LOC257354 (Accession XM_170810) is another VGAM1998 host target gene. LOC257354 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257354, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257354 BINDING SITE, designated SEQ ID:45583, to

the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70371] Another function of VGAM1998 is therefore inhibition of LOC257354 (Accession XM_170810). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257354. LOC51236 (Accession NM_016458) is another VGAM1998 host target gene. LOC51236 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51236, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51236 BINDING SITE, designated SEQ ID:18574, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70372] Another function of VGAM1998 is therefore inhibition of LOC51236 (Accession NM_016458). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51236. LOC90268 (Accession XM_030424) is another VGAM1998 host target gene. LOC90268 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC90268, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90268 BINDING SITE, designated SEQ ID:31042, to the nucleotide sequence of VGAM1998 RNA, herein designated VGAM RNA, also designated SEQ ID:4709.

[70373] Another function of VGAM1998 is therefore inhibition of LOC90268 (Accession XM_030424). Accordingly, utilities of VGAM1998 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90268. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 1999 (VGAM1999) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70374] VGAM1999 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM1999 was detected is described hereinabove with reference to Figs. 1-8.

[70375] VGAM1999 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Nipah Virus. VGAM1999 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70376] VGAM1999 gene encodes a VGAM1999 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM1999 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM1999 precursor RNA is designated SEQ ID:1985, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1985 is located at position 11709 relative to the genome of Nipah Virus.

[70377] VGAM1999 precursor RNA folds onto itself, forming VGAM1999 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70378] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM1999 folded precursor RNA into VGAM1999 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM1999 RNA is designated SEQ ID:4710, and is provided hereinbelow with reference to the sequence listing part.

[70379] VGAM1999 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM1999 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM1999 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70380] VGAM1999 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM1999 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM1999 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM1999 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM1999 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70381] The complementary binding of VGAM1999 RNA, herein designated VGAM RNA, to host target binding sites on VGAM1999 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM1999 host target RNA into VGAM1999 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70382] It is appreciated that VGAM1999 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM1999 host target genes. The mRNA of each one of this plurality of VGAM1999 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM1999 RNA, herein designated VGAM RNA, and which when bound by VGAM1999 RNA causes inhibition of translation of respective one or more VGAM1999 host target proteins.

[70383] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM1999 gene, herein designated VGAM GENE, on one or more VGAM1999 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70384] It is yet further appreciated that a function of VGAM1999 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM1999 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM1999 correlate with, and may be deduced from, the identity of the host target genes which VGAM1999 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70385] Nucleotide sequences of the VGAM1999 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM1999 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM1999 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM1999 are further described hereinbelow with reference to Table 1.

[70386] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM1999 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM1999 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70387] As mentioned hereinabove with reference to Fig. 1, a function of VGAM1999 gene, herein designated VGAM is inhibition of expression of VGAM1999 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM1999 correlate with, and may be deduced from, the identity of the target genes which VGAM1999 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70388] Fer (fps/fes related) Tyrosine Kinase (phosphoprotein NCP94) (FER, Accession NM_005246) is a VGAM1999 host target gene. FER BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FER, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FER BINDING SITE, designated SEQ ID:11754,

to the nucleotide sequence of VGAM1999 RNA, herein designated VGAM RNA, also designated SEQ ID:4710.

[70389] A function of VGAM1999 is therefore inhibition of Fer (fps/fes related) Tyrosine Kinase (phosphoprotein NCP94) (FER, Accession NM_005246), a gene which Non-receptor protein tyrosine kinase; member of the Src family. Accordingly, utilities of VGAM1999 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FER. The function of FER and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM224.FLJ13385 (Accession NM_024853) is another VGAM1999 host target gene. FLJ13385 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13385, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13385 BINDING SITE, designated SEQ ID:24283, to the nucleotide sequence of VGAM1999 RNA, herein designated VGAM RNA, also designated SEQ ID:4710.

[70390] Another function of VGAM1999 is therefore inhibition of

FLJ13385 (Accession NM_024853). Accordingly, utilities of VGAM1999 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13385. KIAA0555 (Accession NM_014790) is another VGAM1999 host target gene. KIAA0555 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0555, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0555 BINDING SITE, designated SEQ ID:16677, to the nucleotide sequence of VGAM1999 RNA, herein designated VGAM RNA, also designated SEQ ID:4710.

[70391] Another function of VGAM1999 is therefore inhibition of KIAA0555 (Accession NM_014790). Accordingly, utilities of VGAM1999 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0555. PDZ Domain Containing 2 (PDZD2, Accession XM_087705) is another VGAM1999 host target gene. PDZD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDZD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of PDZD2 BINDING SITE, designated SEQ ID:39385, to the nucleotide sequence of VGAM1999 RNA, herein designated VGAM RNA, also designated SEQ ID:4710.

[70392] Another function of VGAM1999 is therefore inhibition of PDZ Domain Containing 2 (PDZD2, Accession XM_087705). Accordingly, utilities of VGAM1999 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDZD2. LOC203411 (Accession XM_117547) is another VGAM1999 host target gene. LOC203411 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203411, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203411 BINDING SITE, designated SEQ ID:43563, to the nucleotide sequence of VGAM1999 RNA, herein designated VGAM RNA, also designated SEQ ID:4710.

[70393] Another function of VGAM1999 is therefore inhibition of LOC203411 (Accession XM_117547). Accordingly, utilities of VGAM1999 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC203411. LOC54499 (Accession XM_047479) is another VGAM1999 host target gene. LOC54499 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC54499, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC54499 BINDING SITE, designated SEQ ID:34966, to the nucleotide sequence of VGAM1999 RNA, herein designated VGAM RNA, also designated SEQ ID:4710.

[70394] Another function of VGAM1999 is therefore inhibition of LOC54499 (Accession XM_047479). Accordingly, utilities of VGAM1999 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC54499. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2000 (VGAM2000) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70395] VGAM2000 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2000 was detected is described hereinabove with reference to Figs. 1-8.

[70396] VGAM2000 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah Virus. VGAM2000 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70397] VGAM2000 gene encodes a VGAM2000 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2000 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2000 precursor RNA is designated SEQ ID:1986, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1986 is located at position 10918 relative to the genome of Nipah Virus.

[70398] VGAM2000 precursor RNA folds onto itself, forming VGAM2000 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70399] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2000 folded precursor RNA into VGAM2000 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2000 RNA is designated SEQ ID:4711, and is provided hereinbelow with reference to the sequence listing part.

[70400] VGAM2000 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2000 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2000 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70401] VGAM2000 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2000 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2000 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2000 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2000 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70402] The complementary binding of VGAM2000 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2000 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2000 host target RNA into VGAM2000 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70403] It is appreciated that VGAM2000 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2000 host target genes. The mRNA of each one of this plurality of VGAM2000 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2000 RNA, herein designated VGAM RNA, and which when bound by VGAM2000 RNA causes inhibition of translation of respective one or more VGAM2000 host target proteins.

[70404] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2000 gene, herein designated VGAM GENE, on one or more VGAM2000 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70405] It is yet further appreciated that a function of VGAM2000 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2000 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM2000 correlate with, and may be deduced from, the identity of the host target genes which VGAM2000 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70406] Nucleotide sequences of the VGAM2000 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2000 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2000 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2000 are further described hereinbelow with reference to Table 1.

[70407] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2000 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2000 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70408] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2000 gene, herein designated VGAM is inhibition of expression of VGAM2000 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2000 correlate with, and may be deduced from, the identity of the target genes which VGAM2000 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70409] Cytochrome P450, Subfamily IVF, Polypeptide 3 (leukotriene B4 omega hydroxylase) (CYP4F3, Accession NM_000896) is a VGAM2000 host target gene. CYP4F3 BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by CYP4F3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP4F3 BINDING SITE, designated SEQ ID:6590, to the nucleotide sequence of VGAM2000 RNA, herein designated VGAM RNA, also designated SEQ ID:4711.

[70410] A function of VGAM2000 is therefore inhibition of Cytochrome P450, Subfamily IVF, Polypeptide 3 (leukotriene B4 omega hydroxylase) (CYP4F3, Accession NM_000896), a gene which converts leukotriene B4 into the less active 20-hydroxy-leukotriene B4. Accordingly, utilities of VGAM2000 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP4F3. The function of CYP4F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM186.MHC Class II Transactivator (MHC2TA, Accession NM_000246) is another VGAM2000 host target gene. MHC2TA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MHC2TA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MHC2TA BINDING SITE, designated SEQ ID:5782, to the nucleotide sequence of VGAM2000 RNA, herein designated VGAM RNA, also designated SEQ ID:4711.

[70411] Another function of VGAM2000 is therefore inhibition of MHC Class II Transactivator (MHC2TA, Accession NM_000246). Accordingly, utilities of VGAM2000 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MHC2TA. Kruppel-like Factor 3 (basic) (KLF3, Accession NM_016531) is another VGAM2000 host target gene. KLF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLF3 BINDING SITE, designated SEQ ID:18595, to the nucleotide sequence of VGAM2000 RNA, herein designated VGAM RNA, also designated SEQ ID:4711.

[70412] Another function of VGAM2000 is therefore inhibition of Kruppel-like Factor 3 (basic) (KLF3, Accession NM_016531). Accordingly, utilities of VGAM2000 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF3. LOC201626 (Accession XM_114349) is another VGAM2000 host target gene. LOC201626 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201626, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201626 BINDING SITE, designated SEQ ID:42890, to the nucleotide sequence of VGAM2000 RNA, herein designated VGAM RNA, also designated SEQ ID:4711.

[70413] Another function of VGAM2000 is therefore inhibition of LOC201626 (Accession XM_114349). Accordingly, utilities of VGAM2000 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201626. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2001 (VGAM2001) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70414] VGAM2001 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2001 was detected is described hereinabove with reference to Figs. 1-8.

[70415] VGAM2001 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah Virus. VGAM2001 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70416] VGAM2001 gene encodes a VGAM2001 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2001 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2001 precursor RNA is designated SEQ ID:1987, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1987 is located at position 2273 relative to the genome of Nipah Virus.

[70417] VGAM2001 precursor RNA folds onto itself, forming VGAM2001 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70418] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2001 folded precursor RNA into VGAM2001 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM2001 RNA is designated SEQ ID:4712, and is provided hereinbelow with reference to the sequence listing part.

[70419] VGAM2001 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2001 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2001 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70420] VGAM2001 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2001 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2001 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2001 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2001 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70421] The complementary binding of VGAM2001 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2001 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2001 host target RNA into VGAM2001 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70422] It is appreciated that VGAM2001 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2001 host target genes. The mRNA of each one of this plurality of VGAM2001 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2001 RNA, herein designated VGAM RNA, and which when bound by VGAM2001 RNA causes inhibition of translation of respective one or more VGAM2001 host target proteins.

[70423] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2001 gene, herein designated VGAM GENE, on one or more VGAM2001 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70424] It is yet further appreciated that a function of VGAM2001 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2001 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM2001 correlate with, and may be deduced from, the identity of the host target genes which VGAM2001 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70425] Nucleotide sequences of the VGAM2001 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2001 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2001 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2001 are further described hereinbelow with reference to Table 1.

[70426] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2001 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2001 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70427] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2001 gene, herein designated VGAM is inhibition of expression of VGAM2001 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2001 correlate with, and may be deduced from, the identity of the target genes which VGAM2001 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70428] Ring Finger Protein 12 (RNF12, Accession NM_016120) is a VGAM2001 host target gene. RNF12 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by RNF12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF12 BINDING SITE, designated SEQ ID:18202, to the nucleotide sequence of VGAM2001 RNA, herein designated VGAM RNA, also designated SEQ ID:4712.

[70429] A function of VGAM2001 is therefore inhibition of Ring Finger Protein 12 (RNF12, Accession NM_016120), a gene which acts as a negative coregulator for LIM homeodomain transcription factors. Accordingly, utilities of VGAM2001 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF12. The function of RNF12 has been established by previous studies. RNF12 encodes a RING H2 zinc finger protein, RLIM, that acts as a negative coregulator for LIM homeodomain transcription factors. Scanlan et al. (1999) isolated a human RNF12 cDNA by screening antigens recognized by autologous antibodies in patients with renal cell carcinoma. Using PCR, Ostendorff et al. (2000) amplified an RNF12 cDNA encoding a deduced 624-amino acid protein that shares 89% and 85% sequence identity with the mouse and chick Rlim proteins, respectively. Northern blot

analysis detected wide expression of mouse Rnf12. Ostendorff et al. (2002) examined RLIM as a mediator of cofactor exchange on DNA-bound transcription factors. SDS-PAGE and mutation analysis showed the RLIM, dependent on the RING finger, is ubiquitinated in the presence of UBCH5 (OMIM Ref. No. 602961). RLIM, however, is unable to ubiquitinate LHX1 (OMIM Ref. No. 601999), LXH3 (OMIM Ref. No. 600577), or ISL1 (OMIM Ref. No. 600366) transcription factors. RLIM efficiently ubiquitinates LMO2 (OMIM Ref. No. 180385) and LMO4 (OMIM Ref. No. 603129), but only in the absence of LIM interaction domain of CLIM1 (OMIM Ref. No. 603450) or CLIM2 (OMIM Ref. No. 603451). The CLIM proteins themselves are specifically polyubiquitinated in the presence of RLIM in the presence or absence of LMO2 or LHX3. Western blot analysis and fluorescence microscopy showed that proteosomal degradation of CLIM depends on the presence of the RLIM RING finger and that RLIM and CLIM levels are reciprocally correlated. Analysis of mutated or truncated forms of RLIM demonstrated that the interaction domain is restricted to a basic evolutionarily conserved and centrally located region of approximately 100 amino acids. A combined EMSA and in vitro ubiquitination analysis, as

well as chromatin immunoprecipitation analysis, indicated that RLIM, dependent on the presence of the RING finger, is able to ubiquitinate CLIM cofactors associated with DNA-bound LHX3. Ostendorff et al. (2002) proposed a model of cofactor exchange which depends on the nuclear concentrations of these components and the availability of other LIM-domain interaction partners

[70430] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[70431] Ostendorff, H. P.; Peirano, R. I.; Peters, M. A.; Schluter, A.; Bossenz, M.; Scheffner, M.; Bach, I. : Ubiquitination-dependent cofactor exchange on LIM homeodomain transcription factors. Nature 416: 99-103, 2002. ; and

[70432] Scanlan, M. J.; Gordan, J. D.; Williamson, B.; Stockert, E.; Bander, N. H.; Jongeneel, V.; Gure, A. O.; Jager, D.; Jager, E.; Knuth, A.; Chen, Y.-T.; Old, L. J. : Antigens recognized by.

[70433] Further studies establishing the function and utilities of RNF12 are found in John Hopkins OMIM database record ID 300379, and in sited publications numbered 986-98 and 9448 listed in the bibliography section hereinbelow, which are also hereby incorporated by refer-

ence.KIAA0680 (Accession NM_014721) is another VGAM2001 host target gene. KIAA0680 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0680, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0680 BINDING SITE, designated SEQ ID:16286, to the nucleotide sequence of VGAM2001 RNA, herein designated VGAM RNA, also designated SEQ ID:4712.

[70434] Another function of VGAM2001 is therefore inhibition of KIAA0680 (Accession NM_014721). Accordingly, utilities of VGAM2001 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0680. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2002 (VGAM2002) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70435] VGAM2002 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2002 was detected is described hereinabove with reference to Figs. 1-8.

[70436] VGAM2002 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah Virus. VGAM2002 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70437] VGAM2002 gene encodes a VGAM2002 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2002 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2002 precursor RNA is designated SEQ ID:1988, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1988 is located at position 1516 relative to the genome of Nipah Virus.

[70438] VGAM2002 precursor RNA folds onto itself, forming VGAM2002 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70439] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2002 folded precursor RNA into VGAM2002 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2002 RNA is designated SEQ ID:4713, and is provided hereinbelow with reference to the sequence listing part.

[70440] VGAM2002 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2002 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2002 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70441] VGAM2002 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2002 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2002 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2002 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2002 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70442] The complementary binding of VGAM2002 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2002 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2002 host target RNA into VGAM2002 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70443] It is appreciated that VGAM2002 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2002 host target genes. The mRNA of each one of this plurality of VGAM2002 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2002 RNA, herein designated VGAM RNA, and which when bound by VGAM2002 RNA causes inhibition of translation of respective one or more VGAM2002 host target proteins.

[70444] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2002 gene, herein designated VGAM GENE, on one or more VGAM2002 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70445] It is yet further appreciated that a function of VGAM2002 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2002 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM2002 correlate with, and may be deduced from, the identity of the host target genes which VGAM2002 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70446] Nucleotide sequences of the VGAM2002 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2002 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2002 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2002 are further described hereinbelow with reference to Table 1.

[70447] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2002 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2002 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70448] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2002 gene, herein designated VGAM is inhibition of expression of VGAM2002 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2002 correlate with, and may be deduced from, the identity of the target genes which VGAM2002 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70449] Fibroblast Growth Factor 2 (basic) (FGF2, Accession NM_002006) is a VGAM2002 host target gene. FGF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGF2, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF2 BINDING SITE, designated SEQ ID:7731, to the nucleotide sequence of VGAM2002 RNA, herein designated VGAM RNA, also designated SEQ ID:4713.

[70450] A function of VGAM2002 is therefore inhibition of Fibroblast Growth Factor 2 (basic) (FGF2, Accession NM_002006), a gene which probably involved in nervous system development and function. Accordingly, utilities of VGAM2002 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF2. The function of FGF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM51.Follistatin-like 3 (secreted glycoprotein) (FSTL3, Accession NM_005860) is another VGAM2002 host target gene. FSTL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FSTL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FSTL3 BINDING SITE, designated SEQ ID:12471, to the nucleotide sequence of

VGAM2002 RNA, herein designated VGAM RNA, also designated SEQ ID:4713.

[70451] Another function of VGAM2002 is therefore inhibition of Follistatin-like 3 (secreted glycoprotein) (FSTL3, Accession NM_005860), a gene which is a member of the follistatin-module-protein family. Accordingly, utilities of VGAM2002 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FSTL3. The function of FSTL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Prostaglandin-endoperoxide Synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2, Accession NM_000963) is another VGAM2002 host target gene. PTGS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTGS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTGS2 BINDING SITE, designated SEQ ID:6685, to the nucleotide sequence of VGAM2002 RNA, herein designated VGAM RNA, also designated SEQ ID:4713.

[70452] Another function of VGAM2002 is therefore inhibition of Prostaglandin-endoperoxide Synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2, Accession NM_000963), a gene which may have a role as a major mediator of inflammation and/or a role for prostanoid signaling in activity-dependent plasticity. Accordingly, utilities of VGAM2002 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGS2. The function of PTGS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM292.X-ray Repair Complementing Defective Repair In Chinese Hamster Cells 2 (XRCC2, Accession NM_005431) is another VGAM2002 host target gene. XRCC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XRCC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XRCC2 BINDING SITE, designated SEQ ID:11904, to the nucleotide sequence of VGAM2002 RNA, herein designated VGAM RNA, also designated SEQ ID:4713.

[70453] Another function of VGAM2002 is therefore inhibition of X-ray Repair Complementing Defective Repair In Chinese Hamster Cells 2 (XRCC2, Accession NM_005431), a gene which involves in the homologous recombination repair (hrr) pathway of double-stranded dna. Accordingly, utilities of VGAM2002 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XRCC2. The function of XRCC2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM241.FLJ20445 (Accession NM_017824) is another VGAM2002 host target gene. FLJ20445 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20445 BINDING SITE, designated SEQ ID:19475, to the nucleotide sequence of VGAM2002 RNA, herein designated VGAM RNA, also designated SEQ ID:4713.

[70454] Another function of VGAM2002 is therefore inhibition of FLJ20445 (Accession NM_017824). Accordingly, utilities of

VGAM2002 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20445. KIAA1328 (Accession XM_029429) is another VGAM2002 host target gene. KIAA1328 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1328, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1328 BINDING SITE, designated SEQ ID:30888, to the nucleotide sequence of VGAM2002 RNA, herein designated VGAM RNA, also designated SEQ ID:4713.

[70455] Another function of VGAM2002 is therefore inhibition of KIAA1328 (Accession XM_029429). Accordingly, utilities of VGAM2002 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1328. KIAA1361 (Accession XM_030845) is another VGAM2002 host target gene. KIAA1361 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1361, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1361 BINDING SITE, designated SEQ ID:31170, to the nucleotide sequence of VGAM2002 RNA, herein designated VGAM RNA, also designated SEQ ID:4713.

[70456] Another function of VGAM2002 is therefore inhibition of KIAA1361 (Accession XM_030845). Accordingly, utilities of VGAM2002 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1361. Rab11-FIP2 (Accession NM_014904) is another VGAM2002 host target gene. Rab11-FIP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Rab11-FIP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rab11-FIP2 BINDING SITE, designated SEQ ID:17094, to the nucleotide sequence of VGAM2002 RNA, herein designated VGAM RNA, also designated SEQ ID:4713.

[70457] Another function of VGAM2002 is therefore inhibition of Rab11-FIP2 (Accession NM_014904). Accordingly, utilities of VGAM2002 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Rab11-FIP2. LOC146136 (Accession XM_053737) is another VGAM2002 host target gene. LOC146136 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146136, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146136 BINDING SITE, designated SEQ ID:36110, to the nucleotide sequence of VGAM2002 RNA, herein designated VGAM RNA, also designated SEQ ID:4713.

[70458] Another function of VGAM2002 is therefore inhibition of LOC146136 (Accession XM_053737). Accordingly, utilities of VGAM2002 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146136. LOC150577 (Accession XM_097918) is another VGAM2002 host target gene. LOC150577 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150577 BINDING SITE, designated SEQ ID:41223, to the nucleotide sequence of VGAM2002 RNA, herein designated VGAM RNA, also designated SEQ ID:4713.

[70459] Another function of VGAM2002 is therefore inhibition of

LOC150577 (Accession XM_097918). Accordingly, utilities of VGAM2002 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150577. LOC220565 (Accession XM_165417) is another VGAM2002 host target gene. LOC220565 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220565, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220565 BINDING SITE, designated SEQ ID:43629, to the nucleotide sequence of VGAM2002 RNA, herein designated VGAM RNA, also designated SEQ ID:4713.

[70460] Another function of VGAM2002 is therefore inhibition of LOC220565 (Accession XM_165417). Accordingly, utilities of VGAM2002 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220565. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2003 (VGAM2003) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[70461] VGAM2003 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2003 was detected is described hereinabove with reference to Figs. 1-8.

[70462] VGAM2003 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Nipah Virus. VGAM2003 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70463] VGAM2003 gene encodes a VGAM2003 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2003 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2003 precursor RNA is designated SEQ ID:1989, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1989 is located at position 5319 relative to the genome of Nipah Virus.

[70464] VGAM2003 precursor RNA folds onto itself, forming VGAM2003 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70465] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2003 folded precursor RNA into VGAM2003 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2003 RNA is designated SEQ ID:4714, and is provided hereinbelow with reference to the sequence listing part.

[70466] VGAM2003 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2003 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2003 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[70467] VGAM2003 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2003 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2003 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2003 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2003 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70468] The complementary binding of VGAM2003 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2003 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2003 host target RNA into VGAM2003 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70469] It is appreciated that VGAM2003 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2003 host target genes. The mRNA of each one of this plurality of VGAM2003 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2003 RNA, herein designated VGAM RNA, and which when bound by VGAM2003 RNA causes inhibition of translation of respective one or more VGAM2003 host target proteins.

[70470] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2003 gene, herein designated VGAM GENE, on one or more VGAM2003 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70471] It is yet further appreciated that a function of VGAM2003 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of viral infection by Nipah Virus. Specific functions, and accordingly utilities, of VGAM2003 correlate with, and may be deduced from, the identity of the host target genes which VGAM2003 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70472] Nucleotide sequences of the VGAM2003 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2003 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2003 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2003 are further described hereinbelow with reference to Table 1.

[70473] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2003 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2003 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70474] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2003 gene, herein designated VGAM is inhibition of expression of VGAM2003 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2003 correlate with, and may be deduced from, the identity of the target genes which VGAM2003 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70475] Ankyrin 3, Node of Ranvier (ankyrin G) (ANK3, Accession NM_020987) is a VGAM2003 host target gene. ANK3

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANK3 BINDING SITE, designated SEQ ID:21983, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70476] A function of VGAM2003 is therefore inhibition of Ankyrin 3, Node of Ranvier (ankyrin G) (ANK3, Accession NM_020987), a gene which plays key roles in activities such as cell motility, activation, proliferation. Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANK3. The function of ANK3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1527.Adaptor-related Protein Complex 2, Beta 1 Subunit (AP2B1, Accession NM_001282) is another VGAM2003 host target gene. AP2B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP2B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP2B1 BINDING SITE, designated SEQ ID:6956, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70477] Another function of VGAM2003 is therefore inhibition of Adaptor-related Protein Complex 2, Beta 1 Subunit (AP2B1, Accession NM_001282), a gene which links clathrin to receptors in coated vesicles. Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP2B1. The function of AP2B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1126.Beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1, Accession NM_054025) is another VGAM2003 host target gene. B3GAT1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by B3GAT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of B3GAT1 BINDING SITE, designated SEQ ID:27632, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70478] Another function of VGAM2003 is therefore inhibition of Beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1, Accession NM_054025). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B3GAT1. Developmentally Regulated GTP Binding Protein 2 (DRG2, Accession NM_001388) is another VGAM2003 host target gene. DRG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DRG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DRG2 BINDING SITE, designated SEQ ID:7076, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70479] Another function of VGAM2003 is therefore inhibition of Developmentally Regulated GTP Binding Protein 2 (DRG2, Accession NM_001388), a gene which may play a role in

cell proliferation, differentiation and death. Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRG2. The function of DRG2 has been established by previous studies. Using a subtractive hybridization strategy, Schenker et al. (1994) identified embryonic lung fibroblast cDNAs whose expression was selectively repressed in SV40-transformed cells. One cDNA encoded a predicted 364-amino acid protein that was designated DRG2. DRG2 contains the 5 sequence motifs that are conserved in all GTP-binding proteins. Northern blot analysis detected DRG2 expression as a major 2-kb and a minor 1.5-kb transcript in various tissues. The shorter mRNA appeared to result from use of an alternative polyadenylation site. By fluorescence in situ hybridization, Schenker and Trueb (1997) mapped the DRG2 gene to 17p13-p12. Vlangos et al. (2000) mapped the DRG2 gene to 17p11.2 within the Smith-Magenis syndrome critical region by somatic cell hybrid analysis.

[70480] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[70481] Schenker, T.; Lach, C.; Kessler, B.; Calderara, S.; Trueb, B. :

A novel GTP-binding protein which is selectively repressed in SV40 transformed fibroblasts. J. Biol. Chem. 269: 25447-25453, 1994. ; and

[70482] Vlangos, C. N.; Das, P.; Patel, P. I.; Elsea, S. H. : Assignment of developmentally regulated GTP-binding protein (DRG2) to human chromosome band 17p11.2 with somatic cell hybrids and l.

[70483] Further studies establishing the function and utilities of DRG2 are found in John Hopkins OMIM database record ID 602986, and in sited publications numbered 122 and 8846 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.GM2 Ganglioside Activator Protein (GM2A, Accession XM_041978) is another VGAM2003 host target gene. GM2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GM2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GM2A BINDING SITE, designated SEQ ID:33661, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70484] Another function of VGAM2003 is therefore inhibition of

GM2 Ganglioside Activator Protein (GM2A, Accession XM_041978). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GM2A. GRAF (Accession NM_015071) is another VGAM2003 host target gene. GRAF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRAF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRAF BINDING SITE, designated SEQ ID:17443, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70485] Another function of VGAM2003 is therefore inhibition of GRAF (Accession NM_015071), a gene which ia a GTPase activating protein for p21-rac. Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRAF. The function of GRAF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM430.MAX Gene Associated (MGA, Accession XM_031689) is another VGAM2003 host target gene. MGA

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGA BINDING SITE, designated SEQ ID:31454, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70486] Another function of VGAM2003 is therefore inhibition of MAX Gene Associated (MGA, Accession XM_031689), a gene which plays a role in the final steps of digestion of starch. Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGA. The function of MGA has been established by previous studies. Maltase-glucoamylase (MGA; EC 3.2.1.20) is a brush border membrane enzyme that plays a role in the final steps of digestion of starch. Naim et al. (1988) showed that it is synthesized as a single-chain polypeptide precursor, acquires N- and O-linked carbohydrates, and does not undergo intracellular or extracellular proteolytic cleavage. Nichols et al. (1998) purified and partially sequenced the human maltase-glucoamylase protein. By RT-PCR using degener-

ate oligonucleotides based on the MGA protein sequence, they isolated human small intestine MGA cDNAs. The deduced 1,857-amino acid MGA protein has a putative type II membrane anchor, 2 WIDMNE catalytic sites, which are characteristic of carbohydrate hydrolases such as sucrase-isomaltase (SI; 222900), and 2 glycosyl hydrolase family 31 signature 2 sequences. MGA also has 19 potential N-glycosylation sites and 253 potential O-glycosylation sites. The MGA protein shares 59% sequence identity with SI. RT-PCR detected MGA expression in human small intestine, granulocyte, and kidney but not in salivary gland or pancreas.

[70487] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[70488] Naim, H. Y.; Sterchi, E. E.; Lentze, M. J. : Structure, biosynthesis, and glycosylation of human small intestinal maltase-glucoamylase. J. Biol. Chem. 263: 19709-19717, 1988. ; and

[70489] Nichols, B. L.; Eldering, J.; Avery, S.; Hahn, D.; Quaroni, A.; Sterchi, E. : Human small intestinal maltase-glucoamylase cDNA cloning: homology to sucrase-isomaltase. J. Biol. Chem. 273: 3.

[70490] Further studies establishing the function and utilities of MGA are found in John Hopkins OMIM database record ID 154360, and in sited publications numbered 12706-12708 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Neuroligin 2 (NLGN2, Accession XM_113932) is another VGAM2003 host target gene. NLGN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NLGN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NLGN2 BINDING SITE, designated SEQ ID:42550, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70491] Another function of VGAM2003 is therefore inhibition of Neuroligin 2 (NLGN2, Accession XM_113932), a gene which rapidly hydrolyzes choline released into the synapse. Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NLGN2. The function of NLGN2 and its association with various diseases and clinical conditions, has been established by previous studies, as de-

scribed hereinabove with reference to VGAM178.Nebulin-related Anchoring Protein (NRAP, Accession NM_006175) is another VGAM2003 host target gene. NRAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NRAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NRAP BINDING SITE, designated SEQ ID:12834, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70492] Another function of VGAM2003 is therefore inhibition of Nebulin-related Anchoring Protein (NRAP, Accession NM_006175), a gene which performs an anchoring function to link the terminal actin filaments of myofibrils to protein complexes located beneath the sarcolemma. Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRAP. The function of NRAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM649.Ret Proto-oncogene (multiple endocrine neoplasia and medullary thyroid car-

cinoma 1, Hirschsprung disease) (RET, Accession NM_020630) is another VGAM2003 host target gene. RET BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RET, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RET BINDING SITE, designated SEQ ID:21785, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70493] Another function of VGAM2003 is therefore inhibition of Ret Proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease) (RET, Accession NM_020630), a gene which transduces signals for cell growth and differentiation. Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RET. The function of RET and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Tumor Necrosis Factor (ligand) Superfamily, Member 11 (TNFSF11, Accession NM_033012) is another VGAM2003 host target gene. TNFSF11 BINDING

SITE1 and TNFSF11 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TNFSF11, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFSF11 BINDING SITE1 and TNFSF11 BINDING SITE2, designated SEQ ID:26898 and SEQ ID:9801 respectively, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70494] Another function of VGAM2003 is therefore inhibition of Tumor Necrosis Factor (ligand) Superfamily, Member 11 (TNFSF11, Accession NM_033012), a gene which may be an important regulator of interactions between t cells and dendritic cells and may play a may play a role in the regulation of the t cell-dependent immune response. may also play an important role in enhanced bone-resorption in humoral hypercalcemia of malignancy. Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFSF11. The function of TNFSF11 has been established by previous studies. Croucher et al. (2001) demonstrated that myeloma cells express the critical osteoclas-

togenic factor RANKL. Injection of myeloma cells into a C57BL strain of mice resulted in development of bone disease characterized by a significant decrease in cancellous bone volume in the tibial and femoral metaphyses, an increase in osteoclast formation, and radiologic evidence of osteolytic bone lesions. Treatment of mice with established myeloma with recombinant OPG protein, the soluble decoy receptor for RANKL, prevented the development of lytic bone lesions. OPG treatment was associated with preservation of cancellous bone volume and inhibition of osteoclast formation. OPG also promoted an increase in femoral, tibial, and vertebral BMD. The data suggested that the RANKL/RANK/OPG system may play a critical role in the development of osteolytic bone disease in multiple myeloma and that targeting this system may have therapeutic potential. Takayanagi et al. (2002) demonstrated that RANKL induces the IFN-beta (OMIM Ref. No. 147640) gene in osteoclast precursor cells, and that IFN-beta inhibits the differentiation of osteoclasts by interfering with the RANKL-induced expression of c-Fos (OMIM Ref. No. 164810), an essential transcription factor for the formation of osteoclasts. This IFN-beta gene induction mechanism is distinct from that induced by virus, and is depen-

dent on c-Fos itself. Thus an autoregulatory mechanism operates--the RANKL-induced c-Fos induces its own inhibitor. The importance of this regulatory mechanism for bone homeostasis is emphasized by the observation that mice deficient in IFN-beta signaling exhibit severe osteopenia accompanied by enhanced osteoclastogenesis.

[70495] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[70496] Croucher, P. I.; Shipman, C. M.; Lippitt, J.; Perry, M.; Asosingh, K.; Hijzen, A.; Brabbs, A. C.; van Beek, E. J. R.; Holen, I.; Skerry, T. M.; Dunstan, C. R.; Russell, G. R.; Van Camp, B.; Vanderkerken, K. : Osteoprotegerin inhibits the development of osteolytic bone disease in multiple myeloma. Blood 98: 3534-3540, 2001. ; and

[70497] Fata, J. E.; Kong, Y.-Y.; Li, J.; Sasaki, T.; Irie-Sasaki, J.; Moorehead, R. A.; Elliott, R.; Scully, S.; Voura, E. B.; Lacey, D. L.; Boyle, W. J.; Khokha, R.; Penninger, J. M. : The o.

[70498] Further studies establishing the function and utilities of TNFSF11 are found in John Hopkins OMIM database record ID 602642, and in sited publications numbered 2390-2396, 1147 and 8538 listed in the bibliography section hereinbelow, which are also hereby incorporated

by reference.Chromosome 20 Open Reading Frame 142 (C20orf142, Accession XM_059257) is another VGAM2003 host target gene. C20orf142 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf142, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf142 BINDING SITE, designated SEQ ID:36931, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70499] Another function of VGAM2003 is therefore inhibition of Chromosome 20 Open Reading Frame 142 (C20orf142, Accession XM_059257). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf142. DKFZP564O0423 (Accession XM_166254) is another VGAM2003 host target gene. DKFZP564O0423 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O0423, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of DKFZP564O0423 BINDING SITE, designated SEQ ID:44068, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70500] Another function of VGAM2003 is therefore inhibition of DKFZP564O0423 (Accession XM_166254). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564O0423. FLJ20232 (Accession NM_019008) is another VGAM2003 host target gene. FLJ20232 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20232, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20232 BINDING SITE, designated SEQ ID:21088, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70501] Another function of VGAM2003 is therefore inhibition of FLJ20232 (Accession NM_019008). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20232. FLJ20686 (Accession NM_017925) is another

VGAM2003 host target gene. FLJ20686 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20686, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20686 BINDING SITE, designated SEQ ID:19594, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70502] Another function of VGAM2003 is therefore inhibition of FLJ20686 (Accession NM_017925). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20686. FLJ22501 (Accession NM_024747) is another VGAM2003 host target gene. FLJ22501 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22501, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22501 BINDING SITE, designated SEQ ID:24082, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70503] Another function of VGAM2003 is therefore inhibition of FLJ22501 (Accession NM_024747). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22501. FLJ23120 (Accession XM_097961) is another VGAM2003 host target gene. FLJ23120 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23120, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23120 BINDING SITE, designated SEQ ID:41265, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70504] Another function of VGAM2003 is therefore inhibition of FLJ23120 (Accession XM_097961). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23120. FLJ23309 (Accession NM_024896) is another VGAM2003 host target gene. FLJ23309 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23309, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23309 BINDING SITE, designated SEQ ID:24379, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70505] Another function of VGAM2003 is therefore inhibition of FLJ23309 (Accession NM_024896). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23309. FLJ25438 (Accession NM_144696) is another VGAM2003 host target gene. FLJ25438 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ25438, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ25438 BINDING SITE, designated SEQ ID:29521, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70506] Another function of VGAM2003 is therefore inhibition of FLJ25438 (Accession NM_144696). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ25438. Kruppel-like Factor 5 (intestinal) (KLF5, Accession NM_001730) is another VGAM2003 host target gene. KLF5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLF5 BINDING SITE, designated SEQ ID:7464, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70507] Another function of VGAM2003 is therefore inhibition of Kruppel-like Factor 5 (intestinal) (KLF5, Accession NM_001730). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF5. PRO0659 (Accession NM_014138) is another VGAM2003 host target gene. PRO0659 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO0659, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0659 BINDING SITE, designated SEQ ID:15407, to the nucleotide sequence of VGAM2003 RNA,

herein designated VGAM RNA, also designated SEQ ID:4714.

[70508] Another function of VGAM2003 is therefore inhibition of PRO0659 (Accession NM_014138). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0659. LOC144453 (Accession XM_084869) is another VGAM2003 host target gene. LOC144453 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144453, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144453 BINDING SITE, designated SEQ ID:37748, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70509] Another function of VGAM2003 is therefore inhibition of LOC144453 (Accession XM_084869). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144453. LOC148223 (Accession XM_086101) is another VGAM2003 host target gene. LOC148223 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC148223, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148223 BINDING SITE, designated SEQ ID:38495, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70510] Another function of VGAM2003 is therefore inhibition of LOC148223 (Accession XM_086101). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148223. LOC158819 (Accession XM_098995) is another VGAM2003 host target gene. LOC158819 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158819, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158819 BINDING SITE, designated SEQ ID:42027, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70511] Another function of VGAM2003 is therefore inhibition of LOC158819 (Accession XM_098995). Accordingly, utilities

of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158819. LOC202934 (Accession XM_117486) is another VGAM2003 host target gene. LOC202934 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202934, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE, designated SEQ ID:43462, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70512] Another function of VGAM2003 is therefore inhibition of LOC202934 (Accession XM_117486). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202934. LOC206426 (Accession XM_116505) is another VGAM2003 host target gene. LOC206426 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC206426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC206426 BINDING SITE, designated SEQ ID:43118, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70513] Another function of VGAM2003 is therefore inhibition of LOC206426 (Accession XM_116505). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC206426. LOC255465 (Accession XM_173206) is another VGAM2003 host target gene. LOC255465 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255465, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255465 BINDING SITE, designated SEQ ID:46454, to the nucleotide sequence of VGAM2003 RNA, herein designated VGAM RNA, also designated SEQ ID:4714.

[70514] Another function of VGAM2003 is therefore inhibition of LOC255465 (Accession XM_173206). Accordingly, utilities of VGAM2003 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255465. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2004 (VGAM2004) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70515] VGAM2004 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2004 was detected is described hereinabove with reference to Figs. 1-8.

[70516] VGAM2004 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee Cytomegalovirus. VGAM2004 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70517] VGAM2004 gene encodes a VGAM2004 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2004 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2004 precursor RNA is designated SEQ ID:1990, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1990 is located at position 177784 relative to the

genome of Chimpanzee Cytomegalovirus.

[70518] VGAM2004 precursor RNA folds onto itself, forming VGAM2004 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70519] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2004 folded precursor RNA into VGAM2004 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2004 RNA is designated SEQ ID:4715, and is provided hereinbelow with reference to the sequence listing part.

[70520] VGAM2004 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2004 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2004 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70521] VGAM2004 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2004 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2004 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2004 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2004 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70522] The complementary binding of VGAM2004 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2004 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2004 host target RNA into VGAM2004 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70523] It is appreciated that VGAM2004 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2004 host target genes. The mRNA of each one of this plurality of VGAM2004 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2004 RNA, herein designated VGAM RNA, and which when bound by VGAM2004 RNA causes inhibition of translation of respective one or more VGAM2004 host target proteins.

[70524] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2004 gene, herein designated VGAM GENE, on one or more VGAM2004 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70525] It is yet further appreciated that a function of VGAM2004 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2004 include diagnosis, prevention and treatment of viral infection by Chimpanzee Cytomegalovirus. Specific functions, and accordingly utili-

ties, of VGAM2004 correlate with, and may be deduced from, the identity of the host target genes which VGAM2004 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70526] Nucleotide sequences of the VGAM2004 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2004 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2004 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2004 are further described hereinbelow with reference to Table 1.

[70527] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2004 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2004 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70528] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2004 gene, herein designated VGAM is inhibition of expression of VGAM2004 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2004 correlate with, and may be deduced

from, the identity of the target genes which VGAM2004 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70529] G Protein-coupled Receptor 61 (GPR61, Accession XM_086232) is a VGAM2004 host target gene. GPR61 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPR61, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR61 BINDING SITE, designated SEQ ID:38564, to the nucleotide sequence of VGAM2004 RNA, herein designated VGAM RNA, also designated SEQ ID:4715.

[70530] A function of VGAM2004 is therefore inhibition of G Protein-coupled Receptor 61 (GPR61, Accession XM_086232), a gene which transduces extracellular signals through heterotrimeric G proteins. Accordingly, utilities of VGAM2004 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR61. The function of GPR61 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Fig. 1 further provides a conceptual de-

scription of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2005 (VGAM2005) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70531] VGAM2005 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2005 was detected is described hereinabove with reference to Figs. 1-8.

[70532] VGAM2005 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee Cytomegalovirus. VGAM2005 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70533] VGAM2005 gene encodes a VGAM2005 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2005 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2005 precursor RNA is designated SEQ ID:1991, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:1991 is located at position 177914 relative to the genome of Chimpanzee Cytomegalovirus.

[70534] VGAM2005 precursor RNA folds onto itself, forming VGAM2005 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70535] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2005 folded precursor RNA into VGAM2005 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2005 RNA is designated SEQ ID:4716, and is provided hereinbelow with reference to the sequence listing part.

[70536] VGAM2005 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2005 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2005 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70537] VGAM2005 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2005 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2005 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2005 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2005 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70538] The complementary binding of VGAM2005 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2005 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2005 host target RNA into VGAM2005 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70539] It is appreciated that VGAM2005 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2005 host target genes. The mRNA of each one of this plurality of VGAM2005 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2005 RNA, herein designated VGAM RNA, and which when bound by VGAM2005 RNA causes inhibition of translation of respective one or more

VGAM2005 host target proteins.

[70540] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2005 gene, herein designated VGAM GENE, on one or more VGAM2005 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70541] It is yet further appreciated that a function of VGAM2005 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2005 include diagnosis, prevention and treatment of viral infection by Chimpanzee Cy-

tomegalovirus. Specific functions, and accordingly utilities, of VGAM2005 correlate with, and may be deduced from, the identity of the host target genes which VGAM2005 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70542] Nucleotide sequences of the VGAM2005 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2005 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2005 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2005 are further described hereinbelow with reference to Table 1.

[70543] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2005 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2005 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70544] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2005 gene, herein designated VGAM is inhibition of expression of VGAM2005 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2005 correlate with, and may be deduced from, the identity of the target genes which VGAM2005 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70545] V-akt Murine Thymoma Viral Oncogene Homolog 2 (AKT2, Accession NM_001626) is a VGAM2005 host target gene. AKT2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AKT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKT2 BINDING SITE, designated SEQ ID:7338, to the nucleotide sequence of VGAM2005 RNA, herein designated VGAM RNA, also designated SEQ ID:4716.

[70546] A function of VGAM2005 is therefore inhibition of V-akt Murine Thymoma Viral Oncogene Homolog 2 (AKT2, Accession NM_001626). Accordingly, utilities of VGAM2005 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKT2. Tec Protein Tyrosine Kinase (TEC, Accession NM_003215) is another VGAM2005 host target gene. TEC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEC, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEC BINDING SITE, designated SEQ ID:9218, to the nucleotide sequence of VGAM2005 RNA, herein designated VGAM RNA, also designated SEQ ID:4716.

[70547] Another function of VGAM2005 is therefore inhibition of Tec Protein Tyrosine Kinase (TEC, Accession NM_003215). Accordingly, utilities of VGAM2005 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEC. KIAA0429 (Accession NM_014751) is another VGAM2005 host target gene. KIAA0429 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0429, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0429 BINDING SITE, designated SEQ ID:16473, to the nucleotide sequence of VGAM2005 RNA, herein designated VGAM RNA, also designated SEQ ID:4716.

[70548] Another function of VGAM2005 is therefore inhibition of KIAA0429 (Accession NM_014751). Accordingly, utilities

of VGAM2005 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0429. LOC147841 (Accession XM_085924) is another VGAM2005 host target gene. LOC147841 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147841 BINDING SITE, designated SEQ ID:38399, to the nucleotide sequence of VGAM2005 RNA, herein designated VGAM RNA, also designated SEQ ID:4716.

[70549] Another function of VGAM2005 is therefore inhibition of LOC147841 (Accession XM_085924). Accordingly, utilities of VGAM2005 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147841. LOC152048 (Accession XM_098158) is another VGAM2005 host target gene. LOC152048 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152048, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC152048 BINDING SITE, designated SEQ ID:41425, to the nucleotide sequence of VGAM2005 RNA, herein designated VGAM RNA, also designated SEQ ID:4716.

[70550] Another function of VGAM2005 is therefore inhibition of LOC152048 (Accession XM_098158). Accordingly, utilities of VGAM2005 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152048. LOC152271 (Accession XM_087419) is another VGAM2005 host target gene. LOC152271 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152271 BINDING SITE, designated SEQ ID:39240, to the nucleotide sequence of VGAM2005 RNA, herein designated VGAM RNA, also designated SEQ ID:4716.

[70551] Another function of VGAM2005 is therefore inhibition of LOC152271 (Accession XM_087419). Accordingly, utilities of VGAM2005 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152271. LOC199796 (Accession XM_058994) is another VGAM2005 host target gene. LOC199796 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC199796, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199796 BINDING SITE, designated SEQ ID:36811, to the nucleotide sequence of VGAM2005 RNA, herein designated VGAM RNA, also designated SEQ ID:4716.

[70552] Another function of VGAM2005 is therefore inhibition of LOC199796 (Accession XM_058994). Accordingly, utilities of VGAM2005 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199796. LOC56270 (Accession NM_019613) is another VGAM2005 host target gene. LOC56270 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC56270, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56270 BINDING SITE, designated SEQ ID:21232, to the nucleotide sequence of VGAM2005 RNA, herein designated VGAM RNA, also designated SEQ ID:4716.

[70553] Another function of VGAM2005 is therefore inhibition of

LOC56270 (Accession NM_019613). Accordingly, utilities of VGAM2005 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56270. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2006 (VGAM2006) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70554] VGAM2006 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2006 was detected is described hereinabove with reference to Figs. 1-8.

[70555] VGAM2006 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Chimpanzee Cytomegalovirus. VGAM2006 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70556] VGAM2006 gene encodes a VGAM2006 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2006 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2006 precursor RNA is designated SEQ ID:1992, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1992 is located at position 191561 relative to the genome of Chimpanzee Cytomegalovirus.

[70557] VGAM2006 precursor RNA folds onto itself, forming VGAM2006 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70558] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2006 folded precursor RNA into VGAM2006 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide se-

quence of VGAM2006 RNA is designated SEQ ID:4717, and is provided hereinbelow with reference to the sequence listing part.

[70559] VGAM2006 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2006 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2006 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70560] VGAM2006 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2006 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2006 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2006 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2006 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70561] The complementary binding of VGAM2006 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2006 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2006 host target RNA into VGAM2006 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70562] It is appreciated that VGAM2006 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2006 host target genes. The mRNA of each one of this plurality of VGAM2006 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2006 RNA, herein designated VGAM RNA, and which when bound by VGAM2006 RNA causes inhibition of translation of respective one or more VGAM2006 host target proteins.

[70563] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2006 gene, herein designated VGAM GENE, on one or more VGAM2006 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70564] It is yet further appreciated that a function of VGAM2006

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of viral infection by Chimpanzee Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2006 correlate with, and may be deduced from, the identity of the host target genes which VGAM2006 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70565] Nucleotide sequences of the VGAM2006 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2006 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2006 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2006 are further described hereinbelow with reference to Table 1.

[70566] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2006 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2006 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70567] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2006 gene, herein designated VGAM is inhibition of expression of VGAM2006 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2006 correlate with, and may be deduced from, the identity of the target genes which VGAM2006 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70568] Formin 2 (FMN2, Accession XM_086525) is a VGAM2006 host target gene. FMN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FMN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FMN2 BINDING SITE, designated SEQ ID:38741, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70569] A function of VGAM2006 is therefore inhibition of Formin 2 (FMN2, Accession XM_086525). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FMN2. Homeo Box C13 (HOXC13, Accession XM_006804) is an-

other VGAM2006 host target gene. HOXC13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HOXC13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOXC13 BINDING SITE, designated SEQ ID:30015, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70570] Another function of VGAM2006 is therefore inhibition of Homeo Box C13 (HOXC13, Accession XM_006804). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXC13. Hypoxia Up-regulated 1 (HYOU1, Accession XM_006464) is another VGAM2006 host target gene. HYOU1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HYOU1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HYOU1 BINDING SITE, designated SEQ ID:30003, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4717.

[70571] Another function of VGAM2006 is therefore inhibition of Hypoxia Up-regulated 1 (HYOU1, Accession XM_006464). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HYOU1. RAP1, GTPase Activating Protein 1 (RAP1GA1, Accession NM_002885) is another VGAM2006 host target gene. RAP1GA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAP1GA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAP1GA1 BINDING SITE, designated SEQ ID:8796, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70572] Another function of VGAM2006 is therefore inhibition of RAP1, GTPase Activating Protein 1 (RAP1GA1, Accession NM_002885). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP1GA1. DKFZP434E2318 (Accession NM_032138) is another VGAM2006 host target gene. DKFZP434E2318 BINDING SITE is HOST TARGET

binding site found in the 5` untranslated region of mRNA encoded by DKFZP434E2318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434E2318 BINDING SITE, designated SEQ ID:25816, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70573] Another function of VGAM2006 is therefore inhibition of DKFZP434E2318 (Accession NM_032138). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434E2318. Family with Sequence Similarity 3, Member A (FAM3A, Accession NM_021806) is another VGAM2006 host target gene. FAM3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FAM3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FAM3A BINDING SITE, designated SEQ ID:22357, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70574] Another function of VGAM2006 is therefore inhibition of Family with Sequence Similarity 3, Member A (FAM3A, Accession NM_021806). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAM3A. FGD1 Family, Member 3 (FGD3, Accession XM_053487) is another VGAM2006 host target gene. FGD3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGD3 BINDING SITE, designated SEQ ID:36090, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70575] Another function of VGAM2006 is therefore inhibition of FGD1 Family, Member 3 (FGD3, Accession XM_053487). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGD3. KIAA0014 (Accession NM_014665) is another VGAM2006 host target gene. KIAA0014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

KIAA0014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0014 BINDING SITE, designated SEQ ID:16114, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70576] Another function of VGAM2006 is therefore inhibition of KIAA0014 (Accession NM_014665). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0014. KIAA0152 (Accession NM_014730) is another VGAM2006 host target gene. KIAA0152 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0152, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0152 BINDING SITE, designated SEQ ID:16335, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70577] Another function of VGAM2006 is therefore inhibition of KIAA0152 (Accession NM_014730). Accordingly, utilities

of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0152. KIAA0753 (Accession NM_014804) is another VGAM2006 host target gene. KIAA0753 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0753, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0753 BINDING SITE, designated SEQ ID:16735, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70578] Another function of VGAM2006 is therefore inhibition of KIAA0753 (Accession NM_014804). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0753. KIAA1404 (Accession XM_030494) is another VGAM2006 host target gene. KIAA1404 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1404, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1404 BINDING SITE, designated SEQ ID:31051, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70579] Another function of VGAM2006 is therefore inhibition of KIAA1404 (Accession XM_030494). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1404. KIAA1987 (Accession XM_113870) is another VGAM2006 host target gene. KIAA1987 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1987, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1987 BINDING SITE, designated SEQ ID:42495, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70580] Another function of VGAM2006 is therefore inhibition of KIAA1987 (Accession XM_113870). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1987. Neuron Navigator 3 (NAV3, Accession NM_014903) is another VGAM2006 host target gene.

NAV3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NAV3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAV3 BINDING SITE, designated SEQ ID:17090, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70581] Another function of VGAM2006 is therefore inhibition of Neuron Navigator 3 (NAV3, Accession NM_014903). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAV3. PDEF (Accession NM_012391) is another VGAM2006 host target gene. PDEF BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PDEF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDEF BINDING SITE, designated SEQ ID:14746, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70582] Another function of VGAM2006 is therefore inhibition of

PDEF (Accession NM_012391). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDEF. RoXaN (Accession NM_025013) is another VGAM2006 host target gene. RoXaN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RoXaN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RoXaN BINDING SITE, designated SEQ ID:24603, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70583] Another function of VGAM2006 is therefore inhibition of RoXaN (Accession NM_025013). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RoXaN. LOC145813 (Accession XM_096873) is another VGAM2006 host target gene. LOC145813 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145813, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC145813 BINDING SITE, designated SEQ ID:40598, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70584] Another function of VGAM2006 is therefore inhibition of LOC145813 (Accession XM_096873). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145813. LOC152426 (Accession XM_098225) is another VGAM2006 host target gene. LOC152426 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152426 BINDING SITE, designated SEQ ID:41498, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70585] Another function of VGAM2006 is therefore inhibition of LOC152426 (Accession XM_098225). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152426. LOC157254 (Accession XM_088279) is an-

other VGAM2006 host target gene. LOC157254 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157254, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157254 BINDING SITE, designated SEQ ID:39579, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70586] Another function of VGAM2006 is therefore inhibition of LOC157254 (Accession XM_088279). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157254. LOC158382 (Accession XM_098931) is another VGAM2006 host target gene. LOC158382 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158382, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158382 BINDING SITE, designated SEQ ID:41964, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70587] Another function of VGAM2006 is therefore inhibition of LOC158382 (Accession XM_098931). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158382. LOC221393 (Accession XM_166435) is another VGAM2006 host target gene. LOC221393 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221393, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221393 BINDING SITE, designated SEQ ID:44337, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70588] Another function of VGAM2006 is therefore inhibition of LOC221393 (Accession XM_166435). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221393. LOC51285 (Accession NM_016563) is another VGAM2006 host target gene. LOC51285 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51285, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51285 BINDING SITE, designated SEQ ID:18638, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70589] Another function of VGAM2006 is therefore inhibition of LOC51285 (Accession NM_016563). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51285. LOC90342 (Accession XM_031009) is another VGAM2006 host target gene. LOC90342 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90342, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90342 BINDING SITE, designated SEQ ID:31253, to the nucleotide sequence of VGAM2006 RNA, herein designated VGAM RNA, also designated SEQ ID:4717.

[70590] Another function of VGAM2006 is therefore inhibition of LOC90342 (Accession XM_031009). Accordingly, utilities of VGAM2006 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC90342. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2007 (VGAM2007) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70591] VGAM2007 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2007 was detected is described hereinabove with reference to Figs. 1-8.

[70592] VGAM2007 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola Virus (REBOV). VGAM2007 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70593] VGAM2007 gene encodes a VGAM2007 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2007 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2007 precursor RNA is designated SEQ ID:1993, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:1993 is located at position 5965 relative to the genome of Reston Ebola Virus (REBOV).

[70594] VGAM2007 precursor RNA folds onto itself, forming VGAM2007 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70595] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2007 folded precursor RNA into VGAM2007 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2007 RNA is designated SEQ ID:4718, and is provided hereinbelow with reference to the sequence listing part.

[70596] VGAM2007 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2007 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2007 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70597] VGAM2007 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2007 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2007 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2007 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2007 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70598] The complementary binding of VGAM2007 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2007 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2007 host target RNA into VGAM2007 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70599] It is appreciated that VGAM2007 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2007 host target genes. The mRNA of each one of this plurality of VGAM2007 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2007 RNA, herein designated VGAM RNA, and which when bound by VGAM2007 RNA causes

inhibition of translation of respective one or more VGAM2007 host target proteins.

[70600] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2007 gene, herein designated VGAM GENE, on one or more VGAM2007 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70601] It is yet further appreciated that a function of VGAM2007 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2007 include diagnosis, prevention and

treatment of viral infection by Reston Ebola Virus (REBOV). Specific functions, and accordingly utilities, of VGAM2007 correlate with, and may be deduced from, the identity of the host target genes which VGAM2007 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70602] Nucleotide sequences of the VGAM2007 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2007 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2007 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2007 are further described hereinbelow with reference to Table 1.

[70603] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2007 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2007 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70604] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2007 gene, herein designated VGAM is inhibition of expression of VGAM2007 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2007 correlate with, and may be deduced from, the identity of the target genes which VGAM2007 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70605] Adenylate Cyclase 8 (brain) (ADCY8, Accession NM_001115) is a VGAM2007 host target gene. ADCY8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ADCY8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADCY8 BINDING SITE, designated SEQ ID:6787, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70606] A function of VGAM2007 is therefore inhibition of Adenylate Cyclase 8 (brain) (ADCY8, Accession NM_001115), a gene which this a membrane-bound, ca(2+)-inhibitable adenylyl cyclase. Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY8. The function of ADCY8 and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to VGAM1169.Aldehyde Dehydrogenase 3 Family, Member B1 (ALDH3B1, Accession XM_166190) is another VGAM2007 host target gene. ALDH3B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALDH3B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALDH3B1 BINDING SITE, designated SEQ ID:44002, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70607] Another function of VGAM2007 is therefore inhibition of Aldehyde Dehydrogenase 3 Family, Member B1 (ALDH3B1, Accession XM_166190), a gene which may play a major role in the detoxification of aldehydes generated by alcohol metabolism and lipid peroxidation. Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH3B1. The function of ALDH3B1 has been established by previous studies. The aldehyde dehydrogenases are a family of isozymes that may play a major role in the detoxification of aldehydes generated by alcohol

metabolism and lipid peroxidation. Hsu et al. (1994) reported the cloning and sequencing of a cDNA encoding a new human ALDH, designated ALDH7. Degenerate oligodeoxyribonucleotides derived from conserved regions of known ALDH cDNAs amplified a 408-bp product from human kidney total RNA by the reverse transcription-PCR procedure. This PCR product was subcloned, selected, and used as a probe to screen a human kidney cDNA library. The full-length human kidney cDNA of ALDH7 is 2,791 bp long and contains an open reading frame encoding 468 amino acids. The deduced sequence of ALDH7 was longer than that of human stomach ALDH3 (OMIM Ref. No. 100660) by 15 amino acids at the C terminus. The degree of identity between the 2 isozymes was 52% with a positional alignment of 453 amino acids. Northern blot analysis demonstrated that lung is another major tissue expressing ALDH7. Hsu et al. (1997) determined the structure of the ALDH7 and ALDH8 (OMIM Ref. No. 601917) genes. The ALDH7 gene spans about 20 kb of genomic DNA and is composed of 9 coding exons. The ALDH8 gene is over 10 kb in length and consists of at least 10 exons. The ALDH8 gene contains an in-frame stop codon at the seventeenth codon position from the

first initiator Met. The coding region of the ALDH7 gene shows about 86% nucleotide identity with the corresponding region of the ALDH8 gene. The numbers and positions of the introns of the 2 genes are conserved, suggesting that gene duplication is involved in the expansion of the ALDH gene family. The human ALDH7 and ALDH8 genes have a close evolutionary relationship with human ALDH3. The International Radiation Hybrid Mapping Consortium mapped the ALDH7 gene to chromosome 11 (RH69713).

[70608] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[70609] Hsu, L. C.; Chang, W.-C.; Yoshida, A. : Human aldehyde dehydrogenase genes, ALDH7 and ALDH8: genomic organization and gene structure comparison. Gene 189: 89-94, 1997. ; and

[70610] Hsu, L. C.; Chang, W.-C.; Yoshida, A. : Cloning of a cDNA encoding human ALDH7, a new member of the aldehyde dehydrogenase family. Gene 151: 285-289, 1994.

[70611] Further studies establishing the function and utilities of ALDH3B1 are found in John Hopkins OMIM database record ID 600466, and in sited publications numbered 7732-7733 listed in the bibliography section hereinbelow,

which are also hereby incorporated by reference.Aprataxin (APTX, Accession NM_017692) is another VGAM2007 host target gene. APTX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APTX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APTX BINDING SITE, designated SEQ ID:19249, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70612] Another function of VGAM2007 is therefore inhibition of Aprataxin (APTX, Accession NM_017692). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APTX. UDP-Gal:betaGlcNAc Beta 1,4- Galactosyl-transferase, Polypeptide 6 (B4GALT6, Accession XM_008799) is another VGAM2007 host target gene. B4GALT6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by B4GALT6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of B4GALT6 BINDING SITE, designated SEQ ID:30093, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70613] Another function of VGAM2007 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 6 (B4GALT6, Accession XM_008799). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT6. Collagen, Type V, Alpha 3 (COL5A3, Accession NM_015719) is another VGAM2007 host target gene. COL5A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL5A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL5A3 BINDING SITE, designated SEQ ID:17932, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70614] Another function of VGAM2007 is therefore inhibition of Collagen, Type V, Alpha 3 (COL5A3, Accession NM_015719). Accordingly, utilities of VGAM2007 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with COL5A3. Enamelin (ENAM, Accession NM_031889) is another VGAM2007 host target gene. ENAM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ENAM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ENAM BINDING SITE, designated SEQ ID:25634, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70615] Another function of VGAM2007 is therefore inhibition of Enamelin (ENAM, Accession NM_031889). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENAM. FBJ Murine Osteosarcoma Viral Oncogene Homolog B (FOSB, Accession NM_006732) is another VGAM2007 host target gene. FOSB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FOSB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOSB BINDING SITE,

designated SEQ ID:13584, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70616] Another function of VGAM2007 is therefore inhibition of FBJ Murine Osteosarcoma Viral Oncogene Homolog B (FOSB, Accession NM_006732), a gene which interacts with jun proteins enhancing their dna binding activity. Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOSB. The function of FOSB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM747.Interleukin 1, Beta (IL1B, Accession NM_000576) is another VGAM2007 host target gene. IL1B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1B BINDING SITE, designated SEQ ID:6176, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70617] Another function of VGAM2007 is therefore inhibition of

Interleukin 1, Beta (IL1B, Accession NM_000576), a gene which stimulates thymocyte proliferation. Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1B. The function of IL1B has been established by previous studies. Interleukin-1, produced mainly by blood monocytes, mediates the panoply of host reactions collectively known as acute phase response. It is identical to endogenous pyrogen. The multiple biologic activities that define IL1 are properties of a 15- to 18-kD protein that is derived from a 30- to 35-kD precursor. El-Omar et al. (2000) reported that interleukin-1 gene cluster polymorphisms suspected of enhancing production of interleukin-1-beta are associated with an increased risk of both hypochlorhydria induced by Helicobacter pylori and gastric cancer. Two of these polymorphisms are in near-complete linkage disequilibrium, and 1 is a TATA-box polymorphism that markedly affects DNA-protein interactions in vitro. The association with disease may be explained by the biologic properties of interleukin-1-beta, which is an important proinflammatory cytokine and a powerful inhibitor of gastric acid secretion. Host genetic factors that affect interleukin-1-beta may determine why

some individuals infected with H. pylori develop gastric cancer while others do not. IL1-beta is upregulated in the presence of H. pylori and is important in initiating and amplifying the inflammatory response to this infection. Three diallelic polymorphisms in IL1B have been reported, all representing C-to-T base transitions, at positions -511, -31, and +3954 basepairs from the transcriptional start site. To determine whether these polymorphisms are important with respect to different outcomes of H. pylori infections, El-Omar et al. (2000) studied their effects on gastric physiology in healthy subjects. Carriers of the ILB -31T allele (147720.0001) had an age-adjusted odds ratio of 9.1 (95% confidence interval, 2.2-37) for low acid secretion, and there was little difference between homozygous and heterozygous carriers. The IL1B +3954 genotype was not associated with the risk of hypochlorhydria. Carriers of IL1B -31T had an increased gastric cancer risk at an odds ratio of 1.9 (95% confidence interval, 1.5-2.6), with no significant difference between homozygotes and heterozygotes Hamajima et al. (2001) determined that the C-to-T transition at position -31, creating a TATA box, is associated with vulnerability to persistent H. pylori infection, and that the susceptibility is modified by smoking

Animal model experiments lend further support to the function of IL1B. Mature IL1-beta levels are a sensitive and specific indicator of caspase-1 (OMIM Ref. No. 147678) activation. Ona et al. (1999) studied the effect of inhibition of caspase-1 on the progression of Huntington disease (OMIM Ref. No. 143100) in the mouse model developed by Mangiarini et al. (1996), which they called R6/2 mice. Ona et al. (1999) crossed R6/2 mice with a well-characterized transgenic mouse strain expressing a dominant-negative mutant of caspase-1 in the brain (NSE M17Z). Double mutant mice showed extended survival and delayed appearance of neuronal inclusions, neurotransmitter receptor alterations, and onset of symptoms, indicating that caspase-1 is important in the pathogenesis of Huntington disease. Mature IL1-beta levels in R6/2 mice were elevated to 268% of those in wildtype controls. This increase was significantly inhibited in the R6/2-NSE M17Z mice. IL1-beta levels in the brains of human patients also exhibited significant increases, to 213% of those in normal controls

[70618] It is appreciated that the abovementioned animal model for IL1B is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appre-

ciated from the publications sited hereinbelow.

[70619] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[70620] El-Omar, E. M.; Carrington, M.; Chow, W.-H.; McColl, K. E. L.; Bream, J. H.; Young, H. A.; Herrera, J.; Lissowska, J.; Yuan, C.-C.; Rothman, N.; Lanyon, G.; Martin, M.; Fraumeni, J. F., Jr.; Rabkin, C. S. : Interleukin-1 polymorphisms associated with increased risk of gastric cancer. Nature 404: 398-402, 2000. Note: Erratum: Nature 412: 99 only, 2001. ; and

[70621] Ona, V. O.; Li, M.; Vonsattel, J. P. G.; Andrews, L. J.; Khan, S. Q.; Chung, W. M.; Frey, A. S.; Menon, A. S.; Li, X.-J.; Stieg, P. E.; Yuan, J.; Penney, J. B.; Young, A. B.; Cha, J.-H.

[70622] Further studies establishing the function and utilities of IL1B are found in John Hopkins OMIM database record ID 147720, and in sited publications numbered 5261, 11182-11184, 11189-11186, 472, 11187, 11188, 4805, 11170, 1119 and 11191-11192 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Membrane Protein, Palmitoylated 2 (MAGUK p55 subfamily member 2) (MPP2, Accession XM_008355) is another VGAM2007 host target gene. MPP2 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MPP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MPP2 BINDING SITE, designated SEQ ID:30085, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70623] Another function of VGAM2007 is therefore inhibition of Membrane Protein, Palmitoylated 2 (MAGUK p55 subfamily member 2) (MPP2, Accession XM_008355). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPP2. Male-specific Lethal 3-like 1 (Drosophila) (MSL3L1, Accession NM_078628) is another VGAM2007 host target gene. MSL3L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MSL3L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MSL3L1 BINDING SITE, designated SEQ ID:27812, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4718.

[70624] Another function of VGAM2007 is therefore inhibition of Male-specific Lethal 3-like 1 (Drosophila) (MSL3L1, Accession NM_078628). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSL3L1. Mature T-cell Proliferation 1 (MTCP1, Accession NM_014221) is another VGAM2007 host target gene. MTCP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MTCP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTCP1 BINDING SITE, designated SEQ ID:15491, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70625] Another function of VGAM2007 is therefore inhibition of Mature T-cell Proliferation 1 (MTCP1, Accession NM_014221). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTCP1. SRGAP1 (Accession XM_051143) is another VGAM2007 host target gene. SRGAP1 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by SRGAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SRGAP1 BINDING SITE, designated SEQ ID:35760, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70626] Another function of VGAM2007 is therefore inhibition of SRGAP1 (Accession XM_051143). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRGAP1. C(27)-3BETA-HSD (Accession NM_025193) is another VGAM2007 host target gene. C(27)-3BETA-HSD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C(27)-3BETA-HSD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C(27)-3BETA-HSD BINDING SITE, designated SEQ ID:24850, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70627] Another function of VGAM2007 is therefore inhibition of C(27)-3BETA-HSD (Accession NM_025193). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C(27)-3BETA-HSD. DKFZp547M072 (Accession XM_028067) is another VGAM2007 host target gene. DKFZp547M072 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp547M072, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547M072 BINDING SITE, designated SEQ ID:30619, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70628] Another function of VGAM2007 is therefore inhibition of DKFZp547M072 (Accession XM_028067). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547M072. FLJ14594 (Accession NM_032808) is another VGAM2007 host target gene. FLJ14594 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14594, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14594 BINDING SITE, designated SEQ ID:26568, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70629] Another function of VGAM2007 is therefore inhibition of FLJ14594 (Accession NM_032808). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14594. FUS Interacting Protein (serine-arginine rich) 1 (FUSIP1, Accession NM_006625) is another VGAM2007 host target gene. FUSIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FUSIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FUSIP1 BINDING SITE, designated SEQ ID:13411, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70630] Another function of VGAM2007 is therefore inhibition of FUS Interacting Protein (serine-arginine rich) 1 (FUSIP1,

Accession NM_006625). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUSIP1. KIAA0193 (Accession NM_014766) is another VGAM2007 host target gene. KIAA0193 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0193, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0193 BINDING SITE, designated SEQ ID:16548, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70631] Another function of VGAM2007 is therefore inhibition of KIAA0193 (Accession NM_014766). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0193. KIAA0435 (Accession NM_014801) is another VGAM2007 host target gene. KIAA0435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0435 BINDING SITE, designated SEQ ID:16724, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70632] Another function of VGAM2007 is therefore inhibition of KIAA0435 (Accession NM_014801). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0435. KIAA1755 (Accession XM_028810) is another VGAM2007 host target gene. KIAA1755 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1755, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1755 BINDING SITE, designated SEQ ID:30753, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70633] Another function of VGAM2007 is therefore inhibition of KIAA1755 (Accession XM_028810). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1755. Lysosomal-associated Membrane Protein 3

(LAMP3, Accession XM_003022) is another VGAM2007 host target gene. LAMP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LAMP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAMP3 BINDING SITE, designated SEQ ID:29917, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70634] Another function of VGAM2007 is therefore inhibition of Lysosomal-associated Membrane Protein 3 (LAMP3, Accession XM_003022). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMP3. MacGAP (Accession NM_033515) is another VGAM2007 host target gene. MacGAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MacGAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MacGAP BINDING SITE, designated SEQ ID:27290, to the nucleotide sequence of VGAM2007 RNA,

herein designated VGAM RNA, also designated SEQ ID:4718.

[70635] Another function of VGAM2007 is therefore inhibition of MacGAP (Accession NM_033515). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Mac-GAP. MGC12217 (Accession NM_032771) is another VGAM2007 host target gene. MGC12217 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC12217, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC12217 BINDING SITE, designated SEQ ID:26518, to the nucleotide sequence of VGAM2007 RNA, herein desig-nated VGAM RNA, also designated SEQ ID:4718.

[70636] Another function of VGAM2007 is therefore inhibition of MGC12217 (Accession NM_032771). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treat-ment of diseases and clinical conditions associated with MGC12217. Protein Tyrosine Phosphatase, Receptor Type, F Polypeptide (PTPRF), Interacting Protein (liprin), Alpha 4 (PPFIA4, Accession XM_046751) is another VGAM2007

host target gene. PPFIA4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPFIA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPFIA4 BINDING SITE, designated SEQ ID:34822, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70637] Another function of VGAM2007 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, F Polypeptide (PTPRF), Interacting Protein (liprin), Alpha 4 (PPFIA4, Accession XM_046751). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPFIA4. RAB6C, Member RAS Oncogene Family (RAB6C, Accession NM_032144) is another VGAM2007 host target gene. RAB6C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB6C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB6C BINDING SITE, designated SEQ

ID:25837, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70638] Another function of VGAM2007 is therefore inhibition of RAB6C, Member RAS Oncogene Family (RAB6C, Accession NM_032144). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB6C. SARM (Accession NM_015077) is another VGAM2007 host target gene. SARM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SARM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SARM BINDING SITE, designated SEQ ID:17463, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70639] Another function of VGAM2007 is therefore inhibition of SARM (Accession NM_015077). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SARM. LOC148823 (Accession NM_145278) is another VGAM2007 host target gene. LOC148823 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148823, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148823 BINDING SITE, designated SEQ ID:29791, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70640] Another function of VGAM2007 is therefore inhibition of LOC148823 (Accession NM_145278). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148823. LOC159121 (Accession XM_099028) is another VGAM2007 host target gene. LOC159121 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC159121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159121 BINDING SITE, designated SEQ ID:42065, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70641] Another function of VGAM2007 is therefore inhibition of

LOC159121 (Accession XM_099028). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159121. LOC164955 (Accession XM_092265) is another VGAM2007 host target gene. LOC164955 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC164955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164955 BINDING SITE, designated SEQ ID:40114, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70642] Another function of VGAM2007 is therefore inhibition of LOC164955 (Accession XM_092265). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164955. LOC200269 (Accession XM_114175) is another VGAM2007 host target gene. LOC200269 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200269, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC200269 BINDING SITE, designated SEQ ID:42758, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70643] Another function of VGAM2007 is therefore inhibition of LOC200269 (Accession XM_114175). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200269. LOC200830 (Accession XM_117287) is another VGAM2007 host target gene. LOC200830 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200830, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200830 BINDING SITE, designated SEQ ID:43348, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70644] Another function of VGAM2007 is therefore inhibition of LOC200830 (Accession XM_117287). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200830. LOC256946 (Accession XM_170543) is an-

other VGAM2007 host target gene. LOC256946 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256946, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256946 BINDING SITE, designated SEQ ID:45361, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70645] Another function of VGAM2007 is therefore inhibition of LOC256946 (Accession XM_170543). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256946. LOC85414 (Accession NM_033102) is another VGAM2007 host target gene. LOC85414 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC85414, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC85414 BINDING SITE, designated SEQ ID:26949, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70646] Another function of VGAM2007 is therefore inhibition of LOC85414 (Accession NM_033102). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC85414. LOC90110 (Accession XM_029046) is another VGAM2007 host target gene. LOC90110 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90110 BINDING SITE, designated SEQ ID:30841, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70647] Another function of VGAM2007 is therefore inhibition of LOC90110 (Accession XM_029046). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90110. LOC92659 (Accession XM_046434) is another VGAM2007 host target gene. LOC92659 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92659, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92659 BINDING SITE, designated SEQ ID:34716, to the nucleotide sequence of VGAM2007 RNA, herein designated VGAM RNA, also designated SEQ ID:4718.

[70648] Another function of VGAM2007 is therefore inhibition of LOC92659 (Accession XM_046434). Accordingly, utilities of VGAM2007 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92659. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2008 (VGAM2008) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70649] VGAM2008 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2008 was detected is described hereinabove with reference to Figs. 1-8.

[70650] VGAM2008 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola Virus (REBOV). VGAM2008 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70651] VGAM2008 gene encodes a VGAM2008 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2008 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2008 precursor RNA is designated SEQ ID:1994, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1994 is located at position 11658 relative to the genome of Reston Ebola Virus (REBOV).

[70652] VGAM2008 precursor RNA folds onto itself, forming VGAM2008 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70653] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2008 folded precursor RNA into VGAM2008

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2008 RNA is designated SEQ ID:4719, and is provided hereinbelow with reference to the sequence listing part.

[70654] VGAM2008 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2008 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2008 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70655] VGAM2008 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2008 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2008 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2008 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2008 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70656] The complementary binding of VGAM2008 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2008 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2008 host target RNA into VGAM2008 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[70657] It is appreciated that VGAM2008 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2008 host target genes. The mRNA of each one of this plurality of VGAM2008 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2008 RNA, herein designated VGAM RNA, and which when bound by VGAM2008 RNA causes inhibition of translation of respective one or more VGAM2008 host target proteins.

[70658] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2008 gene, herein designated VGAM GENE, on one or more VGAM2008 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70659] It is yet further appreciated that a function of VGAM2008 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2008 include diagnosis, prevention and treatment of viral infection by Reston Ebola Virus (REBOV). Specific functions, and accordingly utilities, of VGAM2008 correlate with, and may be deduced from, the identity of the host target genes which VGAM2008 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70660] Nucleotide sequences of the VGAM2008 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2008 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2008 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2008 are further described hereinbelow with reference to Table 1.

[70661] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2008 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2008 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70662] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2008 gene, herein designated VGAM is inhibition of expression of VGAM2008 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2008 correlate with, and may be deduced from, the identity of the target genes which VGAM2008 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70663] Chromosome 8 Open Reading Frame 1 (C8orf1, Accession NM_004337) is a VGAM2008 host target gene. C8orf1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C8orf1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C8orf1 BINDING SITE, designated SEQ ID:10530, to the nucleotide sequence of VGAM2008 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4719.

[70664] A function of VGAM2008 is therefore inhibition of Chromosome 8 Open Reading Frame 1 (C8orf1, Accession NM_004337). Accordingly, utilities of VGAM2008 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf1. Synaptotagmin I (SYT1, Accession NM_005639) is another VGAM2008 host target gene. SYT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYT1 BINDING SITE, designated SEQ ID:12169, to the nucleotide sequence of VGAM2008 RNA, herein designated VGAM RNA, also designated SEQ ID:4719.

[70665] Another function of VGAM2008 is therefore inhibition of Synaptotagmin I (SYT1, Accession NM_005639), a gene which may have a regulatory role in the membrane interactions during trafficking of synaptic vesicles at the active zone of the synapse. Accordingly, utilities of VGAM2008 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT1. The function

of SYT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM739.Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273) is another VGAM2008 host target gene. CHST3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHST3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHST3 BINDING SITE, designated SEQ ID:10474, to the nucleotide sequence of VGAM2008 RNA, herein designated VGAM RNA, also designated SEQ ID:4719.

[70666] Another function of VGAM2008 is therefore inhibition of Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273). Accordingly, utilities of VGAM2008 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHST3. KIAA1055 (Accession XM_038509) is another VGAM2008 host target gene. KIAA1055 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1055, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1055 BINDING SITE, designated SEQ ID:32849, to the nucleotide sequence of VGAM2008 RNA, herein designated VGAM RNA, also designated SEQ ID:4719.

[70667] Another function of VGAM2008 is therefore inhibition of KIAA1055 (Accession XM_038509). Accordingly, utilities of VGAM2008 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1055. Syndecan 3 (N-syndecan) (SDC3, Accession NM_014654) is another VGAM2008 host target gene. SDC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SDC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDC3 BINDING SITE, designated SEQ ID:16077, to the nucleotide sequence of VGAM2008 RNA, herein designated VGAM RNA, also designated SEQ ID:4719.

[70668] Another function of VGAM2008 is therefore inhibition of Syndecan 3 (N-syndecan) (SDC3, Accession NM_014654). Accordingly, utilities of VGAM2008 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with SDC3. Zinc Finger Protein 387 (ZNF387, Accession NM_014682) is another VGAM2008 host target gene. ZNF387 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF387, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF387 BINDING SITE, designated SEQ ID:16171, to the nucleotide sequence of VGAM2008 RNA, herein designated VGAM RNA, also designated SEQ ID:4719.

[70669] Another function of VGAM2008 is therefore inhibition of Zinc Finger Protein 387 (ZNF387, Accession NM_014682). Accordingly, utilities of VGAM2008 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF387. LOC151234 (Accession XM_087136) is another VGAM2008 host target gene. LOC151234 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151234, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of LOC151234 BINDING SITE, designated SEQ ID:39078, to the nucleotide sequence of VGAM2008 RNA, herein designated VGAM RNA, also designated SEQ ID:4719.

[70670] Another function of VGAM2008 is therefore inhibition of LOC151234 (Accession XM_087136). Accordingly, utilities of VGAM2008 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151234. LOC96597 (Accession XM_039922) is another VGAM2008 host target gene. LOC96597 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC96597, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC96597 BINDING SITE, designated SEQ ID:33225, to the nucleotide sequence of VGAM2008 RNA, herein designated VGAM RNA, also designated SEQ ID:4719.

[70671] Another function of VGAM2008 is therefore inhibition of LOC96597 (Accession XM_039922). Accordingly, utilities of VGAM2008 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC96597. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2009 (VGAM2009) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70672] VGAM2009 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2009 was detected is described hereinabove with reference to Figs. 1-8.

[70673] VGAM2009 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola Virus (REBOV). VGAM2009 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70674] VGAM2009 gene encodes a VGAM2009 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2009 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2009 precursor RNA is designated SEQ ID:1995, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:1995 is located at position 12590 relative to the genome of Reston Ebola Virus (REBOV).

[70675] VGAM2009 precursor RNA folds onto itself, forming VGAM2009 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70676] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2009 folded precursor RNA into VGAM2009 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2009 RNA is designated SEQ ID:4720, and is provided hereinbelow with reference to the sequence listing part.

[70677] VGAM2009 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2009 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2009 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70678] VGAM2009 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2009 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2009 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2009 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2009 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70679] The complementary binding of VGAM2009 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2009 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2009 host target RNA into VGAM2009 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70680] It is appreciated that VGAM2009 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2009 host target genes. The mRNA of each one of this plurality of VGAM2009 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2009 RNA, herein designated VGAM RNA, and which when bound by VGAM2009 RNA causes inhibition of translation of respective one or more

VGAM2009 host target proteins.

[70681] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2009 gene, herein designated VGAM GENE, on one or more VGAM2009 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70682] It is yet further appreciated that a function of VGAM2009 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of viral infection by Reston Ebola Virus (REBOV).

Specific functions, and accordingly utilities, of VGAM2009 correlate with, and may be deduced from, the identity of the host target genes which VGAM2009 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70683] Nucleotide sequences of the VGAM2009 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2009 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2009 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2009 are further described hereinbelow with reference to Table 1.

[70684] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2009 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2009 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70685] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2009 gene, herein designated VGAM is inhibition of expression of VGAM2009 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2009 correlate with, and may be deduced from, the identity of the target genes which VGAM2009 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70686] Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 1 (p85 alpha) (PIK3R1, Accession XM_043865) is a VGAM2009 host target gene. PIK3R1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIK3R1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIK3R1 BINDING SITE, designated SEQ ID:34039, to the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, also designated SEQ ID:4720.

[70687] A function of VGAM2009 is therefore inhibition of Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 1 (p85 alpha) (PIK3R1, Accession XM_043865), a gene which acts as an adapter, for the insulin-stimulated increase in glucose uptake and glycogen synthesis. Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3R1. The function of PIK3R1 and its association

with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM826.Suppression of Tumorigenicity 7 (ST7, Accession NM_013437) is another VGAM2009 host target gene. ST7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ST7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ST7 BINDING SITE, designated SEQ ID:15099, to the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, also designated SEQ ID:4720.

[70688] Another function of VGAM2009 is therefore inhibition of Suppression of Tumorigenicity 7 (ST7, Accession NM_013437), a gene which has a role in regulating cell-environment or cell-cell interactions. Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ST7. The function of ST7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM107.Supervillin (SVIL, Accession NM_003174) is another VGAM2009 host target gene. SVIL BINDING SITE1

and SVIL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SVIL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SVIL BINDING SITE1 and SVIL BINDING SITE2, designated SEQ ID:9151 and SEQ ID:22348 respectively, to the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, also designated SEQ ID:4720.

[70689] Another function of VGAM2009 is therefore inhibition of Supervillin (SVIL, Accession NM_003174), a gene which binds actin, links filamentous actin with the plasma membrane; and contains putative nuclear localization signals. Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SVIL. The function of SVIL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1459.GNB4 (Accession NM_021629) is another VGAM2009 host target gene. GNB4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNB4, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNB4 BINDING SITE, designated SEQ ID:22269, to the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, also designated SEQ ID:4720.

[70690] Another function of VGAM2009 is therefore inhibition of GNB4 (Accession NM_021629). Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNB4. KIAA0530 (Accession XM_048070) is another VGAM2009 host target gene. KIAA0530 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0530, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0530 BINDING SITE, designated SEQ ID:35099, to the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, also designated SEQ ID:4720.

[70691] Another function of VGAM2009 is therefore inhibition of KIAA0530 (Accession XM_048070). Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0530. KIAA1265 (Accession XM_047707) is another VGAM2009 host target gene. KIAA1265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1265 BINDING SITE, designated SEQ ID:35032, to the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, also designated SEQ ID:4720.

[70692] Another function of VGAM2009 is therefore inhibition of KIAA1265 (Accession XM_047707). Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1265. Testis-specific Transcript, Y-linked 9 (TTTY9, Accession NM_031927) is another VGAM2009 host target gene. TTTY9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TTTY9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTTY9 BINDING SITE, designated SEQ ID:25677, to the nucleotide sequence of VGAM2009 RNA,

herein designated VGAM RNA, also designated SEQ ID:4720.

[70693] Another function of VGAM2009 is therefore inhibition of Testis-specific Transcript, Y-linked 9 (TTTY9, Accession NM_031927). Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTTY9. LOC120856 (Accession XM_058509) is another VGAM2009 host target gene. LOC120856 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120856, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120856 BINDING SITE, designated SEQ ID:36634, to the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, also designated SEQ ID:4720.

[70694] Another function of VGAM2009 is therefore inhibition of LOC120856 (Accession XM_058509). Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120856. LOC157278 (Accession XM_098741) is another VGAM2009 host target gene. LOC157278 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157278, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157278 BINDING SITE, designated SEQ ID:41777, to the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, also designated SEQ ID:4720.

[70695] Another function of VGAM2009 is therefore inhibition of LOC157278 (Accession XM_098741). Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157278. LOC221962 (Accession XM_166554) is another VGAM2009 host target gene. LOC221962 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221962, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221962 BINDING SITE, designated SEQ ID:44528, to the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, also designated SEQ ID:4720.

[70696] Another function of VGAM2009 is therefore inhibition of

LOC221962 (Accession XM_166554). Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221962. LOC255461 (Accession XM_173207) is another VGAM2009 host target gene. LOC255461 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255461, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255461 BINDING SITE, designated SEQ ID:46463, to the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, also designated SEQ ID:4720.

[70697] Another function of VGAM2009 is therefore inhibition of LOC255461 (Accession XM_173207). Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255461. LOC255516 (Accession XM_173212) is another VGAM2009 host target gene. LOC255516 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC255516 BINDING SITE, designated SEQ ID:46469, to the nucleotide sequence of VGAM2009 RNA, herein designated VGAM RNA, also designated SEQ ID:4720.

[70698] Another function of VGAM2009 is therefore inhibition of LOC255516 (Accession XM_173212). Accordingly, utilities of VGAM2009 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255516. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2010 (VGAM2010) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70699] VGAM2010 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2010 was detected is described hereinabove with reference to Figs. 1-8.

[70700] VGAM2010 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola Virus (REBOV). VGAM2010 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in

the human genome.

[70701] VGAM2010 gene encodes a VGAM2010 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2010 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2010 precursor RNA is designated SEQ ID:1996, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1996 is located at position 17622 relative to the genome of Reston Ebola Virus (REBOV).

[70702] VGAM2010 precursor RNA folds onto itself, forming VGAM2010 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70703] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2010 folded precursor RNA into VGAM2010 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM2010 RNA is designated SEQ ID:4721, and is provided hereinbelow with reference to the sequence listing part.

[70704] VGAM2010 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2010 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2010 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70705] VGAM2010 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2010 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2010 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2010 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2010 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70706] The complementary binding of VGAM2010 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2010 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2010 host target RNA into VGAM2010 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70707] It is appreciated that VGAM2010 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2010 host target genes. The mRNA of each one of this plurality of VGAM2010 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2010 RNA, herein designated VGAM RNA, and which when bound by VGAM2010 RNA causes inhibition of translation of respective one or more VGAM2010 host target proteins.

[70708] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2010 gene, herein designated VGAM GENE, on one or more VGAM2010 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70709] It is yet further appreciated that a function of VGAM2010 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2010 include diagnosis, prevention and treatment of viral infection by Reston Ebola Virus (REBOV). Specific functions, and accordingly utilities, of VGAM2010 correlate with, and may be deduced from, the identity of the host target genes which VGAM2010 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70710] Nucleotide sequences of the VGAM2010 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2010 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2010 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2010 are further described hereinbelow with reference to Table 1.

[70711] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2010 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2010 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70712] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2010 gene, herein designated VGAM is inhibition of expression of VGAM2010 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2010 correlate with, and may be deduced from, the identity of the target genes which VGAM2010 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70713] Complement Component (3b/4b) Receptor 1, Including Knops Blood Group System (CR1, Accession NM_000573) is a VGAM2010 host target gene. CR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CR1 BINDING SITE, designated SEQ ID:6173, to the nucleotide sequence of VGAM2010 RNA, herein designated VGAM RNA, also

designated SEQ ID:4721.

[70714] A function of VGAM2010 is therefore inhibition of Complement Component (3b/4b) Receptor 1, Including Knops Blood Group System (CR1, Accession NM_000573). Accordingly, utilities of VGAM2010 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CR1. Interleukin-1 Receptor-associated Kinase 1 (IRAK1, Accession NM_001569) is another VGAM2010 host target gene. IRAK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IRAK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRAK1 BINDING SITE, designated SEQ ID:7299, to the nucleotide sequence of VGAM2010 RNA, herein designated VGAM RNA, also designated SEQ ID:4721.

[70715] Another function of VGAM2010 is therefore inhibition of Interleukin-1 Receptor-associated Kinase 1 (IRAK1, Accession NM_001569). Accordingly, utilities of VGAM2010 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRAK1. DKFZp547I014 (Accession NM_020217) is another

VGAM2010 host target gene. DKFZp547I014 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp547I014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547I014 BINDING SITE, designated SEQ ID:21470, to the nucleotide sequence of VGAM2010 RNA, herein designated VGAM RNA, also designated SEQ ID:4721.

[70716] Another function of VGAM2010 is therefore inhibition of DKFZp547I014 (Accession NM_020217). Accordingly, utilities of VGAM2010 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547I014. Erythroblast Membrane-associated Protein (ERMAP, Accession NM_018538) is another VGAM2010 host target gene. ERMAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERMAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERMAP BINDING SITE, designated SEQ ID:20605, to the nucleotide sequence of VGAM2010 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4721.

[70717] Another function of VGAM2010 is therefore inhibition of Erythroblast Membrane-associated Protein (ERMAP, Accession NM_018538). Accordingly, utilities of VGAM2010 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERMAP. KIAA0527 (Accession XM_171054) is another VGAM2010 host target gene. KIAA0527 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0527, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0527 BINDING SITE, designated SEQ ID:45849, to the nucleotide sequence of VGAM2010 RNA, herein designated VGAM RNA, also designated SEQ ID:4721.

[70718] Another function of VGAM2010 is therefore inhibition of KIAA0527 (Accession XM_171054). Accordingly, utilities of VGAM2010 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0527. Rab11-FIP2 (Accession NM_014904) is another VGAM2010 host target gene. Rab11-FIP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by Rab11-FIP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rab11-FIP2 BINDING SITE, designated SEQ ID:17096, to the nucleotide sequence of VGAM2010 RNA, herein designated VGAM RNA, also designated SEQ ID:4721.

[70719] Another function of VGAM2010 is therefore inhibition of Rab11-FIP2 (Accession NM_014904). Accordingly, utilities of VGAM2010 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Rab11-FIP2. RING1 and YY1 Binding Protein (RYBP, Accession XM_002853) is another VGAM2010 host target gene. RYBP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RYBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RYBP BINDING SITE, designated SEQ ID:29908, to the nucleotide sequence of VGAM2010 RNA, herein designated VGAM RNA, also designated SEQ ID:4721.

[70720] Another function of VGAM2010 is therefore inhibition of RING1 and YY1 Binding Protein (RYBP, Accession

XM_002853). Accordingly, utilities of VGAM2010 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RYBP. LOC221035 (Accession XM_167640) is another VGAM2010 host target gene. LOC221035 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221035, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221035 BINDING SITE, designated SEQ ID:44744, to the nucleotide sequence of VGAM2010 RNA, herein designated VGAM RNA, also designated SEQ ID:4721.

[70721] Another function of VGAM2010 is therefore inhibition of LOC221035 (Accession XM_167640). Accordingly, utilities of VGAM2010 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221035. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2011 (VGAM2011) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[70722] VGAM2011 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2011 was detected is described hereinabove with reference to Figs. 1-8.

[70723] VGAM2011 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola Virus (REBOV). VGAM2011 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70724] VGAM2011 gene encodes a VGAM2011 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2011 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2011 precursor RNA is designated SEQ ID:1997, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1997 is located at position 4098 relative to the genome of Reston Ebola Virus (REBOV).

[70725] VGAM2011 precursor RNA folds onto itself, forming VGAM2011 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70726] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2011 folded precursor RNA into VGAM2011 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2011 RNA is designated SEQ ID:4722, and is provided hereinbelow with reference to the sequence listing part.

[70727] VGAM2011 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2011 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2011 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70728] VGAM2011 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2011 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2011 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2011 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2011 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[70729] The complementary binding of VGAM2011 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2011 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2011 host target RNA into VGAM2011 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70730] It is appreciated that VGAM2011 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2011 host target genes. The mRNA of each one of this plurality of VGAM2011 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2011 RNA, herein designated VGAM RNA, and which when bound by VGAM2011 RNA causes inhibition of translation of respective one or more VGAM2011 host target proteins.

[70731] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2011 gene, herein designated VGAM GENE, on one

or more VGAM2011 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70732] It is yet further appreciated that a function of VGAM2011 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of viral infection by Reston Ebola Virus (REBOV). Specific functions, and accordingly utilities, of VGAM2011 correlate with, and may be deduced from, the identity of the host target genes which VGAM2011 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70733] Nucleotide sequences of the VGAM2011 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2011 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2011 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2011 are further described hereinbelow with reference to Table 1.

[70734] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2011 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2011 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70735] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2011 gene, herein designated VGAM is inhibition of expression of VGAM2011 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2011 correlate with, and may be deduced from, the identity of the target genes which VGAM2011 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70736] Cold Shock Domain Protein A (CSDA, Accession

NM_003651) is a VGAM2011 host target gene. CSDA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSDA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSDA BINDING SITE, designated SEQ ID:9728, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70737] A function of VGAM2011 is therefore inhibition of Cold Shock Domain Protein A (CSDA, Accession NM_003651), a gene which binds to the gm-csf promoter and seems to act as a repressor. Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSDA. The function of CSDA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1615.Leucine-zipper-like Transcriptional Regulator, 1 (LZTR1, Accession NM_006767) is another VGAM2011 host target gene. LZTR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LZTR1, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LZTR1 BINDING SITE, designated SEQ ID:13636, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70738] Another function of VGAM2011 is therefore inhibition of Leucine-zipper-like Transcriptional Regulator, 1 (LZTR1, Accession NM_006767). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LZTR1. SORCS2 (Accession NM_020777) is another VGAM2011 host target gene. SORCS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SORCS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SORCS2 BINDING SITE, designated SEQ ID:21872, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70739] Another function of VGAM2011 is therefore inhibition of SORCS2 (Accession NM_020777). Accordingly, utilities of

VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SORCS2. KIAA1922 (Accession XM_057040) is another VGAM2011 host target gene. KIAA1922 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1922, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1922 BINDING SITE, designated SEQ ID:36456, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70740] Another function of VGAM2011 is therefore inhibition of KIAA1922 (Accession XM_057040). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1922. MGC19556 (Accession NM_033551) is another VGAM2011 host target gene. MGC19556 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC19556, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

MGC19556 BINDING SITE, designated SEQ ID:27315, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70741] Another function of VGAM2011 is therefore inhibition of MGC19556 (Accession NM_033551). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC19556. NY-REN-25 (Accession XM_027116) is another VGAM2011 host target gene. NY-REN-25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NY-REN-25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NY-REN-25 BINDING SITE, designated SEQ ID:30415, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70742] Another function of VGAM2011 is therefore inhibition of NY-REN-25 (Accession XM_027116). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NY-REN-25. PF1 (Accession XM_170828) is another VGAM2011 host target gene. PF1 BINDING SITE is HOST

TARGET binding site found in the 5` untranslated region of mRNA encoded by PF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PF1 BINDING SITE, designated SEQ ID:45603, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70743] Another function of VGAM2011 is therefore inhibition of PF1 (Accession XM_170828). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PF1. SARM (Accession NM_015077) is another VGAM2011 host target gene. SARM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SARM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SARM BINDING SITE, designated SEQ ID:17459, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70744] Another function of VGAM2011 is therefore inhibition of

SARM (Accession NM_015077). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SARM. SCAMP-4 (Accession NM_079834) is another VGAM2011 host target gene. SCAMP-4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCAMP-4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAMP-4 BINDING SITE, designated SEQ ID:27820, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70745] Another function of VGAM2011 is therefore inhibition of SCAMP-4 (Accession NM_079834). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP-4. WIT-1 (Accession NM_015855) is another VGAM2011 host target gene. WIT-1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by WIT-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of WIT-1 BINDING SITE, designated SEQ ID:17989, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70746] Another function of VGAM2011 is therefore inhibition of WIT-1 (Accession NM_015855). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WIT-1. LOC149271 (Accession XM_086475) is another VGAM2011 host target gene. LOC149271 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149271 BINDING SITE, designated SEQ ID:38673, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70747] Another function of VGAM2011 is therefore inhibition of LOC149271 (Accession XM_086475). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149271. LOC221288 (Accession XM_168058) is an-

other VGAM2011 host target gene. LOC221288 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221288 BINDING SITE, designated SEQ ID:44967, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70748] Another function of VGAM2011 is therefore inhibition of LOC221288 (Accession XM_168058). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221288. LOC255299 (Accession XM_173564) is another VGAM2011 host target gene. LOC255299 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255299, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255299 BINDING SITE, designated SEQ ID:46548, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70749] Another function of VGAM2011 is therefore inhibition of LOC255299 (Accession XM_173564). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255299. LOC90092 (Accession XM_028862) is another VGAM2011 host target gene. LOC90092 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90092 BINDING SITE, designated SEQ ID:30788, to the nucleotide sequence of VGAM2011 RNA, herein designated VGAM RNA, also designated SEQ ID:4722.

[70750] Another function of VGAM2011 is therefore inhibition of LOC90092 (Accession XM_028862). Accordingly, utilities of VGAM2011 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90092. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2012 (VGAM2012) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[70751] VGAM2012 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2012 was detected is described hereinabove with reference to Figs. 1-8.

[70752] VGAM2012 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola Virus (REBOV). VGAM2012 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70753] VGAM2012 gene encodes a VGAM2012 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2012 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2012 precursor RNA is designated SEQ ID:1998, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1998 is located at position 16890 relative to the genome of Reston Ebola Virus (REBOV).

[70754] VGAM2012 precursor RNA folds onto itself, forming VGAM2012 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70755] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2012 folded precursor RNA into VGAM2012 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2012 RNA is designated SEQ ID:4723, and is provided hereinbelow with reference to the sequence listing part.

[70756] VGAM2012 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2012 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2012 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70757] VGAM2012 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2012 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2012 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2012 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2012 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70758] The complementary binding of VGAM2012 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2012 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2012 host target RNA into VGAM2012 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70759] It is appreciated that VGAM2012 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2012 host target genes. The mRNA of each one of this plurality of VGAM2012 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2012 RNA, herein designated VGAM RNA, and which when bound by VGAM2012 RNA causes inhibition of translation of respective one or more VGAM2012 host target proteins.

[70760] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2012 gene, herein designated VGAM GENE, on one or more VGAM2012 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70761] It is yet further appreciated that a function of VGAM2012 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2012 include diagnosis, prevention and treatment of viral infection by Reston Ebola Virus (REBOV). Specific functions, and accordingly utilities, of VGAM2012 correlate with, and may be deduced from, the identity of the host target genes which VGAM2012 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[70762] Nucleotide sequences of the VGAM2012 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2012 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2012 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2012 are further described hereinbelow with reference to Table 1.

[70763] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2012 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2012 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70764] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2012 gene, herein designated VGAM is inhibition of expression of VGAM2012 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2012 correlate with, and may be deduced from, the identity of the target genes which VGAM2012 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70765] Beclin 1 (coiled-coil, myosin-like BCL2 interacting protein) (BECN1, Accession NM_003766) is a VGAM2012 host target gene. BECN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BECN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BECN1 BINDING SITE, designated SEQ ID:9844, to the nucleotide sequence of VGAM2012 RNA, herein designated VGAM RNA, also designated SEQ ID:4723.

[70766] A function of VGAM2012 is therefore inhibition of Beclin 1 (coiled-coil, myosin-like BCL2 interacting protein) (BECN1, Accession NM_003766), a gene which protects cell from viral-induced apoptosis. Accordingly, utilities of VGAM2012 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BECN1. The function of BECN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1246.Dmx-like 1 (DMXL1, Accession NM_005509) is another VGAM2012 host target gene. DMXL1 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by DMXL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DMXL1 BINDING SITE, designated SEQ ID:12023, to the nucleotide sequence of VGAM2012 RNA, herein designated VGAM RNA, also designated SEQ ID:4723.

[70767] Another function of VGAM2012 is therefore inhibition of Dmx-like 1 (DMXL1, Accession NM_005509). Accordingly, utilities of VGAM2012 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMXL1. Nuclear Transcription Factor Y, Gamma (NFYC, Accession NM_014223) is another VGAM2012 host target gene. NFYC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NFYC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFYC BINDING SITE, designated SEQ ID:15493, to the nucleotide sequence of VGAM2012 RNA, herein designated VGAM RNA, also designated SEQ ID:4723.

[70768] Another function of VGAM2012 is therefore inhibition of Nuclear Transcription Factor Y, Gamma (NFYC, Accession NM_014223). Accordingly, utilities of VGAM2012 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFYC. Plastin 3 (T isoform) (PLS3, Accession NM_005032) is another VGAM2012 host target gene. PLS3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLS3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLS3 BINDING SITE, designated SEQ ID:11471, to the nucleotide sequence of VGAM2012 RNA, herein designated VGAM RNA, also designated SEQ ID:4723.

[70769] Another function of VGAM2012 is therefore inhibition of Plastin 3 (T isoform) (PLS3, Accession NM_005032), a gene which binds actin. Accordingly, utilities of VGAM2012 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLS3. The function of PLS3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM1754.Protein Tyrosine Phosphatase, Receptor Type, J (PTPRJ, Accession NM_002843) is another VGAM2012 host target gene. PTPRJ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPRJ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRJ BINDING SITE, designated SEQ ID:8730, to the nucleotide sequence of VGAM2012 RNA, herein designated VGAM RNA, also designated SEQ ID:4723.

[70770] Another function of VGAM2012 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, J (PTPRJ, Accession NM_002843), a gene which Receptor-type protein tyrosine phosphatase J. Accordingly, utilities of VGAM2012 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRJ. The function of PTPRJ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM552.JDD1 (Accession XM_032515) is another VGAM2012 host target gene. JDD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by JDD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JDD1 BINDING SITE, designated SEQ ID:31666, to the nucleotide sequence of VGAM2012 RNA, herein designated VGAM RNA, also designated SEQ ID:4723.

[70771] Another function of VGAM2012 is therefore inhibition of JDD1 (Accession XM_032515). Accordingly, utilities of VGAM2012 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JDD1. KIAA1878 (Accession XM_166256) is another VGAM2012 host target gene. KIAA1878 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1878, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1878 BINDING SITE, designated SEQ ID:44077, to the nucleotide sequence of VGAM2012 RNA, herein designated VGAM RNA, also designated SEQ ID:4723.

[70772] Another function of VGAM2012 is therefore inhibition of KIAA1878 (Accession XM_166256). Accordingly, utilities

of VGAM2012 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1878. LOC157867 (Accession XM_098831) is another VGAM2012 host target gene. LOC157867 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157867, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157867 BINDING SITE, designated SEQ ID:41854, to the nucleotide sequence of VGAM2012 RNA, herein designated VGAM RNA, also designated SEQ ID:4723.

[70773] Another function of VGAM2012 is therefore inhibition of LOC157867 (Accession XM_098831). Accordingly, utilities of VGAM2012 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157867. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2013 (VGAM2013) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70774] VGAM2013 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2013 was detected is described hereinabove with reference to Figs. 1-8.

[70775] VGAM2013 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola Virus (REBOV). VGAM2013 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70776] VGAM2013 gene encodes a VGAM2013 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2013 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2013 precursor RNA is designated SEQ ID:1999, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:1999 is located at position 12733 relative to the genome of Reston Ebola Virus (REBOV).

[70777] VGAM2013 precursor RNA folds onto itself, forming VGAM2013 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70778] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2013 folded precursor RNA into VGAM2013 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2013 RNA is designated SEQ ID:4724, and is provided hereinbelow with reference to the sequence listing part.

[70779] VGAM2013 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2013 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2013 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[70780] VGAM2013 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2013 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2013 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2013 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2013 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70781] The complementary binding of VGAM2013 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2013 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2013 host target RNA into VGAM2013 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70782] It is appreciated that VGAM2013 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2013 host target genes. The mRNA of each one of this plurality of VGAM2013 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2013 RNA, herein designated VGAM RNA, and which when bound by VGAM2013 RNA causes inhibition of translation of respective one or more VGAM2013 host target proteins.

[70783] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2013 gene, herein designated VGAM GENE, on one or more VGAM2013 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70784] It is yet further appreciated that a function of VGAM2013 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2013 include diagnosis, prevention and treatment of viral infection by Reston Ebola Virus (REBOV). Specific functions, and accordingly utilities, of VGAM2013 correlate with, and may be deduced from, the identity of the host target genes which VGAM2013 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70785] Nucleotide sequences of the VGAM2013 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2013 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2013 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2013 are further described hereinbelow with reference to Table 1.

[70786] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2013 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2013 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70787] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2013 gene, herein designated VGAM is inhibition of expression of VGAM2013 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2013 correlate with, and may be deduced from, the identity of the target genes which VGAM2013 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70788] Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858) is a VGAM2013 host target gene. COL19A1

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL19A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL19A1 BINDING SITE, designated SEQ ID:7593, to the nucleotide sequence of VGAM2013 RNA, herein designated VGAM RNA, also designated SEQ ID:4724.

[70789] A function of VGAM2013 is therefore inhibition of Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858), a gene which may act as a cross-bridge between fibrils and other extracellular matrix molecules. Accordingly, utilities of VGAM2013 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL19A1. The function of COL19A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM19.Filamin B, Beta (actin binding protein 278) (FLNB, Accession XM_030806) is another VGAM2013 host target gene. FLNB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLNB BINDING SITE, designated SEQ ID:31145, to the nucleotide sequence of VGAM2013 RNA, herein designated VGAM RNA, also designated SEQ ID:4724.

[70790] Another function of VGAM2013 is therefore inhibition of Filamin B, Beta (actin binding protein 278) (FLNB, Accession XM_030806), a gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. Accordingly, utilities of VGAM2013 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLNB. The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM416.FLJ23322 (Accession XM_114207) is another VGAM2013 host target gene. FLJ23322 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23322, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23322 BINDING SITE, designated SEQ

ID:42799, to the nucleotide sequence of VGAM2013 RNA, herein designated VGAM RNA, also designated SEQ ID:4724.

[70791] Another function of VGAM2013 is therefore inhibition of FLJ23322 (Accession XM_114207). Accordingly, utilities of VGAM2013 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23322. KIAA1317 (Accession XM_098368) is another VGAM2013 host target gene. KIAA1317 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1317, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1317 BINDING SITE, designated SEQ ID:41622, to the nucleotide sequence of VGAM2013 RNA, herein designated VGAM RNA, also designated SEQ ID:4724.

[70792] Another function of VGAM2013 is therefore inhibition of KIAA1317 (Accession XM_098368). Accordingly, utilities of VGAM2013 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1317. Testis-specific Transcript, Y-linked 9 (TTTY9, Accession NM_031927) is another VGAM2013 host target

gene. TTTY9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TTTY9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTTY9 BINDING SITE, designated SEQ ID:25676, to the nucleotide sequence of VGAM2013 RNA, herein designated VGAM RNA, also designated SEQ ID:4724.

[70793] Another function of VGAM2013 is therefore inhibition of Testis-specific Transcript, Y-linked 9 (TTTY9, Accession NM_031927). Accordingly, utilities of VGAM2013 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTTY9. LOC146287 (Accession XM_096967) is another VGAM2013 host target gene. LOC146287 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146287, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146287 BINDING SITE, designated SEQ ID:40688, to the nucleotide sequence of VGAM2013 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4724.

[70794] Another function of VGAM2013 is therefore inhibition of LOC146287 (Accession XM_096967). Accordingly, utilities of VGAM2013 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146287. LOC253039 (Accession XM_171203) is another VGAM2013 host target gene. LOC253039 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253039, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253039 BINDING SITE, designated SEQ ID:45992, to the nucleotide sequence of VGAM2013 RNA, herein designated VGAM RNA, also designated SEQ ID:4724.

[70795] Another function of VGAM2013 is therefore inhibition of LOC253039 (Accession XM_171203). Accordingly, utilities of VGAM2013 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253039. LOC257235 (Accession XM_173124) is another VGAM2013 host target gene. LOC257235 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257235, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257235 BINDING SITE, designated SEQ ID:46371, to the nucleotide sequence of VGAM2013 RNA, herein designated VGAM RNA, also designated SEQ ID:4724.

[70796] Another function of VGAM2013 is therefore inhibition of LOC257235 (Accession XM_173124). Accordingly, utilities of VGAM2013 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257235. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2014 (VGAM2014) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70797] VGAM2014 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2014 was detected is described hereinabove with reference to Figs. 1-8.

[70798] VGAM2014 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Reston Ebola Virus

(REBOV). VGAM2014 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70799] VGAM2014 gene encodes a VGAM2014 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2014 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2014 precursor RNA is designated SEQ ID:2000, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2000 is located at position 13026 relative to the genome of Reston Ebola Virus (REBOV).

[70800] VGAM2014 precursor RNA folds onto itself, forming VGAM2014 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70801] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2014 folded precursor RNA into VGAM2014 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2014 RNA is designated SEQ ID:4725, and is provided hereinbelow with reference to the sequence listing part.

[70802] VGAM2014 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2014 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2014 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70803] VGAM2014 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2014 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2014 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2014 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2014 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70804] The complementary binding of VGAM2014 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2014 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2014 host target RNA into VGAM2014 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70805] It is appreciated that VGAM2014 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2014 host target genes. The mRNA of each one of this plurality of VGAM2014 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2014 RNA, herein designated VGAM RNA, and which when bound by VGAM2014 RNA causes inhibition of translation of respective one or more VGAM2014 host target proteins.

[70806] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2014 gene, herein designated VGAM GENE, on one or more VGAM2014 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70807] It is yet further appreciated that a function of VGAM2014 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of viral infection by Reston Ebola Virus (REBOV). Specific functions, and accordingly utilities, of VGAM2014 correlate with, and may be deduced from, the identity of the host target genes which VGAM2014 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70808] Nucleotide sequences of the VGAM2014 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2014 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2014 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2014 are further described hereinbelow with reference to Table 1.

[70809] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2014 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2014 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70810] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2014 gene, herein designated VGAM is inhibition of expression of VGAM2014 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2014 correlate with, and may be deduced from, the identity of the target genes which VGAM2014 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70811] ATPase, Ca++ Transporting, Plasma Membrane 2 (ATP2B2, Accession NM_001683) is a VGAM2014 host target gene. ATP2B2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP2B2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP2B2 BINDING SITE, designated SEQ

ID:7405, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70812] A function of VGAM2014 is therefore inhibition of ATPase, Ca++ Transporting, Plasma Membrane 2 (ATP2B2, Accession NM_001683), a gene which catalyzes the hydrolysis of ATP coupled with the transport of the calcium out of the cell . Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP2B2. The function of ATP2B2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM711.Ceroid-lipofuscinosis, Neuronal 5 (CLN5, Accession NM_006493) is another VGAM2014 host target gene. CLN5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CLN5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLN5 BINDING SITE, designated SEQ ID:13232, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70813] Another function of VGAM2014 is therefore inhibition of Ceroid-lipofuscinosis, Neuronal 5 (CLN5, Accession NM_006493). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLN5. Cathepsin B (CTSB, Accession XM_035662) is another VGAM2014 host target gene. CTSB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CTSB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTSB BINDING SITE, designated SEQ ID:32329, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70814] Another function of VGAM2014 is therefore inhibition of Cathepsin B (CTSB, Accession XM_035662). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSB. Engrailed Homolog 1 (EN1, Accession NM_001426) is another VGAM2014 host target gene. EN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EN1, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EN1 BINDING SITE, designated SEQ ID:7142, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70815] Another function of VGAM2014 is therefore inhibition of Engrailed Homolog 1 (EN1, Accession NM_001426), a gene which is a member of the homeodomain family of DNA binding proteins; may regulate gene expression, morphogenesis, and differentiation;. Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EN1. The function of EN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1615.Potassium Voltage-gated Channel, Shaker-related Subfamily, Member 6 (KCNA6, Accession NM_002235) is another VGAM2014 host target gene. KCNA6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of KCNA6 BINDING SITE, designated SEQ ID:8019, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70816] Another function of VGAM2014 is therefore inhibition of Potassium Voltage-gated Channel, Shaker-related Subfamily, Member 6 (KCNA6, Accession NM_002235), a gene which mediates the voltage-dependent potassium ion permeability of excitable membranes. Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNA6. The function of KCNA6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM893.Ryanodine Receptor 3 (RYR3, Accession NM_001036) is another VGAM2014 host target gene. RYR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RYR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RYR3 BINDING SITE, designated SEQ ID:6701, to the nucleotide sequence of VGAM2014 RNA, herein

designated VGAM RNA, also designated SEQ ID:4725.

[70817] Another function of VGAM2014 is therefore inhibition of Ryanodine Receptor 3 (RYR3, Accession NM_001036), a gene which is involved in communication between transverse-tubules and sarcoplasmic reticulum. Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RYR3. The function of RYR3 has been established by previous studies. Ryanodine receptors are intracellular calcium ion release channels responsible for the release of Ca(2+) from intracellular stores following transduction of many different extracellular stimuli. Hakamata et al. (1992) deduced the complete amino acid sequence of a novel ryanodine receptor/calcium release channel from rabbit brain by cloning and sequence analysis of the cDNA. The protein was composed of 4,872 amino acids and shared characteristic structural features with the skeletal muscle (RYR1; 180901) and cardiac (RYR2; 180902) ryanodine receptors. RNA blot hybridization analysis showed that the brain ryanodine receptor is abundantly expressed in corpus striatum, thalamus, and hippocampus, whereas the cardiac ryanodine receptor is more uniformly expressed in the brain. The brain ryan-

odine receptor gene was also transcribed in smooth muscle. Leeb and Brenig (1998) isolated overlapping human RYR3 clones from a random primed fetal brain cDNA library. The gene encodes a 4,870-amino acid polypeptide that contains 4 RYR repeats, 3 SPRY domains, an ATP/GTP binding site consensus sequence, and 3 potential calmodulin-binding sites. They identified an alternatively spliced transcript that encodes a truncated protein. By isotopic in situ hybridization, Sorrentino et al. (1993) mapped the RYR3 gene to 15q14-q15; 15q15 is a probable location. By in situ hybridization, Mattei et al. (1994) mapped the type 3 ryanodine receptor to mouse chromosome 2E5-2F3. Richard et al. (1994) presented an integrated physical, expression, and genetic map of chromosome 15. They found that the RYR3 gene fell in their region I: 15pter-q14 Animal model experiments lend further support to the function of RYR3. Takeshima et al. (1996), Bertocchini et al. (1997), and Futatsugi et al. (1999) independently generated Ryr3-deficient mice. In all cases, the homozygous mutant mice were fertile and displayed no gross abnormalities. Takeshima et al. (1996) detected increased locomotor activity in Ryr3 knockout mice compared to that of the control mice and concluded that the

lack of Ryr3-mediated Ca(2+) signaling results in abnormalities of certain neurons in the central nervous system. Bertocchini et al. (1997) detected normal Ryr3 expression in murine skeletal muscles during the postnatal phase of muscle development, but not in muscles of adult mice, with the exception of the diaphragm and soleus muscles. The authors demonstrated that skeletal muscle contraction in Ryr3 knockout mice was impaired during the first weeks after birth. They concluded that Ryr3 has a physiologic role in excitation-contraction coupling of neonatal skeletal muscles. Futatsugi et al. (1999) measured the electrophysiologic and pharmacologic properties of synaptic plasticity in the CA1 area of Ryr3-deficient mice. The results suggested that Ryr3-mediated intracellular calcium release from endoplasmic reticulum may inhibit hippocampal LTP and spatial learning. Barone et al. (1998) generated double mutant mice carrying a targeted disruption of both the Ryr1 and Ryr3 genes. Skeletal muscles from mice homozygous for both mutations did not contract in response to caffeine or ryanodine. In addition, these muscles showed very low tension when directly activated with micromolar ionized calcium after membrane permeabilization, indicating either poor development or

degeneration of the myofibrils. This was confirmed by biochemical analysis of contractile proteins. Electron microscopy confirmed small size of myofibrils and showed complete absence of feet (RyRs) in the junctional sarcoplasmic reticulum.

[70818] It is appreciated that the abovementioned animal model for RYR3 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[70819] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[70820] Bertocchini, F.; Ovitt, C. E.; Conti, A.; Barone, V.; Scholer, H. R.; Bottinelli, R.; Reggiani, C.; Sorrentino, V. : Requirement for the ryanodine receptor type 3 for efficient contraction in neonatal skeletal muscles. EMBO J. 16: 6956-6963, 1997. ; and

[70821] Futatsugi, A.; Kato, K.; Ogura, H.; Li, S.-T.; Nagata, E.; Kuwajima, G.; Tanaka, K.; Itohara, S.; Mikoshiba, K. : Facilitation of NMDAR-independent LTP and spatial learning in mutant mic.

[70822] Further studies establishing the function and utilities of RYR3 are found in John Hopkins OMIM database record ID

180903, and in sited publications numbered 10477-10276, 1027 and 10277-10278 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Transmembrane Protein 2 (TMEM2, Accession NM_013390) is another VGAM2014 host target gene. TMEM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TMEM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMEM2 BINDING SITE, designated SEQ ID:15043, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70823] Another function of VGAM2014 is therefore inhibition of Transmembrane Protein 2 (TMEM2, Accession NM_013390). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMEM2. Tumor Necrosis Factor Receptor Superfamily, Member 9 (TNFRSF9, Accession NM_001561) is another VGAM2014 host target gene. TNFRSF9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TN-

FRSF9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFRSF9 BINDING SITE, designated SEQ ID:7290, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70824] Another function of VGAM2014 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 9 (TNFRSF9, Accession NM_001561), a gene which inhibits proliferation of activated T lymphocytes. Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF9. The function of TNFRSF9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1954.Chromosome 20 Open Reading Frame 29 (C20orf29, Accession NM_018347) is another VGAM2014 host target gene. C20orf29 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf29, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of C20orf29 BINDING SITE, designated SEQ ID:20359, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70825] Another function of VGAM2014 is therefore inhibition of Chromosome 20 Open Reading Frame 29 (C20orf29, Accession NM_018347). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf29. DJ971N18.2 (Accession NM_021156) is another VGAM2014 host target gene. DJ971N18.2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DJ971N18.2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DJ971N18.2 BINDING SITE, designated SEQ ID:22137, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70826] Another function of VGAM2014 is therefore inhibition of DJ971N18.2 (Accession NM_021156). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with DJ971N18.2. DKFZP434A0131 (Accession NM_018991) is another VGAM2014 host target gene. DKFZP434A0131 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434A0131, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434A0131 BINDING SITE, designated SEQ ID:21064, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70827] Another function of VGAM2014 is therefore inhibition of DKFZP434A0131 (Accession NM_018991). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434A0131. Endothelial Cell-specific Molecule 1 (ESM1, Accession NM_007036) is another VGAM2014 host target gene. ESM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ESM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of ESM1 BINDING SITE, designated SEQ ID:13915, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70828] Another function of VGAM2014 is therefore inhibition of Endothelial Cell-specific Molecule 1 (ESM1, Accession NM_007036). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESM1. FLJ13910 (Accession NM_022780) is another VGAM2014 host target gene. FLJ13910 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13910, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13910 BINDING SITE, designated SEQ ID:23058, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70829] Another function of VGAM2014 is therefore inhibition of FLJ13910 (Accession NM_022780). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ13910. Golgi Associated, Gamma Adaptin Ear Containing, ARF Binding Protein 2 (GGA2, Accession NM_015044) is another VGAM2014 host target gene. GGA2 BINDING SITE1 and GGA2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GGA2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE1 and GGA2 BINDING SITE2, designated SEQ ID:17403 and SEQ ID:28925 respectively, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70830] Another function of VGAM2014 is therefore inhibition of Golgi Associated, Gamma Adaptin Ear Containing, ARF Binding Protein 2 (GGA2, Accession NM_015044). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2. HSU24186 (Accession NM_013347) is another VGAM2014 host target gene. HSU24186 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HSU24186, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSU24186 BINDING SITE, designated SEQ ID:14992, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70831] Another function of VGAM2014 is therefore inhibition of HSU24186 (Accession NM_013347). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSU24186. KIAA0057 (Accession NM_012288) is another VGAM2014 host target gene. KIAA0057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0057 BINDING SITE, designated SEQ ID:14629, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70832] Another function of VGAM2014 is therefore inhibition of KIAA0057 (Accession NM_012288). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0057. KIAA0483 (Accession NM_015176) is another VGAM2014 host target gene. KIAA0483 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0483, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0483 BINDING SITE, designated SEQ ID:17531, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70833] Another function of VGAM2014 is therefore inhibition of KIAA0483 (Accession NM_015176). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0483. MGC10960 (Accession NM_032653) is another VGAM2014 host target gene. MGC10960 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC10960, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10960 BINDING SITE, designated SEQ ID:26385, to the nucleotide sequence of VGAM2014 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4725.

[70834] Another function of VGAM2014 is therefore inhibition of MGC10960 (Accession NM_032653). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10960. MGC13159 (Accession NM_032927) is another VGAM2014 host target gene. MGC13159 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC13159, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13159 BINDING SITE, designated SEQ ID:26753, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70835] Another function of VGAM2014 is therefore inhibition of MGC13159 (Accession NM_032927). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13159. MGC2721 (Accession NM_032737) is another VGAM2014 host target gene. MGC2721 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2721, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2721 BINDING SITE, designated SEQ ID:26464, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70836] Another function of VGAM2014 is therefore inhibition of MGC2721 (Accession NM_032737). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2721. MGC29937 (Accession NM_144597) is another VGAM2014 host target gene. MGC29937 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC29937, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC29937 BINDING SITE, designated SEQ ID:29411, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70837] Another function of VGAM2014 is therefore inhibition of MGC29937 (Accession NM_144597). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC29937. Phosphodiesterase 8A (PDE8A, Accession XM_031443) is another VGAM2014 host target gene. PDE8A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE8A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE8A BINDING SITE, designated SEQ ID:31381, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70838] Another function of VGAM2014 is therefore inhibition of Phosphodiesterase 8A (PDE8A, Accession XM_031443). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE8A. Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2, Accession NM_014737) is another VGAM2014 host target gene. RASSF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RASSF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:16399, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70839] Another function of VGAM2014 is therefore inhibition of Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2, Accession NM_014737). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2. RYK Receptor-like Tyrosine Kinase (RYK, Accession XM_093692) is another VGAM2014 host target gene. RYK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RYK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RYK BINDING SITE, designated SEQ ID:40207, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70840] Another function of VGAM2014 is therefore inhibition of RYK Receptor-like Tyrosine Kinase (RYK, Accession XM_093692). Accordingly, utilities of VGAM2014 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with RYK. VMP1 (Accession NM_030938) is another VGAM2014 host target gene. VMP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VMP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VMP1 BINDING SITE, designated SEQ ID:25207, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70841] Another function of VGAM2014 is therefore inhibition of VMP1 (Accession NM_030938). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VMP1. LOC151647 (Accession XM_087261) is another VGAM2014 host target gene. LOC151647 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151647, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151647 BINDING SITE, designated SEQ ID:39159, to

the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70842] Another function of VGAM2014 is therefore inhibition of LOC151647 (Accession XM_087261). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151647. LOC158263 (Accession XM_088530) is another VGAM2014 host target gene. LOC158263 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158263, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158263 BINDING SITE, designated SEQ ID:39800, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70843] Another function of VGAM2014 is therefore inhibition of LOC158263 (Accession XM_088530). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158263. LOC158714 (Accession XM_088650) is another VGAM2014 host target gene. LOC158714 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC158714, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158714 BINDING SITE, designated SEQ ID:39887, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70844] Another function of VGAM2014 is therefore inhibition of LOC158714 (Accession XM_088650). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158714. LOC168667 (Accession XM_166592) is another VGAM2014 host target gene. LOC168667 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC168667, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC168667 BINDING SITE, designated SEQ ID:44570, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70845] Another function of VGAM2014 is therefore inhibition of LOC168667 (Accession XM_166592). Accordingly, utilities

of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168667. LOC201229 (Accession XM_113925) is another VGAM2014 host target gene. LOC201229 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201229 BINDING SITE, designated SEQ ID:42545, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70846] Another function of VGAM2014 is therefore inhibition of LOC201229 (Accession XM_113925). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201229. LOC256821 (Accession XM_175144) is another VGAM2014 host target gene. LOC256821 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256821, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC256821 BINDING SITE, designated SEQ ID:46639, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70847] Another function of VGAM2014 is therefore inhibition of LOC256821 (Accession XM_175144). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256821. LOC51141 (Accession XM_043953) is another VGAM2014 host target gene. LOC51141 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51141, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51141 BINDING SITE, designated SEQ ID:34049, to the nucleotide sequence of VGAM2014 RNA, herein designated VGAM RNA, also designated SEQ ID:4725.

[70848] Another function of VGAM2014 is therefore inhibition of LOC51141 (Accession XM_043953). Accordingly, utilities of VGAM2014 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51141. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2015 (VGAM2015) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70849] VGAM2015 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2015 was detected is described hereinabove with reference to Figs. 1-8.

[70850] VGAM2015 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri Green Mottle Mosaic Virus. VGAM2015 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70851] VGAM2015 gene encodes a VGAM2015 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2015 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2015 precursor RNA is designated SEQ ID:2001, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2001 is located at position 4081 relative to the

genome of Kyuri Green Mottle Mosaic Virus.

[70852] VGAM2015 precursor RNA folds onto itself, forming VGAM2015 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70853] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2015 folded precursor RNA into VGAM2015 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2015 RNA is designated SEQ ID:4726, and is provided hereinbelow with reference to the sequence listing part.

[70854] VGAM2015 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2015 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2015 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70855] VGAM2015 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2015 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2015 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2015 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2015 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70856] The complementary binding of VGAM2015 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2015 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2015 host target RNA into VGAM2015 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70857] It is appreciated that VGAM2015 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2015 host target genes. The mRNA of each one of this plurality of VGAM2015 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2015 RNA, herein designated VGAM RNA, and which when bound by VGAM2015 RNA causes inhibition of translation of respective one or more VGAM2015 host target proteins.

[70858] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2015 gene, herein designated VGAM GENE, on one or more VGAM2015 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70859] It is yet further appreciated that a function of VGAM2015 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2015 include diagnosis, prevention and treatment of viral infection by Kyuri Green Mottle Mosaic Virus. Specific functions, and accordingly utilities, of

VGAM2015 correlate with, and may be deduced from, the identity of the host target genes which VGAM2015 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70860] Nucleotide sequences of the VGAM2015 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2015 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2015 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2015 are further described hereinbelow with reference to Table 1.

[70861] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2015 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2015 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70862] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2015 gene, herein designated VGAM is inhibition of expression of VGAM2015 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2015 correlate with, and may be deduced

from, the identity of the target genes which VGAM2015 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70863] Vacuolar Protein Sorting 26 (yeast) (VPS26, Accession NM_004896) is a VGAM2015 host target gene. VPS26 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VPS26, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS26 BINDING SITE, designated SEQ ID:11325, to the nucleotide sequence of VGAM2015 RNA, herein designated VGAM RNA, also designated SEQ ID:4726.

[70864] A function of VGAM2015 is therefore inhibition of Vacuolar Protein Sorting 26 (yeast) (VPS26, Accession NM_004896), a gene which is a sorting protein- ensures the proper delivery of organelle-specific proteins. Accordingly, utilities of VGAM2015 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS26. The function of VPS26 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM315.Chromosome 20

Open Reading Frame 42 (C20orf42, Accession NM_017671) is another VGAM2015 host target gene. C20orf42 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf42, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf42 BINDING SITE, designated SEQ ID:19214, to the nucleotide sequence of VGAM2015 RNA, herein designated VGAM RNA, also designated SEQ ID:4726.

[70865] Another function of VGAM2015 is therefore inhibition of Chromosome 20 Open Reading Frame 42 (C20orf42, Accession NM_017671). Accordingly, utilities of VGAM2015 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf42. HCGIV.9 (Accession NM_018985) is another VGAM2015 host target gene. HCGIV.9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCGIV.9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCGIV.9 BINDING SITE, designated SEQ

ID:21055, to the nucleotide sequence of VGAM2015 RNA, herein designated VGAM RNA, also designated SEQ ID:4726.

[70866] Another function of VGAM2015 is therefore inhibition of HCGIV.9 (Accession NM_018985). Accordingly, utilities of VGAM2015 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCGIV.9. V-maf Musculoaponeurotic Fibrosarcoma Oncogene Homolog B (avian) (MAFB, Accession NM_005461) is another VGAM2015 host target gene. MAFB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAFB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAFB BINDING SITE, designated SEQ ID:11942, to the nucleotide sequence of VGAM2015 RNA, herein designated VGAM RNA, also designated SEQ ID:4726.

[70867] Another function of VGAM2015 is therefore inhibition of V-maf Musculoaponeurotic Fibrosarcoma Oncogene Homolog B (avian) (MAFB, Accession NM_005461). Accordingly, utilities of VGAM2015 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with MAFB. Proline-serine-threonine Phosphatase Interacting Protein 2 (PSTPIP2, Accession NM_024430) is another VGAM2015 host target gene. PSTPIP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSTPIP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSTPIP2 BINDING SITE, designated SEQ ID:23681, to the nucleotide sequence of VGAM2015 RNA, herein designated VGAM RNA, also designated SEQ ID:4726.

[70868] Another function of VGAM2015 is therefore inhibition of Proline-serine-threonine Phosphatase Interacting Protein 2 (PSTPIP2, Accession NM_024430). Accordingly, utilities of VGAM2015 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSTPIP2. LOC148195 (Accession XM_097419) is another VGAM2015 host target gene. LOC148195 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC148195 BINDING SITE, designated SEQ ID:40876, to the nucleotide sequence of VGAM2015 RNA, herein designated VGAM RNA, also designated SEQ ID:4726.

[70869] Another function of VGAM2015 is therefore inhibition of LOC148195 (Accession XM_097419). Accordingly, utilities of VGAM2015 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148195. LOC253981 (Accession XM_171064) is another VGAM2015 host target gene. LOC253981 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253981, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253981 BINDING SITE, designated SEQ ID:45864, to the nucleotide sequence of VGAM2015 RNA, herein designated VGAM RNA, also designated SEQ ID:4726.

[70870] Another function of VGAM2015 is therefore inhibition of LOC253981 (Accession XM_171064). Accordingly, utilities of VGAM2015 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253981. LOC90183 (Accession XM_029709) is another VGAM2015 host target gene. LOC90183 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90183, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90183 BINDING SITE, designated SEQ ID:30925, to the nucleotide sequence of VGAM2015 RNA, herein designated VGAM RNA, also designated SEQ ID:4726.

[70871] Another function of VGAM2015 is therefore inhibition of LOC90183 (Accession XM_029709). Accordingly, utilities of VGAM2015 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90183. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2016 (VGAM2016) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70872] VGAM2016 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2016 was detected is described hereinabove with reference to Figs. 1-8.

[70873] VGAM2016 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri Green Mottle Mosaic Virus. VGAM2016 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70874] VGAM2016 gene encodes a VGAM2016 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2016 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2016 precursor RNA is designated SEQ ID:2002, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2002 is located at position 1496 relative to the genome of Kyuri Green Mottle Mosaic Virus.

[70875] VGAM2016 precursor RNA folds onto itself, forming VGAM2016 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[70876] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2016 folded precursor RNA into VGAM2016 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2016 RNA is designated SEQ ID:4727, and is provided hereinbelow with reference to the sequence listing part.

[70877] VGAM2016 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2016 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2016 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70878] VGAM2016 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2016 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2016 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2016 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2016 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70879] The complementary binding of VGAM2016 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2016 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2016 host target RNA into VGAM2016 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70880] It is appreciated that VGAM2016 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2016 host target genes. The mRNA of each one of this plurality of VGAM2016 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2016 RNA, herein designated VGAM RNA, and which when bound by VGAM2016 RNA causes inhibition of translation of respective one or more VGAM2016 host target proteins.

[70881] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2016 gene, herein designated VGAM GENE, on one or more VGAM2016 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70882] It is yet further appreciated that a function of VGAM2016 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2016 include diagnosis, prevention and treatment of viral infection by Kyuri Green Mottle Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2016 correlate with, and may be deduced from, the identity of the host target genes which VGAM2016 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70883] Nucleotide sequences of the VGAM2016 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2016 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2016 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2016 are further described hereinbelow with reference to Table 1.

[70884] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2016 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2016 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70885] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2016 gene, herein designated VGAM is inhibition of expression of VGAM2016 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2016 correlate with, and may be deduced from, the identity of the target genes which VGAM2016 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70886] Fibroblast Growth Factor Receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) (FGFR1, Accession NM_023107) is a VGAM2016 host target gene. FGFR1 BINDING SITE1 and FGFR1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FGFR1, corresponding to HOST TARGET bind-

ing sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGFR1 BINDING SITE1 and FGFR1 BINDING SITE2, designated SEQ ID:23360 and SEQ ID:23365 respectively, to the nucleotide sequence of VGAM2016 RNA, herein designated VGAM RNA, also designated SEQ ID:4727.

[70887] A function of VGAM2016 is therefore inhibition of Fibroblast Growth Factor Receptor 1 (fms-related tyrosine kinase 2, Pfeiffer syndrome) (FGFR1, Accession NM_023107). Accordingly, utilities of VGAM2016 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR1. Protease, Serine, 8 (prostasin) (PRSS8, Accession NM_002773) is another VGAM2016 host target gene. PRSS8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRSS8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRSS8 BINDING SITE, designated SEQ ID:8663, to the nucleotide sequence of VGAM2016 RNA, herein designated VGAM RNA, also designated SEQ ID:4727.

[70888] Another function of VGAM2016 is therefore inhibition of Protease, Serine, 8 (prostasin) (PRSS8, Accession NM_002773), a gene which is a transmembrane serine protease. Accordingly, utilities of VGAM2016 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRSS8. The function of PRSS8 has been established by previous studies. Human seminal fluid contains a variety of proteolytic enzymes, including prostate-specific antigen (OMIM Ref. No. 176820) and acrosin (OMIM Ref. No. 102480). These enzymes are involved in the postejaculatory hydrolysis of proteins and in semen coagulation and liquefaction. Yu et al. (1995) obtained partial amino acid sequence of a 40-kD protein isolated from seminal fluid originally by Yu et al. (1994). Yu et al. (1995) designed degenerate primers based on the amino acid sequence and used to screen a human prostate cDNA library by PCR. The 3-prime end of the cDNA was obtained by the RACE (rapid amplification of cDNA ends) method. A 1.8-kb cDNA sequence was assembled encoding a predicted protein of 343 amino acids which contains a 32-amino acid signal peptide. The protein, designated serine protease-8 (PRSS8), was called prostasin by the authors. The precursor, proprostasin, is

cleaved between residues 12 and 13 to produce a 12-amino acid light chain and a 299-amino acid heavy chain which are associated through a disulfide bond. The predicted amino acid sequence is between 34 and 42% identical to human acrosin, plasma kallikrein (OMIM Ref. No. 229000), and hepsin (OMIM Ref. No. 142440). The deduced protein has a hydrophobic domain at the C terminus, indicating to the authors that it may be membrane anchored. The authors showed that the hydrophobic region is cleaved between residues 290 and 291 during secretion. Expression levels of the prostasin mRNA were assayed by Southern blots of RT-PCR products. Expression was noted in a wide variety of tissues. In the prostate gland, expression was localized to the epithelial cells. Donaldson et al. (2002) found evidence for the regulation of the epithelial sodium channel (ENaC; OMIM Ref. No. 600228) by prostasin. They cloned prostasin in their search for a human homolog of a channel-activating protease (xCAP1) of Xenopus kidney epithelial cells. They determined that prostasin shares 41% sequence identity with the Xenopus protease and 76% identity with the mouse homolog. --FUNCTION Donaldson et al. (2002) found that coexpression of prostasin with either Xenopus or rat ENaC

in Xenopus oocytes resulted in a 60 to 80% increase in amiloride-sensitive sodium currents, and that the addition of aprotinin, a serine protease inhibitor, completely prevented this activation. By in situ hybridization, they determined that both prostasin and TMPRSS2 (OMIM Ref. No. 602060) show a tissue distribution in human airway epithelia consistent with a role in ENaC regulation. Both had strong expression in superficial epithelial cells lining the nose, trachea, and distal airways, and both were expressed at the alveolar level, most notably at alveolar junctions in a distribution characteristic of type II pneumocytes. Expression was also pronounced in submucosal glands associated with nasal, tracheal, and bronchial tissues. Donaldson et al. (2002) suggested that prostasin is likely to be the more physiologically relevant protease.

[70889] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[70890] Donaldson, S. H.; Hirsh, A.; Li, D. C.; Holloway, G.; Chao, J.; Boucher, R. C.; Gabriel, S. E. : Regulation of the epithelial sodium channel by serine proteases in human airways. J. Biol. Chem. 277: 8338-8345, 2002. ; and

[70891] Yu, J. X.; Chao, L.; Ward, D. C.; Chao, J. : Structure and

chromosomal localization of the human prostasin (PRSS8) gene. Genomics 32: 334-340, 1996.

[70892] Further studies establishing the function and utilities of PRSS8 are found in John Hopkins OMIM database record ID 600823, and in sited publications numbered 755 and 7772-7774 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.DKFZP564K0322 (Accession NM_032040) is another VGAM2016 host target gene. DKFZP564K0322 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP564K0322, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564K0322 BINDING SITE, designated SEQ ID:25740, to the nucleotide sequence of VGAM2016 RNA, herein designated VGAM RNA, also designated SEQ ID:4727.

[70893] Another function of VGAM2016 is therefore inhibition of DKFZP564K0322 (Accession NM_032040). Accordingly, utilities of VGAM2016 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564K0322. FLJ23511 (Accession NM_032239)

is another VGAM2016 host target gene. FLJ23511 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23511, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23511 BINDING SITE, designated SEQ ID:25966, to the nucleotide sequence of VGAM2016 RNA, herein designated VGAM RNA, also designated SEQ ID:4727.

[70894] Another function of VGAM2016 is therefore inhibition of FLJ23511 (Accession NM_032239). Accordingly, utilities of VGAM2016 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23511. MGC12904 (Accession NM_031219) is another VGAM2016 host target gene. MGC12904 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC12904, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC12904 BINDING SITE, designated SEQ ID:25267, to the nucleotide sequence of VGAM2016 RNA, herein designated VGAM RNA, also designated SEQ ID:4727.

[70895] Another function of VGAM2016 is therefore inhibition of MGC12904 (Accession NM_031219). Accordingly, utilities of VGAM2016 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12904. Solute Carrier Family 5 (choline transporter), Member 7 (SLC5A7, Accession NM_021815) is another VGAM2016 host target gene. SLC5A7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC5A7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC5A7 BINDING SITE, designated SEQ ID:22391, to the nucleotide sequence of VGAM2016 RNA, herein designated VGAM RNA, also designated SEQ ID:4727.

[70896] Another function of VGAM2016 is therefore inhibition of Solute Carrier Family 5 (choline transporter), Member 7 (SLC5A7, Accession NM_021815). Accordingly, utilities of VGAM2016 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC5A7. Spir-1 (Accession XM_035640) is another VGAM2016 host target gene. Spir-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by Spir-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Spir-1 BINDING SITE, designated SEQ ID:32307, to the nucleotide sequence of VGAM2016 RNA, herein designated VGAM RNA, also designated SEQ ID:4727.

[70897] Another function of VGAM2016 is therefore inhibition of Spir-1 (Accession XM_035640). Accordingly, utilities of VGAM2016 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Spir-1. LOC163682 (Accession XM_099402) is another VGAM2016 host target gene. LOC163682 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC163682, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163682 BINDING SITE, designated SEQ ID:42092, to the nucleotide sequence of VGAM2016 RNA, herein designated VGAM RNA, also designated SEQ ID:4727.

[70898] Another function of VGAM2016 is therefore inhibition of LOC163682 (Accession XM_099402). Accordingly, utilities

of VGAM2016 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163682. LOC93589 (Accession XM_052387) is another VGAM2016 host target gene. LOC93589 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93589, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93589 BINDING SITE, designated SEQ ID:35979, to the nucleotide sequence of VGAM2016 RNA, herein designated VGAM RNA, also designated SEQ ID:4727.

[70899] Another function of VGAM2016 is therefore inhibition of LOC93589 (Accession XM_052387). Accordingly, utilities of VGAM2016 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93589. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2017 (VGAM2017) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70900] VGAM2017 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2017 was detected is described hereinabove with reference to Figs. 1-8.

[70901] VGAM2017 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2017 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70902] VGAM2017 gene encodes a VGAM2017 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2017 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2017 precursor RNA is designated SEQ ID:2003, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2003 is located at position 15595 relative to the genome of Zaire Ebola Virus (ZEBOV).

[70903] VGAM2017 precursor RNA folds onto itself, forming VGAM2017 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70904] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2017 folded precursor RNA into VGAM2017 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM2017 RNA is designated SEQ ID:4728, and is provided hereinbelow with reference to the sequence listing part.

[70905] VGAM2017 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2017 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2017 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[70906] VGAM2017 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2017 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2017 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2017 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2017 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70907] The complementary binding of VGAM2017 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2017 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2017 host target RNA into VGAM2017 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70908] It is appreciated that VGAM2017 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2017 host target genes. The mRNA of each one of this plurality of VGAM2017 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2017 RNA, herein designated VGAM RNA, and which when bound by VGAM2017 RNA causes inhibition of translation of respective one or more VGAM2017 host target proteins.

[70909] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2017 gene, herein designated VGAM GENE, on one or more VGAM2017 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70910] It is yet further appreciated that a function of VGAM2017 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2017 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2017 correlate with, and may be deduced from, the identity of the host target genes which VGAM2017 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70911] Nucleotide sequences of the VGAM2017 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2017 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2017 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2017 are further described hereinbelow with reference to Table 1.

[70912] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2017 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2017 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70913] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2017 gene, herein designated VGAM is inhibition of expression of VGAM2017 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2017 correlate with, and may be deduced from, the identity of the target genes which VGAM2017 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70914] Fibroblast Growth Factor 2 (basic) (FGF2, Accession NM_002006) is a VGAM2017 host target gene. FGF2

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF2 BINDING SITE, designated SEQ ID:7734, to the nucleotide sequence of VGAM2017 RNA, herein designated VGAM RNA, also designated SEQ ID:4728.

[70915] A function of VGAM2017 is therefore inhibition of Fibroblast Growth Factor 2 (basic) (FGF2, Accession NM_002006), a gene which probably involved in nervous system development and function. Accordingly, utilities of VGAM2017 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF2. The function of FGF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM51.Protein Phosphatase 1, Regulatory (inhibitor) Subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle) (PPP1R3A, Accession NM_002711) is another VGAM2017 host target gene. PPP1R3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

PPP1R3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R3A BINDING SITE, designated SEQ ID:8565, to the nucleotide sequence of VGAM2017 RNA, herein designated VGAM RNA, also designated SEQ ID:4728.

[70916] Another function of VGAM2017 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 3A (glycogen and sarcoplasmic reticulum binding subunit, skeletal muscle) (PPP1R3A, Accession NM_002711), a gene which regulates phosphatase activity towards glycogen synthase, active in skeletal muscle. Accordingly, utilities of VGAM2017 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R3A. The function of PPP1R3A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1872.Ubiquitin-like 3 (UBL3, Accession NM_007106) is another VGAM2017 host target gene. UBL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UBL3, corresponding to a HOST TARGET binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBL3 BINDING SITE, designated SEQ ID:13964, to the nucleotide sequence of VGAM2017 RNA, herein designated VGAM RNA, also designated SEQ ID:4728.

[70917] Another function of VGAM2017 is therefore inhibition of Ubiquitin-like 3 (UBL3, Accession NM_007106), a gene which appears to have a diverse range of cellular functions. Accordingly, utilities of VGAM2017 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBL3. The function of UBL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM459.Nup43 (Accession NM_024647) is another VGAM2017 host target gene. Nup43 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Nup43, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Nup43 BINDING SITE, designated SEQ ID:23933, to the nucleotide sequence of VGAM2017 RNA, herein designated VGAM RNA, also designated SEQ

ID:4728.

[70918] Another function of VGAM2017 is therefore inhibition of Nup43 (Accession NM_024647). Accordingly, utilities of VGAM2017 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Nup43. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 13B (PPP1R13B, Accession NM_015316) is another VGAM2017 host target gene. PPP1R13B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R13B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R13B BINDING SITE, designated SEQ ID:17632, to the nucleotide sequence of VGAM2017 RNA, herein designated VGAM RNA, also designated SEQ ID:4728.

[70919] Another function of VGAM2017 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 13B (PPP1R13B, Accession NM_015316). Accordingly, utilities of VGAM2017 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R13B. LOC148932 (Accession XM_086372) is another VGAM2017 host target gene. LOC148932 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148932, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148932 BINDING SITE, designated SEQ ID:38623, to the nucleotide sequence of VGAM2017 RNA, herein designated VGAM RNA, also designated SEQ ID:4728.

[70920] Another function of VGAM2017 is therefore inhibition of LOC148932 (Accession XM_086372). Accordingly, utilities of VGAM2017 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148932. LOC158376 (Accession XM_098934) is another VGAM2017 host target gene. LOC158376 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158376, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158376 BINDING SITE, designated SEQ ID:41972, to the nucleotide sequence of VGAM2017 RNA, herein designated VGAM RNA, also designated SEQ ID:4728.

[70921] Another function of VGAM2017 is therefore inhibition of

LOC158376 (Accession XM_098934). Accordingly, utilities of VGAM2017 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158376. LOC221042 (Accession XM_167669) is another VGAM2017 host target gene. LOC221042 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221042, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221042 BINDING SITE, designated SEQ ID:44751, to the nucleotide sequence of VGAM2017 RNA, herein designated VGAM RNA, also designated SEQ ID:4728.

[70922] Another function of VGAM2017 is therefore inhibition of LOC221042 (Accession XM_167669). Accordingly, utilities of VGAM2017 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221042. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2018 (VGAM2018) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[70923] VGAM2018 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2018 was detected is described hereinabove with reference to Figs. 1-8.

[70924] VGAM2018 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2018 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70925] VGAM2018 gene encodes a VGAM2018 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2018 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2018 precursor RNA is designated SEQ ID:2004, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2004 is located at position 13583 relative to the genome of Zaire Ebola Virus (ZEBOV).

[70926] VGAM2018 precursor RNA folds onto itself, forming VGAM2018 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70927] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2018 folded precursor RNA into VGAM2018 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM2018 RNA is designated SEQ ID:4729, and is provided hereinbelow with reference to the sequence listing part.

[70928] VGAM2018 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2018 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2018 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70929] VGAM2018 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2018 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2018 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2018 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2018 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[70930] The complementary binding of VGAM2018 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2018 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2018 host target RNA into VGAM2018 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70931] It is appreciated that VGAM2018 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2018 host target genes. The mRNA of each one of this plurality of VGAM2018 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2018 RNA, herein designated VGAM RNA, and which when bound by VGAM2018 RNA causes inhibition of translation of respective one or more VGAM2018 host target proteins.

[70932] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2018 gene, herein designated VGAM GENE, on one

or more VGAM2018 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70933] It is yet further appreciated that a function of VGAM2018 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2018 correlate with, and may be deduced from, the identity of the host target genes which VGAM2018 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70934] Nucleotide sequences of the VGAM2018 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2018 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2018 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2018 are further described hereinbelow with reference to Table 1.

[70935] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2018 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2018 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70936] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2018 gene, herein designated VGAM is inhibition of expression of VGAM2018 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2018 correlate with, and may be deduced from, the identity of the target genes which VGAM2018 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70937] Early Growth Response 3 (EGR3, Accession XM_005040) is

a VGAM2018 host target gene. EGR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EGR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGR3 BINDING SITE, designated SEQ ID:29957, to the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, also designated SEQ ID:4729.

[70938] A function of VGAM2018 is therefore inhibition of Early Growth Response 3 (EGR3, Accession XM_005040), a gene which is a putative transcription factor. Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGR3. The function of EGR3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM189.Inositol Hexaphosphate Kinase 3 (IHPK3, Accession NM_054111) is another VGAM2018 host target gene. IHPK3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IHPK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IHPK3 BINDING SITE, designated SEQ ID:27657, to the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, also designated SEQ ID:4729.

[70939] Another function of VGAM2018 is therefore inhibition of Inositol Hexaphosphate Kinase 3 (IHPK3, Accession NM_054111). Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IHPK3. Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog 2 (mouse) (MEIS2, Accession NM_020149) is another VGAM2018 host target gene. MEIS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEIS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEIS2 BINDING SITE, designated SEQ ID:21347, to the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, also designated SEQ ID:4729.

[70940] Another function of VGAM2018 is therefore inhibition of Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog

2 (mouse) (MEIS2, Accession NM_020149), a gene which may regulate gene expression and control cell differentiation. Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEIS2. The function of MEIS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1244.Proprotein Convertase Subtilisin/kexin Type 2 (PCSK2, Accession NM_002594) is another VGAM2018 host target gene. PCSK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCSK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCSK2 BINDING SITE, designated SEQ ID:8456, to the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, also designated SEQ ID:4729.

[70941] Another function of VGAM2018 is therefore inhibition of Proprotein Convertase Subtilisin/kexin Type 2 (PCSK2, Accession NM_002594), a gene which is involved in the processing of hormone and other protein precursors at sites

comprised of pairs of basic amino acid residues. Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCSK2. The function of PCSK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1120.TAP Binding Protein (tapasin) (TAPBP, Accession NM_003190) is another VGAM2018 host target gene. TAPBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAPBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAPBP BINDING SITE, designated SEQ ID:9178, to the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, also designated SEQ ID:4729.

[70942] Another function of VGAM2018 is therefore inhibition of TAP Binding Protein (tapasin) (TAPBP, Accession NM_003190), a gene which is involved in MHC class I-restricted antigen processing. Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAPBP.

The function of TAPBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM122.KIAA0934 (Accession XM_034536) is another VGAM2018 host target gene. KIAA0934 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0934, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0934 BINDING SITE, designated SEQ ID:32119, to the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, also designated SEQ ID:4729.

[70943] Another function of VGAM2018 is therefore inhibition of KIAA0934 (Accession XM_034536). Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0934. KIAA1184 (Accession NM_022572) is another VGAM2018 host target gene. KIAA1184 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1184, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1184 BINDING SITE, designated SEQ ID:22895, to the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, also designated SEQ ID:4729.

[70944] Another function of VGAM2018 is therefore inhibition of KIAA1184 (Accession NM_022572). Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1184. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840) is another VGAM2018 host target gene. PPP1R16B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R16B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R16B BINDING SITE, designated SEQ ID:30777, to the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, also designated SEQ ID:4729.

[70945] Another function of VGAM2018 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840). Accordingly, utilities of VGAM2018 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with PPP1R16B. Ribosomal Protein S6 Kinase, 52kDa, Polypeptide 1 (RPS6KC1, Accession NM_012424) is another VGAM2018 host target gene. RPS6KC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPS6KC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPS6KC1 BINDING SITE, designated SEQ ID:14799, to the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, also designated SEQ ID:4729.

[70946] Another function of VGAM2018 is therefore inhibition of Ribosomal Protein S6 Kinase, 52kDa, Polypeptide 1 (RPS6KC1, Accession NM_012424). Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPS6KC1. LOC157421 (Accession XM_098756) is another VGAM2018 host target gene. LOC157421 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157421, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC157421 BINDING SITE, designated SEQ ID:41794, to the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, also designated SEQ ID:4729.

[70947] Another function of VGAM2018 is therefore inhibition of LOC157421 (Accession XM_098756). Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157421. LOC158267 (Accession XM_088528) is another VGAM2018 host target gene. LOC158267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158267 BINDING SITE, designated SEQ ID:39795, to the nucleotide sequence of VGAM2018 RNA, herein designated VGAM RNA, also designated SEQ ID:4729.

[70948] Another function of VGAM2018 is therefore inhibition of LOC158267 (Accession XM_088528). Accordingly, utilities of VGAM2018 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158267. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2019 (VGAM2019) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70949] VGAM2019 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2019 was detected is described hereinabove with reference to Figs. 1-8.

[70950] VGAM2019 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri Green Mottle Mosaic Virus. VGAM2019 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70951] VGAM2019 gene encodes a VGAM2019 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2019 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2019 precursor RNA is designated SEQ ID:2005, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2005 is located at position 3691 relative to the genome of Kyuri Green Mottle Mosaic Virus.

[70952] VGAM2019 precursor RNA folds onto itself, forming VGAM2019 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70953] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2019 folded precursor RNA into VGAM2019 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2019 RNA is designated SEQ ID:4730, and is provided hereinbelow with reference to the sequence listing part.

[70954] VGAM2019 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2019 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2019 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70955] VGAM2019 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2019 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2019 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2019 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2019 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70956] The complementary binding of VGAM2019 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2019 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2019 host target RNA into VGAM2019 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[70957] It is appreciated that VGAM2019 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2019 host target genes. The mRNA of each one of this plurality of VGAM2019 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2019 RNA, herein designated VGAM RNA, and which when bound by VGAM2019 RNA causes inhibition of translation of respective one or more

VGAM2019 host target proteins.

[70958] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2019 gene, herein designated VGAM GENE, on one or more VGAM2019 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70959] It is yet further appreciated that a function of VGAM2019 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2019 include diagnosis, prevention and treatment of viral infection by Kyuri Green Mottle Mosaic

Virus. Specific functions, and accordingly utilities, of VGAM2019 correlate with, and may be deduced from, the identity of the host target genes which VGAM2019 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70960] Nucleotide sequences of the VGAM2019 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2019 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2019 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2019 are further described hereinbelow with reference to Table 1.

[70961] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2019 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2019 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70962] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2019 gene, herein designated VGAM is inhibition of expression of VGAM2019 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2019 correlate with, and may be deduced from, the identity of the target genes which VGAM2019 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70963] Selenoprotein X, 1 (SEPX1, Accession NM_016332) is a VGAM2019 host target gene. SEPX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEPX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEPX1 BINDING SITE, designated SEQ ID:18457, to the nucleotide sequence of VGAM2019 RNA, herein designated VGAM RNA, also designated SEQ ID:4730.

[70964] A function of VGAM2019 is therefore inhibition of Selenoprotein X, 1 (SEPX1, Accession NM_016332). Accordingly, utilities of VGAM2019 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEPX1. Solute Carrier Family 1 (glial high affinity glutamate transporter), Member 3 (SLC1A3, Accession NM_004172) is another VGAM2019 host target gene. SLC1A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

SLC1A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC1A3 BINDING SITE, designated SEQ ID:10383, to the nucleotide sequence of VGAM2019 RNA, herein designated VGAM RNA, also designated SEQ ID:4730.

[70965] Another function of VGAM2019 is therefore inhibition of Solute Carrier Family 1 (glial high affinity glutamate transporter), Member 3 (SLC1A3, Accession NM_004172), a gene which is a transporter molecule that regulates neurotransmitter concentrations at excitatory synapses of the mammalian cns. Accordingly, utilities of VGAM2019 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC1A3. The function of SLC1A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM294.TAR (HIV) RNA Binding Protein 2 (TARBP2, Accession NM_134324) is another VGAM2019 host target gene. TARBP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TARBP2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TARBP2 BINDING SITE, designated SEQ ID:28628, to the nucleotide sequence of VGAM2019 RNA, herein designated VGAM RNA, also designated SEQ ID:4730.

[70966] Another function of VGAM2019 is therefore inhibition of TAR (HIV) RNA Binding Protein 2 (TARBP2, Accession NM_134324), a gene which is involved in the regulation of HIV replication. Accordingly, utilities of VGAM2019 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TARBP2. The function of TARBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM95.CEP3 (Accession NM_006449) is another VGAM2019 host target gene. CEP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CEP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CEP3 BINDING SITE, designated SEQ ID:13155, to the nucleotide sequence of

VGAM2019 RNA, herein designated VGAM RNA, also designated SEQ ID:4730.

[70967] Another function of VGAM2019 is therefore inhibition of CEP3 (Accession NM_006449). Accordingly, utilities of VGAM2019 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEP3. FLJ20300 (Accession NM_017753) is another VGAM2019 host target gene. FLJ20300 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20300, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20300 BINDING SITE, designated SEQ ID:19365, to the nucleotide sequence of VGAM2019 RNA, herein designated VGAM RNA, also designated SEQ ID:4730.

[70968] Another function of VGAM2019 is therefore inhibition of FLJ20300 (Accession NM_017753). Accordingly, utilities of VGAM2019 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20300. KIAA0433 (Accession NM_015216) is another VGAM2019 host target gene. KIAA0433 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by KIAA0433, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0433 BINDING SITE, designated SEQ ID:17546, to the nucleotide sequence of VGAM2019 RNA, herein designated VGAM RNA, also designated SEQ ID:4730.

[70969] Another function of VGAM2019 is therefore inhibition of KIAA0433 (Accession NM_015216). Accordingly, utilities of VGAM2019 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0433. Syntrophin, Gamma 1 (SNTG1, Accession NM_018967) is another VGAM2019 host target gene. SNTG1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SNTG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNTG1 BINDING SITE, designated SEQ ID:21038, to the nucleotide sequence of VGAM2019 RNA, herein designated VGAM RNA, also designated SEQ ID:4730.

[70970] Another function of VGAM2019 is therefore inhibition of

Syntrophin, Gamma 1 (SNTG1, Accession NM_018967). Accordingly, utilities of VGAM2019 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNTG1. LOC150225 (Accession XM_097870) is another VGAM2019 host target gene. LOC150225 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150225, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150225 BINDING SITE, designated SEQ ID:41187, to the nucleotide sequence of VGAM2019 RNA, herein designated VGAM RNA, also designated SEQ ID:4730.

[70971] Another function of VGAM2019 is therefore inhibition of LOC150225 (Accession XM_097870). Accordingly, utilities of VGAM2019 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150225. LOC91526 (Accession XM_038985) is another VGAM2019 host target gene. LOC91526 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91526, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91526 BINDING SITE, designated SEQ ID:32971, to the nucleotide sequence of VGAM2019 RNA, herein designated VGAM RNA, also designated SEQ ID:4730.

[70972] Another function of VGAM2019 is therefore inhibition of LOC91526 (Accession XM_038985). Accordingly, utilities of VGAM2019 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91526. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2020 (VGAM2020) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[70973] VGAM2020 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2020 was detected is described hereinabove with reference to Figs. 1-8.

[70974] VGAM2020 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2020 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[70975] VGAM2020 gene encodes a VGAM2020 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2020 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2020 precursor RNA is designated SEQ ID:2006, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2006 is located at position 8150 relative to the genome of Zaire Ebola Virus (ZEBOV).

[70976] VGAM2020 precursor RNA folds onto itself, forming VGAM2020 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[70977] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2020 folded precursor RNA into VGAM2020

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM2020 RNA is designated SEQ ID:4731, and is provided hereinbelow with reference to the sequence listing part.

[70978] VGAM2020 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2020 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2020 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[70979] VGAM2020 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2020 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2020 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2020 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2020 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[70980] The complementary binding of VGAM2020 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2020 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2020 host target RNA into VGAM2020 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[70981] It is appreciated that VGAM2020 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2020 host target genes. The mRNA of each one of this plurality of VGAM2020 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2020 RNA, herein designated VGAM RNA, and which when bound by VGAM2020 RNA causes inhibition of translation of respective one or more VGAM2020 host target proteins.

[70982] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2020 gene, herein designated VGAM GENE, on one or more VGAM2020 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[70983] It is yet further appreciated that a function of VGAM2020 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2020 correlate with, and may be deduced from, the identity of the host target genes which VGAM2020 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[70984] Nucleotide sequences of the VGAM2020 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2020 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2020 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2020 are further described hereinbelow with reference to Table 1.

[70985] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2020 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2020 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[70986] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2020 gene, herein designated VGAM is inhibition of expression of VGAM2020 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2020 correlate with, and may be deduced from, the identity of the target genes which VGAM2020 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[70987] Protein S (alpha) (PROS1, Accession XM_113400) is a VGAM2020 host target gene. PROS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PROS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PROS1 BINDING SITE, designated SEQ ID:42254, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4731.

[70988] A function of VGAM2020 is therefore inhibition of Protein S (alpha) (PROS1, Accession XM_113400). Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROS1. Serine/threonine Kinase 24 (STE20 homolog, yeast) (STK24, Accession NM_003576) is another VGAM2020 host target gene. STK24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STK24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STK24 BINDING SITE, designated SEQ ID:9628, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also designated SEQ ID:4731.

[70989] Another function of VGAM2020 is therefore inhibition of Serine/threonine Kinase 24 (STE20 homolog, yeast) (STK24, Accession NM_003576), a gene which acts on both serine and threonine residues. Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK24. The function of STK24 and its association with

various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.SWAP70 (Accession XM_049197) is another VGAM2020 host target gene. SWAP70 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SWAP70, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SWAP70 BINDING SITE, designated SEQ ID:35351, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also designated SEQ ID:4731.

[70990] Another function of VGAM2020 is therefore inhibition of SWAP70 (Accession XM_049197), a gene which is involved not only in nuclear events but also in signaling in B-cell activation. Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SWAP70. The function of SWAP70 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1090.DKFZP564I122 (Accession XM_032397) is another VGAM2020 host target gene. DKFZP564I122 BIND-

ING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564I122, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564I122 BINDING SITE, designated SEQ ID:31646, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also designated SEQ ID:4731.

[70991] Another function of VGAM2020 is therefore inhibition of DKFZP564I122 (Accession XM_032397). Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564I122. FLJ22724 (Accession NM_024532) is another VGAM2020 host target gene. FLJ22724 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22724, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22724 BINDING SITE, designated SEQ ID:23737, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also designated SEQ ID:4731.

[70992] Another function of VGAM2020 is therefore inhibition of FLJ22724 (Accession NM_024532). Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22724. HERV-H LTR-associating 2 (HHLA2, Accession NM_007072) is another VGAM2020 host target gene. HHLA2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HHLA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HHLA2 BINDING SITE, designated SEQ ID:13938, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also designated SEQ ID:4731.

[70993] Another function of VGAM2020 is therefore inhibition of HERV-H LTR-associating 2 (HHLA2, Accession NM_007072). Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HHLA2. KIAA0871 (Accession NM_014961) is another VGAM2020 host target gene. KIAA0871 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by KIAA0871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0871 BINDING SITE, designated SEQ ID:17335, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also designated SEQ ID:4731.

[70994] Another function of VGAM2020 is therefore inhibition of KIAA0871 (Accession NM_014961). Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0871. KIAA0931 (Accession XM_041191) is another VGAM2020 host target gene. KIAA0931 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0931, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0931 BINDING SITE, designated SEQ ID:33482, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also designated SEQ ID:4731.

[70995] Another function of VGAM2020 is therefore inhibition of KIAA0931 (Accession XM_041191). Accordingly, utilities

of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0931. PTD012 (Accession NM_014039) is another VGAM2020 host target gene. PTD012 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTD012, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTD012 BINDING SITE, designated SEQ ID:15270, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also designated SEQ ID:4731.

[70996] Another function of VGAM2020 is therefore inhibition of PTD012 (Accession NM_014039). Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTD012. TAF9-like RNA Polymerase II, TATA Box Binding Protein (TBP)-associated Factor, 31kDa (TAF9L, Accession NM_015975) is another VGAM2020 host target gene. TAF9L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAF9L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of TAF9L BINDING SITE, designated SEQ ID:18074, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also designated SEQ ID:4731.

[70997] Another function of VGAM2020 is therefore inhibition of TAF9-like RNA Polymerase II, TATA Box Binding Protein (TBP)-associated Factor, 31kDa (TAF9L, Accession NM_015975). Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAF9L. LOC152765 (Accession XM_087519) is another VGAM2020 host target gene. LOC152765 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152765, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152765 BINDING SITE, designated SEQ ID:39311, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also designated SEQ ID:4731.

[70998] Another function of VGAM2020 is therefore inhibition of LOC152765 (Accession XM_087519). Accordingly, utilities

of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152765. LOC203286 (Accession XM_117526) is another VGAM2020 host target gene. LOC203286 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203286, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203286 BINDING SITE, designated SEQ ID:43493, to the nucleotide sequence of VGAM2020 RNA, herein designated VGAM RNA, also designated SEQ ID:4731.

[70999] Another function of VGAM2020 is therefore inhibition of LOC203286 (Accession XM_117526). Accordingly, utilities of VGAM2020 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203286. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2021 (VGAM2021) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71000] VGAM2021 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2021 was detected is described hereinabove with reference to Figs. 1-8.

[71001] VGAM2021 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2021 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71002] VGAM2021 gene encodes a VGAM2021 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2021 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2021 precursor RNA is designated SEQ ID:2007, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2007 is located at position 11857 relative to the genome of Zaire Ebola Virus (ZEBOV).

[71003] VGAM2021 precursor RNA folds onto itself, forming VGAM2021 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71004] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2021 folded precursor RNA into VGAM2021 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2021 RNA is designated SEQ ID:4732, and is provided hereinbelow with reference to the sequence listing part.

[71005] VGAM2021 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2021 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2021 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[71006] VGAM2021 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2021 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2021 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2021 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2021 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71007] The complementary binding of VGAM2021 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2021 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2021 host target RNA into VGAM2021 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71008] It is appreciated that VGAM2021 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2021 host target genes. The mRNA of each one of this plurality of VGAM2021 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2021 RNA, herein designated VGAM RNA, and which when bound by VGAM2021 RNA causes inhibition of translation of respective one or more VGAM2021 host target proteins.

[71009] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2021 gene, herein designated VGAM GENE, on one or more VGAM2021 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71010] It is yet further appreciated that a function of VGAM2021 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2021 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2021 correlate with, and may be deduced from, the identity of the host target genes which VGAM2021 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71011] Nucleotide sequences of the VGAM2021 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2021 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2021 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2021 are further described hereinbelow with reference to Table 1.

[71012] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2021 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2021 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71013] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2021 gene, herein designated VGAM is inhibition of expression of VGAM2021 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2021 correlate with, and may be deduced from, the identity of the target genes which VGAM2021 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71014] DNA (cytosine-5-)-methyltransferase 3 Beta (DNMT3B, Accession NM_006892) is a VGAM2021 host target gene.

DNMT3B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DNMT3B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNMT3B BINDING SITE, designated SEQ ID:13763, to the nucleotide sequence of VGAM2021 RNA, herein designated VGAM RNA, also designated SEQ ID:4732.

[71015] A function of VGAM2021 is therefore inhibition of DNA (cytosine-5-)-methyltransferase 3 Beta (DNMT3B, Accession NM_006892), a gene which is required for genome wide de novo methylation. Accordingly, utilities of VGAM2021 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNMT3B. The function of DNMT3B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM280.Phosphodiesterase 4D, CAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D, Accession XM_056815) is another VGAM2021 host target gene. PDE4D BINDING SITE is HOST TARGET binding site found in the 5` untranslated region

of mRNA encoded by PDE4D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE4D BINDING SITE, designated SEQ ID:36432, to the nucleotide sequence of VGAM2021 RNA, herein designated VGAM RNA, also designated SEQ ID:4732.

[71016] Another function of VGAM2021 is therefore inhibition of Phosphodiesterase 4D, CAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D, Accession XM_056815), a gene which has similarity to Drosophila dnc, which is the affected protein in learning and memory mutant dunce. Accordingly, utilities of VGAM2021 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4D. The function of PDE4D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM180.Interferon Regulatory Factor 7 (IRF7, Accession NM_004030) is another VGAM2021 host target gene. IRF7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IRF7, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRF7 BINDING SITE, designated SEQ ID:10251, to the nucleotide sequence of VGAM2021 RNA, herein designated VGAM RNA, also designated SEQ ID:4732.

[71017] Another function of VGAM2021 is therefore inhibition of Interferon Regulatory Factor 7 (IRF7, Accession NM_004030). Accordingly, utilities of VGAM2021 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRF7. KIAA0226 (Accession XM_032901) is another VGAM2021 host target gene. KIAA0226 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0226, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0226 BINDING SITE, designated SEQ ID:31786, to the nucleotide sequence of VGAM2021 RNA, herein designated VGAM RNA, also designated SEQ ID:4732.

[71018] Another function of VGAM2021 is therefore inhibition of KIAA0226 (Accession XM_032901). Accordingly, utilities of VGAM2021 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0226. KIAA0433 (Accession NM_015216) is another VGAM2021 host target gene. KIAA0433 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0433, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0433 BINDING SITE, designated SEQ ID:17548, to the nucleotide sequence of VGAM2021 RNA, herein designated VGAM RNA, also designated SEQ ID:4732.

[71019] Another function of VGAM2021 is therefore inhibition of KIAA0433 (Accession NM_015216). Accordingly, utilities of VGAM2021 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0433. VPS39 (Accession XM_031720) is another VGAM2021 host target gene. VPS39 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VPS39, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS39 BINDING SITE, designated SEQ ID:31470, to the nucleotide sequence of

VGAM2021 RNA, herein designated VGAM RNA, also designated SEQ ID:4732.

[71020] Another function of VGAM2021 is therefore inhibition of VPS39 (Accession XM_031720). Accordingly, utilities of VGAM2021 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS39. Zinc Finger, DHHC Domain Containing 3 (ZDHHC3, Accession NM_016598) is another VGAM2021 host target gene. ZDHHC3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZDHHC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZDHHC3 BINDING SITE, designated SEQ ID:18688, to the nucleotide sequence of VGAM2021 RNA, herein designated VGAM RNA, also designated SEQ ID:4732.

[71021] Another function of VGAM2021 is therefore inhibition of Zinc Finger, DHHC Domain Containing 3 (ZDHHC3, Accession NM_016598). Accordingly, utilities of VGAM2021 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZDHHC3. LOC200213 (Accession XM_114156) is another VGAM2021 host target

gene. LOC200213 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200213, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200213 BINDING SITE, designated SEQ ID:42740, to the nucleotide sequence of VGAM2021 RNA, herein designated VGAM RNA, also designated SEQ ID:4732.

[71022] Another function of VGAM2021 is therefore inhibition of LOC200213 (Accession XM_114156). Accordingly, utilities of VGAM2021 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200213. LOC222161 (Accession XM_166596) is another VGAM2021 host target gene. LOC222161 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222161, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222161 BINDING SITE, designated SEQ ID:44580, to the nucleotide sequence of VGAM2021 RNA, herein designated VGAM RNA, also designated SEQ ID:4732.

[71023] Another function of VGAM2021 is therefore inhibition of LOC222161 (Accession XM_166596). Accordingly, utilities of VGAM2021 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222161. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2022 (VGAM2022) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71024] VGAM2022 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2022 was detected is described hereinabove with reference to Figs. 1-8.

[71025] VGAM2022 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2022 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71026] VGAM2022 gene encodes a VGAM2022 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2022 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2022 precursor RNA is designated SEQ ID:2008, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2008 is located at position 4390 relative to the genome of Zaire Ebola Virus (ZEBOV).

[71027] VGAM2022 precursor RNA folds onto itself, forming VGAM2022 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71028] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2022 folded precursor RNA into VGAM2022 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2022 RNA is designated SEQ ID:4733, and is provided hereinbelow with reference to the sequence listing part.

[71029] VGAM2022 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2022 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2022 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71030] VGAM2022 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2022 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2022 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2022 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2022 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71031] The complementary binding of VGAM2022 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2022 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2022 host target RNA into VGAM2022 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71032] It is appreciated that VGAM2022 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2022 host target genes. The mRNA of each one of this plurality of VGAM2022 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2022 RNA, herein designated VGAM RNA, and which when bound by VGAM2022 RNA causes inhibition of translation of respective one or more VGAM2022 host target proteins.

[71033] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2022 gene, herein designated VGAM GENE, on one or more VGAM2022 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71034] It is yet further appreciated that a function of VGAM2022 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2022 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2022 correlate with, and may be deduced from, the identity of the host target genes which VGAM2022 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71035] Nucleotide sequences of the VGAM2022 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2022 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2022 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2022 are further described hereinbelow with reference to Table 1.

[71036] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2022 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2022 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[71037] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2022 gene, herein designated VGAM is inhibition of expression of VGAM2022 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2022 correlate with, and may be deduced from, the identity of the target genes which VGAM2022 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71038] NEL-like 2 (chicken) (NELL2, Accession NM_006159) is a VGAM2022 host target gene. NELL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NELL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NELL2 BINDING SITE, designated SEQ ID:12812, to the nucleotide sequence of VGAM2022 RNA, herein designated VGAM RNA, also designated SEQ ID:4733.

[71039] A function of VGAM2022 is therefore inhibition of NEL-like 2 (chicken) (NELL2, Accession NM_006159). Accordingly, utilities of VGAM2022 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with NELL2. AWP1 (Accession NM_019006) is another VGAM2022 host target gene. AWP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AWP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AWP1 BINDING SITE, designated SEQ ID:21080, to the nucleotide sequence of VGAM2022 RNA, herein designated VGAM RNA, also designated SEQ ID:4733.

[71040] Another function of VGAM2022 is therefore inhibition of AWP1 (Accession NM_019006). Accordingly, utilities of VGAM2022 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AWP1. FLJ10520 (Accession NM_018124) is another VGAM2022 host target gene. FLJ10520 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10520, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10520 BINDING SITE, designated SEQ ID:19904, to the nucleotide sequence of VGAM2022 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4733.

[71041] Another function of VGAM2022 is therefore inhibition of FLJ10520 (Accession NM_018124). Accordingly, utilities of VGAM2022 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10520. FLJ13657 (Accession NM_024828) is another VGAM2022 host target gene. FLJ13657 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13657, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13657 BINDING SITE, designated SEQ ID:24219, to the nucleotide sequence of VGAM2022 RNA, herein designated VGAM RNA, also designated SEQ ID:4733.

[71042] Another function of VGAM2022 is therefore inhibition of FLJ13657 (Accession NM_024828). Accordingly, utilities of VGAM2022 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13657. Oxysterol Binding Protein-like 8 (OSBPL8, Accession NM_020841) is another VGAM2022 host target gene. OSBPL8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

OSBPL8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL8 BINDING SITE, designated SEQ ID:21908, to the nucleotide sequence of VGAM2022 RNA, herein designated VGAM RNA, also designated SEQ ID:4733.

[71043] Another function of VGAM2022 is therefore inhibition of Oxysterol Binding Protein-like 8 (OSBPL8, Accession NM_020841). Accordingly, utilities of VGAM2022 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL8. PRO2964 (Accession NM_018547) is another VGAM2022 host target gene. PRO2964 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO2964, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2964 BINDING SITE, designated SEQ ID:20631, to the nucleotide sequence of VGAM2022 RNA, herein designated VGAM RNA, also designated SEQ ID:4733.

[71044] Another function of VGAM2022 is therefore inhibition of

PRO2964 (Accession NM_018547). Accordingly, utilities of VGAM2022 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2964. LOC146237 (Accession XM_096954) is another VGAM2022 host target gene. LOC146237 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146237, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146237 BINDING SITE, designated SEQ ID:40668, to the nucleotide sequence of VGAM2022 RNA, herein designated VGAM RNA, also designated SEQ ID:4733.

[71045] Another function of VGAM2022 is therefore inhibition of LOC146237 (Accession XM_096954). Accordingly, utilities of VGAM2022 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146237. LOC158381 (Accession XM_048461) is another VGAM2022 host target gene. LOC158381 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158381, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC158381 BINDING SITE, designated SEQ ID:35176, to the nucleotide sequence of VGAM2022 RNA, herein designated VGAM RNA, also designated SEQ ID:4733.

[71046] Another function of VGAM2022 is therefore inhibition of LOC158381 (Accession XM_048461). Accordingly, utilities of VGAM2022 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158381. LOC89231 (Accession XM_166577) is another VGAM2022 host target gene. LOC89231 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC89231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC89231 BINDING SITE, designated SEQ ID:44551, to the nucleotide sequence of VGAM2022 RNA, herein designated VGAM RNA, also designated SEQ ID:4733.

[71047] Another function of VGAM2022 is therefore inhibition of LOC89231 (Accession XM_166577). Accordingly, utilities of VGAM2022 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC89231. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2023 (VGAM2023) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71048] VGAM2023 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2023 was detected is described hereinabove with reference to Figs. 1-8.

[71049] VGAM2023 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2023 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71050] VGAM2023 gene encodes a VGAM2023 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2023 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2023 precursor RNA is designated SEQ ID:2009, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2009 is located at position 11139 relative to the genome of Zaire Ebola Virus (ZEBOV).

[71051] VGAM2023 precursor RNA folds onto itself, forming VGAM2023 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71052] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2023 folded precursor RNA into VGAM2023 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2023 RNA is designated SEQ ID:4734, and is provided hereinbelow with reference to the sequence listing part.

[71053] VGAM2023 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2023 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2023 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71054] VGAM2023 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2023 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2023 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2023 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2023 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71055] The complementary binding of VGAM2023 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2023 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2023 host target RNA into VGAM2023 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71056] It is appreciated that VGAM2023 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2023 host target genes. The mRNA of each one of this plurality of VGAM2023 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2023 RNA, herein designated VGAM RNA, and which when bound by VGAM2023 RNA causes inhibition of translation of respective one or more

VGAM2023 host target proteins.

[71057] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2023 gene, herein designated VGAM GENE, on one or more VGAM2023 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71058] It is yet further appreciated that a function of VGAM2023 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2023 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV).

Specific functions, and accordingly utilities, of VGAM2023 correlate with, and may be deduced from, the identity of the host target genes which VGAM2023 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71059] Nucleotide sequences of the VGAM2023 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2023 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2023 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2023 are further described hereinbelow with reference to Table 1.

[71060] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2023 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2023 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71061] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2023 gene, herein designated VGAM is inhibition of expression of VGAM2023 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2023 correlate with, and may be deduced from, the identity of the target genes which VGAM2023 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71062] Chemokine (C-C motif) Receptor 5 (CCR5, Accession NM_000579) is a VGAM2023 host target gene. CCR5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CCR5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCR5 BINDING SITE, designated SEQ ID:6182, to the nucleotide sequence of VGAM2023 RNA, herein designated VGAM RNA, also designated SEQ ID:4734.

[71063] A function of VGAM2023 is therefore inhibition of Chemokine (C-C motif) Receptor 5 (CCR5, Accession NM_000579). Accordingly, utilities of VGAM2023 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCR5. KIAA0310 (Accession XM_088459) is another VGAM2023 host target gene. KIAA0310 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0310, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0310 BINDING SITE, designated SEQ ID:39708, to the nucleotide sequence of VGAM2023 RNA, herein designated VGAM RNA, also designated SEQ ID:4734.

[71064] Another function of VGAM2023 is therefore inhibition of KIAA0310 (Accession XM_088459). Accordingly, utilities of VGAM2023 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0310. POLD3 (Accession XM_166243) is another VGAM2023 host target gene. POLD3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POLD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POLD3 BINDING SITE, designated SEQ ID:44053, to the nucleotide sequence of VGAM2023 RNA, herein designated VGAM RNA, also designated SEQ ID:4734.

[71065] Another function of VGAM2023 is therefore inhibition of POLD3 (Accession XM_166243). Accordingly, utilities of VGAM2023 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with POLD3. LOC161357 (Accession XM_090827) is another VGAM2023 host target gene. LOC161357 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC161357, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161357 BINDING SITE, designated SEQ ID:40016, to the nucleotide sequence of VGAM2023 RNA, herein designated VGAM RNA, also designated SEQ ID:4734.

[71066] Another function of VGAM2023 is therefore inhibition of LOC161357 (Accession XM_090827). Accordingly, utilities of VGAM2023 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161357. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2024 (VGAM2024) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71067] VGAM2024 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2024 was detected is described hereinabove with reference to Figs. 1-8.

[71068] VGAM2024 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri Green Mottle Mosaic Virus. VGAM2024 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71069] VGAM2024 gene encodes a VGAM2024 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2024 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2024 precursor RNA is designated SEQ ID:2010, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2010 is located at position 332 relative to the genome of Kyuri Green Mottle Mosaic Virus.

[71070] VGAM2024 precursor RNA folds onto itself, forming VGAM2024 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71071] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2024 folded precursor RNA into VGAM2024 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM2024 RNA is designated SEQ ID:4735, and is provided hereinbelow with reference to the sequence listing part.

[71072] VGAM2024 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2024 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2024 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71073] VGAM2024 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2024 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2024 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2024 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2024 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71074] The complementary binding of VGAM2024 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2024 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2024 host target RNA into VGAM2024 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71075] It is appreciated that VGAM2024 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2024 host target genes. The mRNA of each one of this plurality of VGAM2024 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2024 RNA, herein designated VGAM RNA, and which when bound by VGAM2024 RNA causes inhibition of translation of respective one or more VGAM2024 host target proteins.

[71076] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2024 gene, herein designated VGAM GENE, on one or more VGAM2024 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71077] It is yet further appreciated that a function of VGAM2024 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2024 include diagnosis, prevention and treatment of viral infection by Kyuri Green Mottle Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2024 correlate with, and may be deduced from, the identity of the host target genes which VGAM2024 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71078] Nucleotide sequences of the VGAM2024 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2024 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2024 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2024 are further described hereinbelow with reference to Table 1.

[71079] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2024 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2024 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71080] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2024 gene, herein designated VGAM is inhibition of expression of VGAM2024 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2024 correlate with, and may be deduced from, the identity of the target genes which VGAM2024 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71081] APM1 (Accession NM_004797) is a VGAM2024 host target gene. APM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

APM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APM1 BINDING SITE, designated SEQ ID:11213, to the nucleotide sequence of VGAM2024 RNA, herein designated VGAM RNA, also designated SEQ ID:4735.

[71082] A function of VGAM2024 is therefore inhibition of APM1 (Accession NM_004797). Accordingly, utilities of VGAM2024 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APM1. Rho GTPase Activating Protein 6 (ARHGAP6, Accession NM_013423) is another VGAM2024 host target gene. ARHGAP6 BINDING SITE1 and ARHGAP6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ARHGAP6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGAP6 BINDING SITE1 and ARHGAP6 BINDING SITE2, designated SEQ ID:15085 and SEQ ID:6847 respectively, to the nucleotide sequence of VGAM2024 RNA, herein designated VGAM RNA, also designated SEQ ID:4735.

[71083] Another function of VGAM2024 is therefore inhibition of

Rho GTPase Activating Protein 6 (ARHGAP6, Accession NM_013423), a gene which activates the rho-type GTPases by converting them to an inactive GTP-bound state. Accordingly, utilities of VGAM2024 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP6. The function of ARHGAP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Vinculin (VCL, Accession NM_014000) is another VGAM2024 host target gene. VCL BINDING SITE1 and VCL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by VCL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VCL BINDING SITE1 and VCL BINDING SITE2, designated SEQ ID:15193 and SEQ ID:9404 respectively, to the nucleotide sequence of VGAM2024 RNA, herein designated VGAM RNA, also designated SEQ ID:4735.

[71084] Another function of VGAM2024 is therefore inhibition of Vinculin (VCL, Accession NM_014000). Accordingly, utilities of VGAM2024 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with VCL. BPES (Accession NM_023067) is another VGAM2024 host target gene. BPES BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BPES, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BPES BINDING SITE, designated SEQ ID:23325, to the nucleotide sequence of VGAM2024 RNA, herein designated VGAM RNA, also designated SEQ ID:4735.

[71085] Another function of VGAM2024 is therefore inhibition of BPES (Accession NM_023067). Accordingly, utilities of VGAM2024 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BPES. FLJ11722 (Accession NM_024970) is another VGAM2024 host target gene. FLJ11722 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11722, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11722 BINDING SITE, designated SEQ ID:24518, to the nucleotide sequence of

VGAM2024 RNA, herein designated VGAM RNA, also designated SEQ ID:4735.

[71086] Another function of VGAM2024 is therefore inhibition of FLJ11722 (Accession NM_024970). Accordingly, utilities of VGAM2024 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11722. pcnp (Accession NM_020357) is another VGAM2024 host target gene. pcnp BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by pcnp, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of pcnp BINDING SITE, designated SEQ ID:21629, to the nucleotide sequence of VGAM2024 RNA, herein designated VGAM RNA, also designated SEQ ID:4735.

[71087] Another function of VGAM2024 is therefore inhibition of pcnp (Accession NM_020357). Accordingly, utilities of VGAM2024 include diagnosis, prevention and treatment of diseases and clinical conditions associated with pcnp. Zinc Finger Protein 297B (ZNF297B, Accession NM_014007) is another VGAM2024 host target gene. ZNF297B BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by ZNF297B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF297B BINDING SITE, designated SEQ ID:15221, to the nucleotide sequence of VGAM2024 RNA, herein designated VGAM RNA, also designated SEQ ID:4735.

[71088] Another function of VGAM2024 is therefore inhibition of Zinc Finger Protein 297B (ZNF297B, Accession NM_014007). Accordingly, utilities of VGAM2024 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF297B. LOC150139 (Accession XM_086794) is another VGAM2024 host target gene. LOC150139 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150139 BINDING SITE, designated SEQ ID:38859, to the nucleotide sequence of VGAM2024 RNA, herein designated VGAM RNA, also designated SEQ ID:4735.

[71089] Another function of VGAM2024 is therefore inhibition of LOC150139 (Accession XM_086794). Accordingly, utilities of VGAM2024 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150139. LOC92597 (Accession XM_046066) is another VGAM2024 host target gene. LOC92597 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92597, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92597 BINDING SITE, designated SEQ ID:34675, to the nucleotide sequence of VGAM2024 RNA, herein designated VGAM RNA, also designated SEQ ID:4735.

[71090] Another function of VGAM2024 is therefore inhibition of LOC92597 (Accession XM_046066). Accordingly, utilities of VGAM2024 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92597. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2025 (VGAM2025) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[71091] VGAM2025 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2025 was detected is described hereinabove with reference to Figs. 1-8.

[71092] VGAM2025 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri Green Mottle Mosaic Virus. VGAM2025 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71093] VGAM2025 gene encodes a VGAM2025 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2025 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2025 precursor RNA is designated SEQ ID:2011, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2011 is located at position 4374 relative to the genome of Kyuri Green Mottle Mosaic Virus.

[71094] VGAM2025 precursor RNA folds onto itself, forming VGAM2025 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71095] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2025 folded precursor RNA into VGAM2025 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2025 RNA is designated SEQ ID:4736, and is provided hereinbelow with reference to the sequence listing part.

[71096] VGAM2025 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2025 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2025 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71097] VGAM2025 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2025 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2025 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2025 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2025 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71098] The complementary binding of VGAM2025 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2025 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2025 host target RNA into VGAM2025 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71099] It is appreciated that VGAM2025 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2025 host target genes. The mRNA of each one of this plurality of VGAM2025 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2025 RNA, herein designated VGAM RNA, and which when bound by VGAM2025 RNA causes inhibition of translation of respective one or more VGAM2025 host target proteins.

[71100] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2025 gene, herein designated VGAM GENE, on one or more VGAM2025 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71101] It is yet further appreciated that a function of VGAM2025 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2025 include diagnosis, prevention and treatment of viral infection by Kyuri Green Mottle Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2025 correlate with, and may be deduced from, the identity of the host target genes which VGAM2025 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[71102] Nucleotide sequences of the VGAM2025 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2025 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2025 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2025 are further described hereinbelow with reference to Table 1.

[71103] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2025 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2025 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71104] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2025 gene, herein designated VGAM is inhibition of expression of VGAM2025 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2025 correlate with, and may be deduced from, the identity of the target genes which VGAM2025 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71105] UMP-CMPK (Accession NM_016308) is a VGAM2025 host target gene. UMP-CMPK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UMP-CMPK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UMP-CMPK BINDING SITE, designated SEQ ID:18426, to the nucleotide sequence of VGAM2025 RNA, herein designated VGAM RNA, also designated SEQ ID:4736.

[71106] A function of VGAM2025 is therefore inhibition of UMP-CMPK (Accession NM_016308). Accordingly, utilities of VGAM2025 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UMP-CMPK. LOC151959 (Accession XM_098144) is another VGAM2025 host target gene. LOC151959 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151959, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151959 BINDING SITE, designated SEQ ID:41409, to the nucleotide sequence of VGAM2025 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4736.

[71107] Another function of VGAM2025 is therefore inhibition of LOC151959 (Accession XM_098144). Accordingly, utilities of VGAM2025 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151959. LOC203197 (Accession XM_114645) is another VGAM2025 host target gene. LOC203197 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203197, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203197 BINDING SITE, designated SEQ ID:43011, to the nucleotide sequence of VGAM2025 RNA, herein designated VGAM RNA, also designated SEQ ID:4736.

[71108] Another function of VGAM2025 is therefore inhibition of LOC203197 (Accession XM_114645). Accordingly, utilities of VGAM2025 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203197. LOC221431 (Accession XM_166380) is another VGAM2025 host target gene. LOC221431 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221431, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221431 BINDING SITE, designated SEQ ID:44220, to the nucleotide sequence of VGAM2025 RNA, herein designated VGAM RNA, also designated SEQ ID:4736.

[71109] Another function of VGAM2025 is therefore inhibition of LOC221431 (Accession XM_166380). Accordingly, utilities of VGAM2025 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221431. LOC93589 (Accession XM_052387) is another VGAM2025 host target gene. LOC93589 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93589, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93589 BINDING SITE, designated SEQ ID:35975, to the nucleotide sequence of VGAM2025 RNA, herein designated VGAM RNA, also designated SEQ ID:4736.

[71110] Another function of VGAM2025 is therefore inhibition of LOC93589 (Accession XM_052387). Accordingly, utilities of VGAM2025 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC93589. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2026 (VGAM2026) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71111] VGAM2026 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2026 was detected is described hereinabove with reference to Figs. 1-8.

[71112] VGAM2026 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2026 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71113] VGAM2026 gene encodes a VGAM2026 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2026 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2026 precursor RNA is desig-

nated SEQ ID:2012, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2012 is located at position 18253 relative to the genome of Zaire Ebola Virus (ZEBOV).

[71114] VGAM2026 precursor RNA folds onto itself, forming VGAM2026 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71115] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2026 folded precursor RNA into VGAM2026 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2026 RNA is designated SEQ ID:4737, and is provided hereinbelow with reference to the sequence

listing part.

[71116] VGAM2026 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2026 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2026 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71117] VGAM2026 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2026 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2026 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2026 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2026 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71118] The complementary binding of VGAM2026 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2026 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2026 host target RNA into VGAM2026 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71119] It is appreciated that VGAM2026 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2026 host target genes. The mRNA of each one of this plurality of VGAM2026 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2026 RNA, herein designated VGAM

RNA, and which when bound by VGAM2026 RNA causes inhibition of translation of respective one or more VGAM2026 host target proteins.

[71120] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2026 gene, herein designated VGAM GENE, on one or more VGAM2026 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71121] It is yet further appreciated that a function of VGAM2026 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2026 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2026 correlate with, and may be deduced from, the identity of the host target genes which VGAM2026 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71122] Nucleotide sequences of the VGAM2026 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2026 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2026 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2026 are further described hereinbelow with reference to Table 1.

[71123] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2026 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2026 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71124] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2026 gene, herein designated VGAM is

inhibition of expression of VGAM2026 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2026 correlate with, and may be deduced from, the identity of the target genes which VGAM2026 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71125] Lysophospholipase I (LYPLA1, Accession NM_006330) is a VGAM2026 host target gene. LYPLA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LYPLA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LYPLA1 BINDING SITE, designated SEQ ID:13029, to the nucleotide sequence of VGAM2026 RNA, herein designated VGAM RNA, also designated SEQ ID:4737.

[71126] A function of VGAM2026 is therefore inhibition of Lysophospholipase I (LYPLA1, Accession NM_006330). Accordingly, utilities of VGAM2026 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LYPLA1. BM-002 (Accession NM_016617) is another VGAM2026 host target gene. BM-002 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by BM-002, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BM-002 BINDING SITE, designated SEQ ID:18727, to the nucleotide sequence of VGAM2026 RNA, herein designated VGAM RNA, also designated SEQ ID:4737.

[71127] Another function of VGAM2026 is therefore inhibition of BM-002 (Accession NM_016617). Accordingly, utilities of VGAM2026 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BM-002. DKFZP564I052 (Accession XM_039660) is another VGAM2026 host target gene. DKFZP564I052 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564I052, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564I052 BINDING SITE, designated SEQ ID:33139, to the nucleotide sequence of VGAM2026 RNA, herein designated VGAM RNA, also designated SEQ ID:4737.

[71128] Another function of VGAM2026 is therefore inhibition of DKFZP564I052 (Accession XM_039660). Accordingly, utili-

ties of VGAM2026 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564I052. Erythroblast Membrane-associated Protein (ERMAP, Accession NM_018538) is another VGAM2026 host target gene. ERMAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERMAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERMAP BINDING SITE, designated SEQ ID:20610, to the nucleotide sequence of VGAM2026 RNA, herein designated VGAM RNA, also designated SEQ ID:4737.

[71129] Another function of VGAM2026 is therefore inhibition of Erythroblast Membrane-associated Protein (ERMAP, Accession NM_018538). Accordingly, utilities of VGAM2026 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERMAP. FLJ13441 (Accession NM_023924) is another VGAM2026 host target gene. FLJ13441 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13441, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13441 BINDING SITE, designated SEQ ID:23400, to the nucleotide sequence of VGAM2026 RNA, herein designated VGAM RNA, also designated SEQ ID:4737.

[71130] Another function of VGAM2026 is therefore inhibition of FLJ13441 (Accession NM_023924). Accordingly, utilities of VGAM2026 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13441. FLJ14751 (Accession NM_032834) is another VGAM2026 host target gene. FLJ14751 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14751, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14751 BINDING SITE, designated SEQ ID:26610, to the nucleotide sequence of VGAM2026 RNA, herein designated VGAM RNA, also designated SEQ ID:4737.

[71131] Another function of VGAM2026 is therefore inhibition of FLJ14751 (Accession NM_032834). Accordingly, utilities of VGAM2026 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ14751. NAG14 (Accession NM_022143) is another VGAM2026 host target gene. NAG14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NAG14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAG14 BINDING SITE, designated SEQ ID:22707, to the nucleotide sequence of VGAM2026 RNA, herein designated VGAM RNA, also designated SEQ ID:4737.

[71132] Another function of VGAM2026 is therefore inhibition of NAG14 (Accession NM_022143). Accordingly, utilities of VGAM2026 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAG14. N-ethylmaleimide-sensitive Factor Attachment Protein, Gamma (NAPG, Accession XM_172983) is another VGAM2026 host target gene. NAPG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NAPG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAPG BINDING SITE, designated SEQ ID:46252, to the nucleotide sequence of

VGAM2026 RNA, herein designated VGAM RNA, also designated SEQ ID:4737.

[71133] Another function of VGAM2026 is therefore inhibition of N-ethylmaleimide-sensitive Factor Attachment Protein, Gamma (NAPG, Accession XM_172983). Accordingly, utilities of VGAM2026 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAPG. LOC91115 (Accession XM_036218) is another VGAM2026 host target gene. LOC91115 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91115, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91115 BINDING SITE, designated SEQ ID:32398, to the nucleotide sequence of VGAM2026 RNA, herein designated VGAM RNA, also designated SEQ ID:4737.

[71134] Another function of VGAM2026 is therefore inhibition of LOC91115 (Accession XM_036218). Accordingly, utilities of VGAM2026 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91115. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2027 (VGAM2027) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71135] VGAM2027 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2027 was detected is described hereinabove with reference to Figs. 1-8.

[71136] VGAM2027 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri Green Mottle Mosaic Virus. VGAM2027 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71137] VGAM2027 gene encodes a VGAM2027 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2027 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2027 precursor RNA is designated SEQ ID:2013, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2013 is located at position 4198 relative to the

genome of Kyuri Green Mottle Mosaic Virus.

[71138] VGAM2027 precursor RNA folds onto itself, forming VGAM2027 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71139] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2027 folded precursor RNA into VGAM2027 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2027 RNA is designated SEQ ID:4738, and is provided hereinbelow with reference to the sequence listing part.

[71140] VGAM2027 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2027 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2027 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71141] VGAM2027 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2027 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2027 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2027 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2027 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71142] The complementary binding of VGAM2027 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2027 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2027 host target RNA into VGAM2027 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71143] It is appreciated that VGAM2027 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2027 host target genes. The mRNA of each one of this plurality of VGAM2027 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2027 RNA, herein designated VGAM RNA, and which when bound by VGAM2027 RNA causes inhibition of translation of respective one or more VGAM2027 host target proteins.

[71144] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2027 gene, herein designated VGAM GENE, on one or more VGAM2027 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71145] It is yet further appreciated that a function of VGAM2027 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2027 include diagnosis, prevention and treatment of viral infection by Kyuri Green Mottle Mosaic Virus. Specific functions, and accordingly utilities, of

VGAM2027 correlate with, and may be deduced from, the identity of the host target genes which VGAM2027 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71146] Nucleotide sequences of the VGAM2027 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2027 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2027 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2027 are further described hereinbelow with reference to Table 1.

[71147] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2027 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2027 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71148] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2027 gene, herein designated VGAM is inhibition of expression of VGAM2027 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2027 correlate with, and may be deduced

from, the identity of the target genes which VGAM2027 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71149] FLJ13769 (Accession NM_025012) is a VGAM2027 host target gene. FLJ13769 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13769, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13769 BINDING SITE, designated SEQ ID:24589, to the nucleotide sequence of VGAM2027 RNA, herein designated VGAM RNA, also designated SEQ ID:4738.

[71150] A function of VGAM2027 is therefore inhibition of FLJ13769 (Accession NM_025012). Accordingly, utilities of VGAM2027 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13769. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2028 (VGAM2028) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[71151] VGAM2028 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2028 was detected is described hereinabove with reference to Figs. 1-8.

[71152] VGAM2028 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2028 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71153] VGAM2028 gene encodes a VGAM2028 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2028 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2028 precursor RNA is designated SEQ ID:2014, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2014 is located at position 16037 relative to the genome of Zaire Ebola Virus (ZEBOV).

[71154] VGAM2028 precursor RNA folds onto itself, forming VGAM2028 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71155] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2028 folded precursor RNA into VGAM2028 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2028 RNA is designated SEQ ID:4739, and is provided hereinbelow with reference to the sequence listing part.

[71156] VGAM2028 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2028 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2028 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71157] VGAM2028 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2028 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2028 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2028 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2028 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[71158] The complementary binding of VGAM2028 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2028 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2028 host target RNA into VGAM2028 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71159] It is appreciated that VGAM2028 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2028 host target genes. The mRNA of each one of this plurality of VGAM2028 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2028 RNA, herein designated VGAM RNA, and which when bound by VGAM2028 RNA causes inhibition of translation of respective one or more VGAM2028 host target proteins.

[71160] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2028 gene, herein designated VGAM GENE, on one

or more VGAM2028 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71161] It is yet further appreciated that a function of VGAM2028 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2028 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2028 correlate with, and may be deduced from, the identity of the host target genes which VGAM2028 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71162] Nucleotide sequences of the VGAM2028 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2028 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2028 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2028 are further described hereinbelow with reference to Table 1.

[71163] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2028 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2028 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71164] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2028 gene, herein designated VGAM is inhibition of expression of VGAM2028 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2028 correlate with, and may be deduced from, the identity of the target genes which VGAM2028 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71165] Hypermethylated In Cancer 2 (HIC2, Accession

XM_036937) is a VGAM2028 host target gene. HIC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HIC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIC2 BINDING SITE, designated SEQ ID:32527, to the nucleotide sequence of VGAM2028 RNA, herein designated VGAM RNA, also designated SEQ ID:4739.

[71166] A function of VGAM2028 is therefore inhibition of Hypermethylated In Cancer 2 (HIC2, Accession XM_036937). Accordingly, utilities of VGAM2028 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIC2. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2029 (VGAM2029) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71167] VGAM2029 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2029 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[71168] VGAM2029 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2029 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71169] VGAM2029 gene encodes a VGAM2029 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2029 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2029 precursor RNA is designated SEQ ID:2015, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2015 is located at position 17355 relative to the genome of Zaire Ebola Virus (ZEBOV).

[71170] VGAM2029 precursor RNA folds onto itself, forming VGAM2029 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71171] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2029 folded precursor RNA into VGAM2029 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2029 RNA is designated SEQ ID:4740, and is provided hereinbelow with reference to the sequence listing part.

[71172] VGAM2029 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2029 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2029 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71173] VGAM2029 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2029 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2029 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2029 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2029 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71174] The complementary binding of VGAM2029 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2029 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2029 host target RNA into VGAM2029 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71175] It is appreciated that VGAM2029 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2029 host target genes. The mRNA of each one of this plurality of VGAM2029 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2029 RNA, herein designated VGAM RNA, and which when bound by VGAM2029 RNA causes inhibition of translation of respective one or more VGAM2029 host target proteins.

[71176] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2029 gene, herein designated VGAM GENE, on one or more VGAM2029 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71177] It is yet further appreciated that a function of VGAM2029 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2029 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2029 correlate with, and may be deduced from, the identity of the host target genes which VGAM2029 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71178] Nucleotide sequences of the VGAM2029 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2029 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2029 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2029 are further described hereinbelow with reference to Table 1.

[71179] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2029 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2029 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71180] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2029 gene, herein designated VGAM is inhibition of expression of VGAM2029 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2029 correlate with, and may be deduced from, the identity of the target genes which VGAM2029 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71181] Heparanase (HPSE, Accession NM_006665) is a VGAM2029 host target gene. HPSE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HPSE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HPSE BINDING SITE, designated SEQ ID:13479, to the nucleotide sequence of VGAM2029 RNA, herein designated VGAM RNA, also designated SEQ ID:4740.

[71182] A function of VGAM2029 is therefore inhibition of Heparanase (HPSE, Accession NM_006665), a gene which is an endoglycosidase that cleaves heparan sulfate. Accordingly, utilities of VGAM2029 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HPSE. The function of HPSE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM374.DAMS (Accession NM_022001) is another VGAM2029 host target gene. DAMS BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DAMS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAMS BINDING SITE, designated SEQ ID:22542, to the nucleotide sequence of VGAM2029 RNA, herein designated VGAM RNA, also designated SEQ ID:4740.

[71183] Another function of VGAM2029 is therefore inhibition of DAMS (Accession NM_022001). Accordingly, utilities of VGAM2029 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAMS. FLJ13262 (Accession NM_024914) is another VGAM2029 host target gene. FLJ13262 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13262, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13262 BINDING SITE, designated SEQ ID:24434, to the nucleotide sequence of VGAM2029 RNA, herein designated VGAM RNA, also designated SEQ ID:4740.

[71184] Another function of VGAM2029 is therefore inhibition of FLJ13262 (Accession NM_024914). Accordingly, utilities of VGAM2029 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13262. SFRS Protein Kinase 1 (SRPK1, Accession NM_003137) is another VGAM2029 host target gene. SRPK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SRPK1, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SRPK1 BINDING SITE, designated SEQ ID:9108, to the nucleotide sequence of VGAM2029 RNA, herein designated VGAM RNA, also designated SEQ ID:4740.

[71185] Another function of VGAM2029 is therefore inhibition of SFRS Protein Kinase 1 (SRPK1, Accession NM_003137). Accordingly, utilities of VGAM2029 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRPK1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2030 (VGAM2030) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71186] VGAM2030 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2030 was detected is described hereinabove with reference to Figs. 1-8.

[71187] VGAM2030 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2030 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71188] VGAM2030 gene encodes a VGAM2030 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2030 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2030 precursor RNA is designated SEQ ID:2016, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2016 is located at position 12693 relative to the genome of Zaire Ebola Virus (ZEBOV).

[71189] VGAM2030 precursor RNA folds onto itself, forming VGAM2030 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71190] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2030 folded precursor RNA into VGAM2030

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2030 RNA is designated SEQ ID:4741, and is provided hereinbelow with reference to the sequence listing part.

[71191] VGAM2030 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2030 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2030 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71192] VGAM2030 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2030 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2030 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2030 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2030 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71193] The complementary binding of VGAM2030 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2030 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2030 host target RNA into VGAM2030 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[71194] It is appreciated that VGAM2030 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2030 host target genes. The mRNA of each one of this plurality of VGAM2030 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2030 RNA, herein designated VGAM RNA, and which when bound by VGAM2030 RNA causes inhibition of translation of respective one or more VGAM2030 host target proteins.

[71195] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2030 gene, herein designated VGAM GENE, on one or more VGAM2030 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71196] It is yet further appreciated that a function of VGAM2030 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2030 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2030 correlate with, and may be deduced from, the identity of the host target genes which VGAM2030 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71197] Nucleotide sequences of the VGAM2030 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2030 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2030 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2030 are further described hereinbelow with reference to Table 1.

[71198] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2030 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2030 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71199] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2030 gene, herein designated VGAM is inhibition of expression of VGAM2030 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2030 correlate with, and may be deduced from, the identity of the target genes which VGAM2030 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71200] Pleiomorphic Adenoma Gene 1 (PLAG1, Accession NM_002655) is a VGAM2030 host target gene. PLAG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLAG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLAG1 BINDING SITE, designated SEQ ID:8524, to the nucleotide sequence of VGAM2030 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4741.

[71201] A function of VGAM2030 is therefore inhibition of Pleiomorphic Adenoma Gene 1 (PLAG1, Accession NM_002655), a gene which contains a zinc finger domain. Accordingly, utilities of VGAM2030 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAG1. The function of PLAG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM29.Oxysterol Binding Protein-like 8 (OSBPL8, Accession NM_020841) is another VGAM2030 host target gene. OSBPL8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL8 BINDING SITE, designated SEQ ID:21907, to the nucleotide sequence of VGAM2030 RNA, herein designated VGAM RNA, also designated SEQ ID:4741.

[71202] Another function of VGAM2030 is therefore inhibition of Oxysterol Binding Protein-like 8 (OSBPL8, Accession NM_020841). Accordingly, utilities of VGAM2030 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL8. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2031 (VGAM2031) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71203] VGAM2031 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2031 was detected is described hereinabove with reference to Figs. 1-8.

[71204] VGAM2031 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2031 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71205] VGAM2031 gene encodes a VGAM2031 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2031 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2031 precursor RNA is desig-

nated SEQ ID:2017, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2017 is located at position 9873 relative to the genome of Zaire Ebola Virus (ZEBOV).

[71206] VGAM2031 precursor RNA folds onto itself, forming VGAM2031 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71207] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2031 folded precursor RNA into VGAM2031 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2031 RNA is designated SEQ ID:4742, and is provided hereinbelow with reference to the sequence

listing part.

[71208] VGAM2031 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2031 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2031 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71209] VGAM2031 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2031 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2031 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2031 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2031 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71210] The complementary binding of VGAM2031 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2031 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2031 host target RNA into VGAM2031 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71211] It is appreciated that VGAM2031 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2031 host target genes. The mRNA of each one of this plurality of VGAM2031 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2031 RNA, herein designated VGAM

RNA, and which when bound by VGAM2031 RNA causes inhibition of translation of respective one or more VGAM2031 host target proteins.

[71212] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2031 gene, herein designated VGAM GENE, on one or more VGAM2031 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71213] It is yet further appreciated that a function of VGAM2031 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2031 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2031 correlate with, and may be deduced from, the identity of the host target genes which VGAM2031 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71214] Nucleotide sequences of the VGAM2031 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2031 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2031 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2031 are further described hereinbelow with reference to Table 1.

[71215] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2031 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2031 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71216] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2031 gene, herein designated VGAM is

inhibition of expression of VGAM2031 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2031 correlate with, and may be deduced from, the identity of the target genes which VGAM2031 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71217] Carcinoembryonic Antigen-related Cell Adhesion Molecule 1 (biliary glycoprotein) (CEACAM1, Accession NM_001712) is a VGAM2031 host target gene. CEACAM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CEACAM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CEACAM1 BINDING SITE, designated SEQ ID:7442, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71218] A function of VGAM2031 is therefore inhibition of Carcinoembryonic Antigen-related Cell Adhesion Molecule 1 (biliary glycoprotein) (CEACAM1, Accession NM_001712), a gene which is a major effector of VEGF and may be a target for the inhibition of tumor angiogenesis. Accordingly, utilities of VGAM2031 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with CEACAM1. The function of CEACAM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM93.EphB2 (EPHB2, Accession NM_004442) is another VGAM2031 host target gene. EPHB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPHB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPHB2 BINDING SITE, designated SEQ ID:10734, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71219] Another function of VGAM2031 is therefore inhibition of EphB2 (EPHB2, Accession NM_004442), a gene which Eph-related receptor tyrosine kinase B2; may have a role in neurogenesis. Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPHB2. The function of EPHB2 and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to VGAM533.Leucine Zipper-EF-hand Containing Transmembrane Protein 1 (LETM1, Accession NM_012318) is another VGAM2031 host target gene. LETM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LETM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LETM1 BINDING SITE, designated SEQ ID:14695, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71220] Another function of VGAM2031 is therefore inhibition of Leucine Zipper-EF-hand Containing Transmembrane Protein 1 (LETM1, Accession NM_012318). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LETM1. Lysozyme (renal amyloidosis) (LYZ, Accession NM_000239) is another VGAM2031 host target gene. LYZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LYZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of LYZ BINDING SITE, designated SEQ ID:5759, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71221] Another function of VGAM2031 is therefore inhibition of Lysozyme (renal amyloidosis) (LYZ, Accession NM_000239), a gene which a bacteriolytic enzyme. Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LYZ. The function of LYZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM929.Microtubule-associated Protein 1B (MAP1B, Accession NM_005909) is another VGAM2031 host target gene. MAP1B BINDING SITE1 and MAP1B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MAP1B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP1B BINDING SITE1 and MAP1B BINDING SITE2, designated SEQ ID:12533 and SEQ ID:25711 respectively, to the nu-

cleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71222] Another function of VGAM2031 is therefore inhibition of Microtubule-associated Protein 1B (MAP1B, Accession NM_005909), a gene which may have a role in neuronal plasticity and brain development. Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP1B. The function of MAP1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM316.Phosphatidylinositol-4-phosphate 5-kinase, Type I, Alpha (PIP5K1A, Accession NM_003557) is another VGAM2031 host target gene. PIP5K1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIP5K1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIP5K1A BINDING SITE, designated SEQ ID:9602, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71223] Another function of VGAM2031 is therefore inhibition of

Phosphatidylinositol-4-phosphate 5-kinase, Type I, Alpha (PIP5K1A, Accession NM_003557), a gene which is responsible for the synthesis of PtdIns(4,5)P2. Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIP5K1A. The function of PIP5K1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM427.Transforming Growth Factor, Beta Receptor II (70/80kDa) (TGFBR2, Accession NM_003242) is another VGAM2031 host target gene. TGFBR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TGFBR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TGFBR2 BINDING SITE, designated SEQ ID:9245, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71224] Another function of VGAM2031 is therefore inhibition of Transforming Growth Factor, Beta Receptor II (70/80kDa) (TGFBR2, Accession NM_003242). Accordingly, utilities of

VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGFBR2. Ubiquitin Specific Protease 6 (Tre-2 oncogene) (USP6, Accession XM_165948) is another VGAM2031 host target gene. USP6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by USP6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP6 BINDING SITE, designated SEQ ID:43808, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71225] Another function of VGAM2031 is therefore inhibition of Ubiquitin Specific Protease 6 (Tre-2 oncogene) (USP6, Accession XM_165948), a gene which has an atp-independent isopeptidase activity, cleaving at the carboxyl terminus of the ubiquitin moiety. Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP6. The function of USP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM296.BTB (POZ) Domain Containing 2 (BTBD2, Accession NM_017797) is another VGAM2031 host target gene. BTBD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTBD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTBD2 BINDING SITE, designated SEQ ID:19439, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71226] Another function of VGAM2031 is therefore inhibition of BTB (POZ) Domain Containing 2 (BTBD2, Accession NM_017797). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTBD2. Chromosome 20 Open Reading Frame 140 (C20orf140, Accession NM_144628) is another VGAM2031 host target gene. C20orf140 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of C20orf140 BINDING SITE, designated SEQ ID:29445, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71227] Another function of VGAM2031 is therefore inhibition of Chromosome 20 Open Reading Frame 140 (C20orf140, Accession NM_144628). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf140. C20orf183 (Accession NM_030776) is another VGAM2031 host target gene. C20orf183 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf183, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf183 BINDING SITE, designated SEQ ID:25061, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71228] Another function of VGAM2031 is therefore inhibition of C20orf183 (Accession NM_030776). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

C20orf183. DKFZp434F142 (Accession NM_032254) is another VGAM2031 host target gene. DKFZp434F142 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434F142, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434F142 BINDING SITE, designated SEQ ID:25997, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71229] Another function of VGAM2031 is therefore inhibition of DKFZp434F142 (Accession NM_032254). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434F142. DKFZP434J193 (Accession XM_048452) is another VGAM2031 host target gene. DKFZP434J193 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434J193, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434J193 BINDING SITE, des-

ignated SEQ ID:35163, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71230] Another function of VGAM2031 is therefore inhibition of DKFZP434J193 (Accession XM_048452). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434J193. DKFZP434L187 (Accession XM_044070) is another VGAM2031 host target gene. DKFZP434L187 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434L187, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434L187 BINDING SITE, designated SEQ ID:34119, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71231] Another function of VGAM2031 is therefore inhibition of DKFZP434L187 (Accession XM_044070). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434L187. DKFZP564C196 (Accession

XM_046405) is another VGAM2031 host target gene. DKFZP564C196 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564C196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564C196 BINDING SITE, designated SEQ ID:34709, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71232] Another function of VGAM2031 is therefore inhibition of DKFZP564C196 (Accession XM_046405). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564C196. Potassium Voltage-gated Channel, Shal-related Subfamily, Member 1 (KCND1, Accession NM_004979) is another VGAM2031 host target gene. KCND1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCND1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCND1 BINDING SITE, designated SEQ

ID:11426, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71233] Another function of VGAM2031 is therefore inhibition of Potassium Voltage-gated Channel, Shal-related Subfamily, Member 1 (KCND1, Accession NM_004979). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCND1. KIAA0155 (Accession NM_014633) is another VGAM2031 host target gene. KIAA0155 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0155, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0155 BINDING SITE, designated SEQ ID:16003, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71234] Another function of VGAM2031 is therefore inhibition of KIAA0155 (Accession NM_014633). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0155. KIAA0169 (Accession XM_052725) is another

VGAM2031 host target gene. KIAA0169 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0169, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0169 BINDING SITE, designated SEQ ID:36052, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71235] Another function of VGAM2031 is therefore inhibition of KIAA0169 (Accession XM_052725). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0169. KIAA0441 (Accession NM_014797) is another VGAM2031 host target gene. KIAA0441 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0441, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0441 BINDING SITE, designated SEQ ID:16715, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71236] Another function of VGAM2031 is therefore inhibition of KIAA0441 (Accession NM_014797). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0441. KIAA0553 (Accession XM_045981) is another VGAM2031 host target gene. KIAA0553 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0553, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0553 BINDING SITE, designated SEQ ID:34635, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71237] Another function of VGAM2031 is therefore inhibition of KIAA0553 (Accession XM_045981). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0553. KIAA1075 (Accession XM_029631) is another VGAM2031 host target gene. KIAA1075 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1075, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1075 BINDING SITE, designated SEQ ID:30917, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71238] Another function of VGAM2031 is therefore inhibition of KIAA1075 (Accession XM_029631). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1075. KIAA1143 (Accession XM_044014) is another VGAM2031 host target gene. KIAA1143 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1143, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1143 BINDING SITE, designated SEQ ID:34073, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71239] Another function of VGAM2031 is therefore inhibition of KIAA1143 (Accession XM_044014). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1143. KIAA1280 (Accession XM_045766) is another VGAM2031 host target gene. KIAA1280 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1280, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1280 BINDING SITE, designated SEQ ID:34557, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71240] Another function of VGAM2031 is therefore inhibition of KIAA1280 (Accession XM_045766). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1280. KIAA1432 (Accession XM_039698) is another VGAM2031 host target gene. KIAA1432 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1432, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1432 BINDING SITE, designated SEQ ID:33159, to the nucleotide sequence of VGAM2031 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4742.

[71241] Another function of VGAM2031 is therefore inhibition of KIAA1432 (Accession XM_039698). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1432. KIAA1856 (Accession XM_166549) is another VGAM2031 host target gene. KIAA1856 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1856, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1856 BINDING SITE, designated SEQ ID:44523, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71242] Another function of VGAM2031 is therefore inhibition of KIAA1856 (Accession XM_166549). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1856. MGC15631 (Accession NM_032753) is another VGAM2031 host target gene. MGC15631 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC15631, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15631 BINDING SITE, designated SEQ ID:26490, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71243] Another function of VGAM2031 is therefore inhibition of MGC15631 (Accession NM_032753). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15631. NLI-IF (Accession NM_021198) is another VGAM2031 host target gene. NLI-IF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NLI-IF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NLI-IF BINDING SITE, designated SEQ ID:22172, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71244] Another function of VGAM2031 is therefore inhibition of NLI-IF (Accession NM_021198). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with NLI-IF. Ornithine Decarboxylase Antizyme 2 (OAZ2, Accession NM_002537) is another VGAM2031 host target gene. OAZ2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OAZ2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OAZ2 BINDING SITE, designated SEQ ID:8375, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71245] Another function of VGAM2031 is therefore inhibition of Ornithine Decarboxylase Antizyme 2 (OAZ2, Accession NM_002537). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OAZ2. PGR1 (Accession NM_033296) is another VGAM2031 host target gene. PGR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PGR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PGR1 BINDING SITE, designated SEQ ID:27123,

to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71246] Another function of VGAM2031 is therefore inhibition of PGR1 (Accession NM_033296). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PGR1. PRAX-1 (Accession NM_004758) is another VGAM2031 host target gene. PRAX-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRAX-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRAX-1 BINDING SITE, designated SEQ ID:11146, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71247] Another function of VGAM2031 is therefore inhibition of PRAX-1 (Accession NM_004758). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRAX-1. Polymerase I and Transcript Release Factor (PTRF, Accession XM_032852) is another VGAM2031 host target gene. PTRF BINDING SITE is HOST TARGET binding site

found in the 5` untranslated region of mRNA encoded by PTRF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTRF BINDING SITE, designated SEQ ID:31785, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71248] Another function of VGAM2031 is therefore inhibition of Polymerase I and Transcript Release Factor (PTRF, Accession XM_032852). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTRF. SCYD1 (Accession XM_165650) is another VGAM2031 host target gene. SCYD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCYD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCYD1 BINDING SITE, designated SEQ ID:43712, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71249] Another function of VGAM2031 is therefore inhibition of

SCYD1 (Accession XM_165650). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCYD1. LOC147093 (Accession XM_097184) is another VGAM2031 host target gene. LOC147093 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147093, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147093 BINDING SITE, designated SEQ ID:40798, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71250] Another function of VGAM2031 is therefore inhibition of LOC147093 (Accession XM_097184). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147093. LOC149132 (Accession XM_086428) is another VGAM2031 host target gene. LOC149132 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149132, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC149132 BINDING SITE, designated SEQ ID:38644, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71251] Another function of VGAM2031 is therefore inhibition of LOC149132 (Accession XM_086428). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149132. LOC201229 (Accession XM_113925) is another VGAM2031 host target gene. LOC201229 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201229 BINDING SITE, designated SEQ ID:42539, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71252] Another function of VGAM2031 is therefore inhibition of LOC201229 (Accession XM_113925). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201229. LOC203257 (Accession XM_113561) is an-

other VGAM2031 host target gene. LOC203257 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203257, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203257 BINDING SITE, designated SEQ ID:42286, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71253] Another function of VGAM2031 is therefore inhibition of LOC203257 (Accession XM_113561). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203257. LOC206426 (Accession XM_116505) is another VGAM2031 host target gene. LOC206426 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC206426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC206426 BINDING SITE, designated SEQ ID:43115, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71254] Another function of VGAM2031 is therefore inhibition of LOC206426 (Accession XM_116505). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC206426. LOC91040 (Accession XM_035641) is another VGAM2031 host target gene. LOC91040 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91040 BINDING SITE, designated SEQ ID:32311, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71255] Another function of VGAM2031 is therefore inhibition of LOC91040 (Accession XM_035641). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91040. LOC91409 (Accession XM_038298) is another VGAM2031 host target gene. LOC91409 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91409, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91409 BINDING SITE, designated SEQ ID:32803, to the nucleotide sequence of VGAM2031 RNA, herein designated VGAM RNA, also designated SEQ ID:4742.

[71256] Another function of VGAM2031 is therefore inhibition of LOC91409 (Accession XM_038298). Accordingly, utilities of VGAM2031 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91409. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2032 (VGAM2032) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71257] VGAM2032 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2032 was detected is described hereinabove with reference to Figs. 1-8.

[71258] VGAM2032 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri Green Mottle Mosaic Virus. VGAM2032 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71259] VGAM2032 gene encodes a VGAM2032 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2032 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2032 precursor RNA is designated SEQ ID:2018, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2018 is located at position 2336 relative to the genome of Kyuri Green Mottle Mosaic Virus.

[71260] VGAM2032 precursor RNA folds onto itself, forming VGAM2032 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71261] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2032 folded precursor RNA into VGAM2032

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2032 RNA is designated SEQ ID:4743, and is provided hereinbelow with reference to the sequence listing part.

[71262] VGAM2032 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2032 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2032 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71263] VGAM2032 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2032 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2032 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2032 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2032 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71264] The complementary binding of VGAM2032 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2032 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2032 host target RNA into VGAM2032 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[71265] It is appreciated that VGAM2032 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2032 host target genes. The mRNA of each one of this plurality of VGAM2032 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2032 RNA, herein designated VGAM RNA, and which when bound by VGAM2032 RNA causes inhibition of translation of respective one or more VGAM2032 host target proteins.

[71266] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2032 gene, herein designated VGAM GENE, on one or more VGAM2032 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71267] It is yet further appreciated that a function of VGAM2032 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2032 include diagnosis, prevention and treatment of viral infection by Kyuri Green Mottle Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2032 correlate with, and may be deduced from, the identity of the host target genes which VGAM2032 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71268] Nucleotide sequences of the VGAM2032 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2032 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2032 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2032 are further described hereinbelow with reference to Table 1.

[71269] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2032 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2032 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71270] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2032 gene, herein designated VGAM is inhibition of expression of VGAM2032 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2032 correlate with, and may be deduced from, the identity of the target genes which VGAM2032 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71271] FLJ20298 (Accession NM_017752) is a VGAM2032 host target gene. FLJ20298 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20298, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20298 BINDING SITE, designated SEQ ID:19362, to the nucleotide sequence of VGAM2032 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4743.

[71272] A function of VGAM2032 is therefore inhibition of FLJ20298 (Accession NM_017752). Accordingly, utilities of VGAM2032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20298. LOC201695 (Accession XM_120432) is another VGAM2032 host target gene. LOC201695 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201695, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201695 BINDING SITE, designated SEQ ID:43609, to the nucleotide sequence of VGAM2032 RNA, herein designated VGAM RNA, also designated SEQ ID:4743.

[71273] Another function of VGAM2032 is therefore inhibition of LOC201695 (Accession XM_120432). Accordingly, utilities of VGAM2032 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201695. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2033 (VGAM2033) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71274] VGAM2033 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2033 was detected is described hereinabove with reference to Figs. 1-8.

[71275] VGAM2033 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2033 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71276] VGAM2033 gene encodes a VGAM2033 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2033 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2033 precursor RNA is designated SEQ ID:2019, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2019 is located at position 4726 relative to the genome of Zaire Ebola Virus (ZEBOV).

[71277] VGAM2033 precursor RNA folds onto itself, forming

VGAM2033 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71278] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2033 folded precursor RNA into VGAM2033 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2033 RNA is designated SEQ ID:4744, and is provided hereinbelow with reference to the sequence listing part.

[71279] VGAM2033 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2033 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2033 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71280] VGAM2033 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2033 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2033 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2033 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2033 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71281] The complementary binding of VGAM2033 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2033 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2033 host target RNA into VGAM2033 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71282] It is appreciated that VGAM2033 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2033 host target genes. The mRNA of each one of this plurality of VGAM2033 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2033 RNA, herein designated VGAM RNA, and which when bound by VGAM2033 RNA causes inhibition of translation of respective one or more VGAM2033 host target proteins.

[71283] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2033 gene, herein designated VGAM GENE, on one or more VGAM2033 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71284] It is yet further appreciated that a function of VGAM2033 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2033 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2033 correlate with, and may be deduced from, the identity of the host target genes which VGAM2033 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[71285] Nucleotide sequences of the VGAM2033 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2033 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2033 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2033 are further described hereinbelow with reference to Table 1.

[71286] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2033 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2033 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71287] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2033 gene, herein designated VGAM is inhibition of expression of VGAM2033 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2033 correlate with, and may be deduced from, the identity of the target genes which VGAM2033 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[71288] KIAA1219 (Accession XM_028835) is a VGAM2033 host target gene. KIAA1219 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1219 BINDING SITE, designated SEQ ID:30759, to the nucleotide sequence of VGAM2033 RNA, herein designated VGAM RNA, also designated SEQ ID:4744.

[71289] A function of VGAM2033 is therefore inhibition of KIAA1219 (Accession XM_028835). Accordingly, utilities of VGAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1219. KIAA1822 (Accession XM_041566) is another VGAM2033 host target gene. KIAA1822 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1822, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1822 BINDING SITE, designated SEQ ID:33549, to the

nucleotide sequence of VGAM2033 RNA, herein designated VGAM RNA, also designated SEQ ID:4744.

[71290] Another function of VGAM2033 is therefore inhibition of KIAA1822 (Accession XM_041566). Accordingly, utilities of VGAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1822. MKP-7 (Accession XM_039106) is another VGAM2033 host target gene. MKP-7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MKP-7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MKP-7 BINDING SITE, designated SEQ ID:33004, to the nucleotide sequence of VGAM2033 RNA, herein designated VGAM RNA, also designated SEQ ID:4744.

[71291] Another function of VGAM2033 is therefore inhibition of MKP-7 (Accession XM_039106). Accordingly, utilities of VGAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKP-7. LOC199858 (Accession XM_114040) is another VGAM2033 host target gene. LOC199858 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by LOC199858, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199858 BINDING SITE, designated SEQ ID:42634, to the nucleotide sequence of VGAM2033 RNA, herein designated VGAM RNA, also designated SEQ ID:4744.

[71292] Another function of VGAM2033 is therefore inhibition of LOC199858 (Accession XM_114040). Accordingly, utilities of VGAM2033 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199858. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2034 (VGAM2034) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71293] VGAM2034 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2034 was detected is described hereinabove with reference to Figs. 1-8.

[71294] VGAM2034 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Kyuri Green Mottle Mosaic Virus. VGAM2034 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71295] VGAM2034 gene encodes a VGAM2034 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2034 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2034 precursor RNA is designated SEQ ID:2020, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2020 is located at position 3084 relative to the genome of Kyuri Green Mottle Mosaic Virus.

[71296] VGAM2034 precursor RNA folds onto itself, forming VGAM2034 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71297] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2034 folded precursor RNA into VGAM2034 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2034 RNA is designated SEQ ID:4745, and is provided hereinbelow with reference to the sequence listing part.

[71298] VGAM2034 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2034 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2034 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71299] VGAM2034 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2034 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2034 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2034 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2034 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71300] The complementary binding of VGAM2034 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2034 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2034

host target RNA into VGAM2034 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71301] It is appreciated that VGAM2034 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2034 host target genes. The mRNA of each one of this plurality of VGAM2034 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2034 RNA, herein designated VGAM RNA, and which when bound by VGAM2034 RNA causes inhibition of translation of respective one or more VGAM2034 host target proteins.

[71302] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2034 gene, herein designated VGAM GENE, on one or more VGAM2034 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71303] It is yet further appreciated that a function of VGAM2034 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of viral infection by Kyuri Green Mottle Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2034 correlate with, and may be deduced from, the identity of the host target genes which VGAM2034 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71304] Nucleotide sequences of the VGAM2034 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2034 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2034 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2034 are further

described hereinbelow with reference to Table 1.

[71305] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2034 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2034 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71306] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2034 gene, herein designated VGAM is inhibition of expression of VGAM2034 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2034 correlate with, and may be deduced from, the identity of the target genes which VGAM2034 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71307] C-reactive Protein, Pentraxin-related (CRP, Accession XM_049673) is a VGAM2034 host target gene. CRP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRP

BINDING SITE, designated SEQ ID:35464, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71308] A function of VGAM2034 is therefore inhibition of C-reactive Protein, Pentraxin-related (CRP, Accession XM_049673). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRP. Huntingtin (Huntington disease) (HD, Accession NM_002111) is another VGAM2034 host target gene. HD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HD BINDING SITE, designated SEQ ID:7898, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71309] Another function of VGAM2034 is therefore inhibition of Huntingtin (Huntington disease) (HD, Accession NM_002111). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HD. LAPTM5 (Accession

NM_006762) is another VGAM2034 host target gene. LAPTM5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LAPTM5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAPTM5 BINDING SITE, designated SEQ ID:13618, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71310] Another function of VGAM2034 is therefore inhibition of LAPTM5 (Accession NM_006762). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAPTM5. Non-POU Domain Containing, Octamer-binding (NONO, Accession XM_088688) is another VGAM2034 host target gene. NONO BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NONO, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NONO BINDING SITE, designated SEQ ID:39901, to the nucleotide sequence of

VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71311] Another function of VGAM2034 is therefore inhibition of Non-POU Domain Containing, Octamer-binding (NONO, Accession XM_088688), a gene which is a nuclear protein which contains RNA recognition motifs. Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NONO. The function of NONO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM95.Proprotein Convertase Subtilisin/kexin Type 1 (PCSK1, Accession NM_000439) is another VGAM2034 host target gene. PCSK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCSK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCSK1 BINDING SITE, designated SEQ ID:6024, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71312] Another function of VGAM2034 is therefore inhibition of

Proprotein Convertase Subtilisin/kexin Type 1 (PCSK1, Accession NM_000439), a gene which processes hormone precursors by cleaving paired basic amino acids; serine protease of the subtilase family. Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCSK1. The function of PCSK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1398.APELIN (Accession NM_017413) is another VGAM2034 host target gene. APELIN BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by APELIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APELIN BINDING SITE, designated SEQ ID:18872, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71313] Another function of VGAM2034 is therefore inhibition of APELIN (Accession NM_017413). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APELIN.

Apoptosis Inhibitor 5 (API5, Accession NM_006595) is another VGAM2034 host target gene. API5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by API5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of API5 BINDING SITE, designated SEQ ID:13363, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71314] Another function of VGAM2034 is therefore inhibition of Apoptosis Inhibitor 5 (API5, Accession NM_006595). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with API5. FLJ20979 (Accession NM_024121) is another VGAM2034 host target gene. FLJ20979 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20979, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20979 BINDING SITE, designated SEQ ID:23575, to the nucleotide sequence of VGAM2034 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4745.

[71315] Another function of VGAM2034 is therefore inhibition of FLJ20979 (Accession NM_024121). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20979. KIAA0441 (Accession NM_014797) is another VGAM2034 host target gene. KIAA0441 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0441, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0441 BINDING SITE, designated SEQ ID:16711, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71316] Another function of VGAM2034 is therefore inhibition of KIAA0441 (Accession NM_014797). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0441. MGC15437 (Accession NM_032873) is another VGAM2034 host target gene. MGC15437 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC15437, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15437 BINDING SITE, designated SEQ ID:26691, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71317] Another function of VGAM2034 is therefore inhibition of MGC15437 (Accession NM_032873). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15437. LOC144079 (Accession XM_084711) is another VGAM2034 host target gene. LOC144079 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144079, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144079 BINDING SITE, designated SEQ ID:37673, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71318] Another function of VGAM2034 is therefore inhibition of LOC144079 (Accession XM_084711). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC144079. LOC146455 (Accession XM_085471) is another VGAM2034 host target gene. LOC146455 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146455, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146455 BINDING SITE, designated SEQ ID:38160, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71319] Another function of VGAM2034 is therefore inhibition of LOC146455 (Accession XM_085471). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146455. LOC152762 (Accession XM_087518) is another VGAM2034 host target gene. LOC152762 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152762, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152762 BINDING SITE, designated SEQ ID:39307, to

the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71320] Another function of VGAM2034 is therefore inhibition of LOC152762 (Accession XM_087518). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152762. LOC153196 (Accession XM_098323) is another VGAM2034 host target gene. LOC153196 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153196 BINDING SITE, designated SEQ ID:41591, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71321] Another function of VGAM2034 is therefore inhibition of LOC153196 (Accession XM_098323). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153196. LOC153505 (Accession XM_087693) is another VGAM2034 host target gene. LOC153505 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC153505, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153505 BINDING SITE, designated SEQ ID:39384, to the nucleotide sequence of VGAM2034 RNA, herein designated VGAM RNA, also designated SEQ ID:4745.

[71322] Another function of VGAM2034 is therefore inhibition of LOC153505 (Accession XM_087693). Accordingly, utilities of VGAM2034 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153505. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2035 (VGAM2035) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71323] VGAM2035 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2035 was detected is described hereinabove with reference to Figs. 1-8.

[71324] VGAM2035 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Zaire Ebola Virus (ZEBOV). VGAM2035 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71325] VGAM2035 gene encodes a VGAM2035 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2035 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2035 precursor RNA is designated SEQ ID:2021, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2021 is located at position 12837 relative to the genome of Zaire Ebola Virus (ZEBOV).

[71326] VGAM2035 precursor RNA folds onto itself, forming VGAM2035 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71327] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2035 folded precursor RNA into VGAM2035 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2035 RNA is designated SEQ ID:4746, and is provided hereinbelow with reference to the sequence listing part.

[71328] VGAM2035 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2035 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2035 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71329] VGAM2035 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2035 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2035 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2035 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2035 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71330] The complementary binding of VGAM2035 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2035 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2035

host target RNA into VGAM2035 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71331] It is appreciated that VGAM2035 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2035 host target genes. The mRNA of each one of this plurality of VGAM2035 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2035 RNA, herein designated VGAM RNA, and which when bound by VGAM2035 RNA causes inhibition of translation of respective one or more VGAM2035 host target proteins.

[71332] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2035 gene, herein designated VGAM GENE, on one or more VGAM2035 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71333] It is yet further appreciated that a function of VGAM2035 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of viral infection by Zaire Ebola Virus (ZEBOV). Specific functions, and accordingly utilities, of VGAM2035 correlate with, and may be deduced from, the identity of the host target genes which VGAM2035 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71334] Nucleotide sequences of the VGAM2035 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2035 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2035 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2035 are further

described hereinbelow with reference to Table 1.

[71335] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2035 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2035 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71336] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2035 gene, herein designated VGAM is inhibition of expression of VGAM2035 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2035 correlate with, and may be deduced from, the identity of the target genes which VGAM2035 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71337] Activating Transcription Factor 5 (ATF5, Accession NM_012068) is a VGAM2035 host target gene. ATF5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ATF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

ATF5 BINDING SITE, designated SEQ ID:14319, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71338] A function of VGAM2035 is therefore inhibition of Activating Transcription Factor 5 (ATF5, Accession NM_012068), a gene which binds to cAMP-inducible promoters and is involved in gene transcription. Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATF5. The function of ATF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM588.Interleukin 8 Receptor, Alpha (IL8RA, Accession NM_000634) is another VGAM2035 host target gene. IL8RA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL8RA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL8RA BINDING SITE, designated SEQ ID:6265, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71339] Another function of VGAM2035 is therefore inhibition of

Interleukin 8 Receptor, Alpha (IL8RA, Accession NM_000634), a gene which is the receptor to interleukin-8, which is a powerful neutrophils chemotactic factor. Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL8RA. The function of IL8RA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM300.Paraoxonase 1 (PON1, Accession NM_000446) is another VGAM2035 host target gene. PON1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PON1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PON1 BINDING SITE, designated SEQ ID:6032, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71340] Another function of VGAM2035 is therefore inhibition of Paraoxonase 1 (PON1, Accession NM_000446), a gene which hydrolyzes the toxic metabolites of a variety of organophosphorus insecticides. Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PON1. The function of PON1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1956.SH3-domain Binding Protein 4 (SH3BP4, Accession NM_014521) is another VGAM2035 host target gene. SH3BP4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3BP4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3BP4 BINDING SITE, designated SEQ ID:15853, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71341] Another function of VGAM2035 is therefore inhibition of SH3-domain Binding Protein 4 (SH3BP4, Accession NM_014521), a gene which is of unknown function, contains SH3-domain binding protein 4; similar to the EH-binding protein. Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BP4. The function of SH3BP4 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM179.FLJ10540 (Accession NM_018131) is another VGAM2035 host target gene. FLJ10540 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10540, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10540 BINDING SITE, designated SEQ ID:19926, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71342] Another function of VGAM2035 is therefore inhibition of FLJ10540 (Accession NM_018131). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10540. FLJ11370 (Accession NM_024961) is another VGAM2035 host target gene. FLJ11370 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11370, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11370

BINDING SITE, designated SEQ ID:24516, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71343] Another function of VGAM2035 is therefore inhibition of FLJ11370 (Accession NM_024961). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11370. FLJ21272 (Accession NM_025032) is another VGAM2035 host target gene. FLJ21272 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21272, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21272 BINDING SITE, designated SEQ ID:24630, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71344] Another function of VGAM2035 is therefore inhibition of FLJ21272 (Accession NM_025032). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21272. HSMPP8 (Accession XM_167894) is another VGAM2035 host target gene. HSMPP8 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSMPP8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSMPP8 BINDING SITE, designated SEQ ID:44903, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71345] Another function of VGAM2035 is therefore inhibition of HSMPP8 (Accession XM_167894). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSMPP8. KIAA0431 (Accession NM_015251) is another VGAM2035 host target gene. KIAA0431 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0431, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0431 BINDING SITE, designated SEQ ID:17578, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71346] Another function of VGAM2035 is therefore inhibition of KIAA0431 (Accession NM_015251). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0431. KIAA0562 (Accession NM_014704) is another VGAM2035 host target gene. KIAA0562 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0562, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0562 BINDING SITE, designated SEQ ID:16241, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71347] Another function of VGAM2035 is therefore inhibition of KIAA0562 (Accession NM_014704). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0562. KIAA1789 (Accession XM_040486) is another VGAM2035 host target gene. KIAA1789 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1789, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1789 BINDING SITE, designated SEQ ID:33308, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71348] Another function of VGAM2035 is therefore inhibition of KIAA1789 (Accession XM_040486). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1789. LIN-7-C (Accession NM_018362) is another VGAM2035 host target gene. LIN-7-C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIN-7-C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIN-7-C BINDING SITE, designated SEQ ID:20371, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71349] Another function of VGAM2035 is therefore inhibition of LIN-7-C (Accession NM_018362). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIN-

7-C. LOC119504 (Accession XM_058400) is another VGAM2035 host target gene. LOC119504 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC119504, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC119504 BINDING SITE, designated SEQ ID:36615, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71350] Another function of VGAM2035 is therefore inhibition of LOC119504 (Accession XM_058400). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC119504. LOC145547 (Accession XM_085167) is another VGAM2035 host target gene. LOC145547 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145547, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145547 BINDING SITE, designated SEQ ID:37895, to the nucleotide sequence of VGAM2035 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4746.

[71351] Another function of VGAM2035 is therefore inhibition of LOC145547 (Accession XM_085167). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145547. LOC203339 (Accession XM_117534) is another VGAM2035 host target gene. LOC203339 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203339, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203339 BINDING SITE, designated SEQ ID:43525, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71352] Another function of VGAM2035 is therefore inhibition of LOC203339 (Accession XM_117534). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203339. LOC253128 (Accession XM_170726) is another VGAM2035 host target gene. LOC253128 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253128, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253128 BINDING SITE, designated SEQ ID:45487, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71353] Another function of VGAM2035 is therefore inhibition of LOC253128 (Accession XM_170726). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253128. LOC254065 (Accession XM_173239) is another VGAM2035 host target gene. LOC254065 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254065, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254065 BINDING SITE, designated SEQ ID:46523, to the nucleotide sequence of VGAM2035 RNA, herein designated VGAM RNA, also designated SEQ ID:4746.

[71354] Another function of VGAM2035 is therefore inhibition of LOC254065 (Accession XM_173239). Accordingly, utilities of VGAM2035 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC254065. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2036 (VGAM2036) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71355] VGAM2036 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2036 was detected is described hereinabove with reference to Figs. 1-8.

[71356] VGAM2036 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Marburg Virus. VGAM2036 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71357] VGAM2036 gene encodes a VGAM2036 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2036 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2036 precursor RNA is desig-

nated SEQ ID:2022, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2022 is located at position 4709 relative to the genome of Marburg Virus.

[71358] VGAM2036 precursor RNA folds onto itself, forming VGAM2036 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71359] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2036 folded precursor RNA into VGAM2036 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2036 RNA is designated SEQ ID:4747, and is provided hereinbelow with reference to the sequence

listing part.

[71360] VGAM2036 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2036 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2036 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71361] VGAM2036 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2036 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2036 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2036 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2036 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71362] The complementary binding of VGAM2036 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2036 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2036 host target RNA into VGAM2036 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71363] It is appreciated that VGAM2036 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2036 host target genes. The mRNA of each one of this plurality of VGAM2036 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2036 RNA, herein designated VGAM

RNA, and which when bound by VGAM2036 RNA causes inhibition of translation of respective one or more VGAM2036 host target proteins.

[71364] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2036 gene, herein designated VGAM GENE, on one or more VGAM2036 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71365] It is yet further appreciated that a function of VGAM2036 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2036 include diagnosis, prevention and treatment of viral infection by Marburg Virus. Specific functions, and accordingly utilities, of VGAM2036 correlate with, and may be deduced from, the identity of the host target genes which VGAM2036 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71366] Nucleotide sequences of the VGAM2036 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2036 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2036 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2036 are further described hereinbelow with reference to Table 1.

[71367] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2036 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2036 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71368] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2036 gene, herein designated VGAM is

inhibition of expression of VGAM2036 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2036 correlate with, and may be deduced from, the identity of the target genes which VGAM2036 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71369] Death-associated Protein (DAP, Accession XM_051902) is a VGAM2036 host target gene. DAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAP BINDING SITE, designated SEQ ID:35915, to the nucleotide sequence of VGAM2036 RNA, herein designated VGAM RNA, also designated SEQ ID:4747.

[71370] A function of VGAM2036 is therefore inhibition of Death-associated Protein (DAP, Accession XM_051902), a gene which mediates in programmed cell death . Accordingly, utilities of VGAM2036 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAP. The function of DAP has been established by previous studies. Deiss et al. (1995) reported that

gamma-interferon (OMIM Ref. No. 147570) induced in HeLa cells a type of death that had cytologic characteristics of programmed cell death. In this system, they identified 2 novel genes whose expression was indispensable for the execution of this type of cell death. The rescue was based on positive growth selection of cells after transfection with antisense cDNA expression libraries. The antisense RNA-mediated inactivation of the 2 novel genes protected the cells from the IFNG-induced cell death, but not from the cytostatic effects of the cytokine or from a necrotic type of cell death. One of these genes was death-associated protein kinase-1 (OMIM Ref. No. 600831). The other, designated death-associated protein (DAP), was expressed as a single 2.4-kb mRNA that encodes a basic, proline-rich, 15-kD protein. The expression levels of the 2 proteins were selectively reduced by the corresponding antisense RNAs. The authors suggested that these 2 novel genes are candidates for positive mediators of programmed cell death that is induced by interferon-gamma. By analysis of rodent-human somatic cell hybrids, Feinstein et al. (1995) found that DAP is located on chromosome 5p15.2 in a region just centromeric to that to which the cri-du-chat syndrome (OMIM Ref. No. 123450) has

been mapped

[71371] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[71372] Deiss, L. P.; Feinstein, E.; Berissi, H.; Cohen, O.; Kimchi, A. : Identification of a novel serine/threonine kinase and a novel 15-kD protein as potential mediators of the gamma interferon-induced cell death. Genes Dev. 9: 15-30, 1995. ; and

[71373] Feinstein, E.; Druck, T.; Kastury, K.; Berissi, H.; Goodart, S. A.; Overhauser, J.; Kimchi, A.; Huebner, K. : Assignment of DAP1 and DAPK: genes that positively mediate pro-grammed cell.

[71374] Further studies establishing the function and utilities of DAP are found in John Hopkins OMIM database record ID 600954, and in sited publications numbered 8217-8218 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Zinc Finger Protein 256 (ZNF256, Accession NM_005773) is another VGAM2036 host target gene. ZNF256 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF256, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF256 BINDING SITE, designated SEQ ID:12346, to the nucleotide sequence of VGAM2036 RNA, herein designated VGAM RNA, also designated SEQ ID:4747.

[71375] Another function of VGAM2036 is therefore inhibition of Zinc Finger Protein 256 (ZNF256, Accession NM_005773). Accordingly, utilities of VGAM2036 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF256. KIAA1843 (Accession XM_030838) is another VGAM2036 host target gene. KIAA1843 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1843, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1843 BINDING SITE, designated SEQ ID:31161, to the nucleotide sequence of VGAM2036 RNA, herein designated VGAM RNA, also designated SEQ ID:4747.

[71376] Another function of VGAM2036 is therefore inhibition of KIAA1843 (Accession XM_030838). Accordingly, utilities of VGAM2036 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1843. PRO0456 (Accession NM_014127) is another VGAM2036 host target gene. PRO0456 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO0456, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0456 BINDING SITE, designated SEQ ID:15393, to the nucleotide sequence of VGAM2036 RNA, herein designated VGAM RNA, also designated SEQ ID:4747.

[71377] Another function of VGAM2036 is therefore inhibition of PRO0456 (Accession NM_014127). Accordingly, utilities of VGAM2036 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0456. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2037 (VGAM2037) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71378] VGAM2037 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2037 was detected is described hereinabove with reference to Figs. 1-8.

[71379] VGAM2037 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Marburg Virus. VGAM2037 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71380] VGAM2037 gene encodes a VGAM2037 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2037 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2037 precursor RNA is designated SEQ ID:2023, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2023 is located at position 17431 relative to the genome of Marburg Virus.

[71381] VGAM2037 precursor RNA folds onto itself, forming VGAM2037 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71382] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2037 folded precursor RNA into VGAM2037 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2037 RNA is designated SEQ ID:4748, and is provided hereinbelow with reference to the sequence listing part.

[71383] VGAM2037 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2037 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2037 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71384] VGAM2037 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2037 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2037 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2037 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2037 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71385] The complementary binding of VGAM2037 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2037 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2037 host target RNA into VGAM2037 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71386] It is appreciated that VGAM2037 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2037 host target genes. The mRNA of each one of this plurality of VGAM2037 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2037 RNA, herein designated VGAM RNA, and which when bound by VGAM2037 RNA causes inhibition of translation of respective one or more VGAM2037 host target proteins.

[71387] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2037 gene, herein designated VGAM GENE, on one or more VGAM2037 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71388] It is yet further appreciated that a function of VGAM2037 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2037 include diagnosis, prevention and treatment of viral infection by Marburg Virus. Specific functions, and accordingly utilities, of VGAM2037 correlate with, and may be deduced from, the identity of the host target genes which VGAM2037 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71389] Nucleotide sequences of the VGAM2037 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2037 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2037 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2037 are further described hereinbelow with reference to Table 1.

[71390] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2037 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2037 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71391] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2037 gene, herein designated VGAM is inhibition of expression of VGAM2037 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2037 correlate with, and may be deduced from, the identity of the target genes which VGAM2037 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71392] FLJ20449 (Accession NM_017826) is a VGAM2037 host target gene. FLJ20449 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by FLJ20449, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20449 BINDING SITE, designated SEQ ID:19486, to the nucleotide sequence of VGAM2037 RNA, herein designated VGAM RNA, also designated SEQ ID:4748.

[71393] A function of VGAM2037 is therefore inhibition of FLJ20449 (Accession NM_017826). Accordingly, utilities of VGAM2037 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20449. FLJ21044 (Accession NM_022370) is another VGAM2037 host target gene. FLJ21044 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ21044, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21044 BINDING SITE, designated SEQ ID:22759, to the nucleotide sequence of VGAM2037 RNA, herein designated VGAM RNA, also designated SEQ ID:4748.

[71394] Another function of VGAM2037 is therefore inhibition of FLJ21044 (Accession NM_022370). Accordingly, utilities of

VGAM2037 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21044. KIAA0354 (Accession NM_014872) is another VGAM2037 host target gene. KIAA0354 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0354, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0354 BINDING SITE, designated SEQ ID:16996, to the nucleotide sequence of VGAM2037 RNA, herein designated VGAM RNA, also designated SEQ ID:4748.

[71395] Another function of VGAM2037 is therefore inhibition of KIAA0354 (Accession NM_014872). Accordingly, utilities of VGAM2037 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0354. KIAA0534 (Accession XM_049349) is another VGAM2037 host target gene. KIAA0534 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0534, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0534 BINDING SITE, designated SEQ ID:35378, to the nucleotide sequence of VGAM2037 RNA, herein designated VGAM RNA, also designated SEQ ID:4748.

[71396] Another function of VGAM2037 is therefore inhibition of KIAA0534 (Accession XM_049349). Accordingly, utilities of VGAM2037 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0534. KIAA0825 (Accession XM_027906) is another VGAM2037 host target gene. KIAA0825 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0825, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0825 BINDING SITE, designated SEQ ID:30591, to the nucleotide sequence of VGAM2037 RNA, herein designated VGAM RNA, also designated SEQ ID:4748.

[71397] Another function of VGAM2037 is therefore inhibition of KIAA0825 (Accession XM_027906). Accordingly, utilities of VGAM2037 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0825. LOC115207 (Accession NM_138444) is another VGAM2037 host target gene. LOC115207 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115207, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115207 BINDING SITE, designated SEQ ID:28808, to the nucleotide sequence of VGAM2037 RNA, herein designated VGAM RNA, also designated SEQ ID:4748.

[71398] Another function of VGAM2037 is therefore inhibition of LOC115207 (Accession NM_138444). Accordingly, utilities of VGAM2037 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115207. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2038 (VGAM2038) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71399] VGAM2038 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2038 was detected is described hereinabove with reference to Figs. 1-8.

[71400] VGAM2038 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Kyuri Green Mottle Mosaic Virus. VGAM2038 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71401] VGAM2038 gene encodes a VGAM2038 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2038 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2038 precursor RNA is designated SEQ ID:2024, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2024 is located at position 2310 relative to the genome of Kyuri Green Mottle Mosaic Virus.

[71402] VGAM2038 precursor RNA folds onto itself, forming VGAM2038 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[71403] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2038 folded precursor RNA into VGAM2038 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2038 RNA is designated SEQ ID:4749, and is provided hereinbelow with reference to the sequence listing part.

[71404] VGAM2038 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2038 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2038 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71405] VGAM2038 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2038 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2038 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2038 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2038 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71406] The complementary binding of VGAM2038 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2038 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2038 host target RNA into VGAM2038 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71407] It is appreciated that VGAM2038 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2038 host target genes. The mRNA of each one of this plurality of VGAM2038 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2038 RNA, herein designated VGAM RNA, and which when bound by VGAM2038 RNA causes inhibition of translation of respective one or more VGAM2038 host target proteins.

[71408] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2038 gene, herein designated VGAM GENE, on one or more VGAM2038 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71409] It is yet further appreciated that a function of VGAM2038 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2038 include diagnosis, prevention and treatment of viral infection by Kyuri Green Mottle Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2038 correlate with, and may be deduced from, the identity of the host target genes which VGAM2038 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71410] Nucleotide sequences of the VGAM2038 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2038 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2038 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2038 are further described hereinbelow with reference to Table 1.

[71411] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2038 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2038 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71412] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2038 gene, herein designated VGAM is inhibition of expression of VGAM2038 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2038 correlate with, and may be deduced from, the identity of the target genes which VGAM2038 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71413] FLJ20298 (Accession NM_017752) is a VGAM2038 host target gene. FLJ20298 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20298, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of FLJ20298 BINDING SITE, designated SEQ ID:19362, to the nucleotide sequence of VGAM2038 RNA, herein designated VGAM RNA, also designated SEQ ID:4749.

[71414] A function of VGAM2038 is therefore inhibition of FLJ20298 (Accession NM_017752). Accordingly, utilities of VGAM2038 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20298. LOC201695 (Accession XM_120432) is another VGAM2038 host target gene. LOC201695 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201695, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201695 BINDING SITE, designated SEQ ID:43609, to the nucleotide sequence of VGAM2038 RNA, herein designated VGAM RNA, also designated SEQ ID:4749.

[71415] Another function of VGAM2038 is therefore inhibition of LOC201695 (Accession XM_120432). Accordingly, utilities of VGAM2038 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201695. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2039 (VGAM2039) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71416] VGAM2039 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2039 was detected is described hereinabove with reference to Figs. 1-8.

[71417] VGAM2039 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Marburg Virus. VGAM2039 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71418] VGAM2039 gene encodes a VGAM2039 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2039 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2039 precursor RNA is designated SEQ ID:2025, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2025 is located at position 2481 relative to the genome of Marburg Virus.

[71419] VGAM2039 precursor RNA folds onto itself, forming VGAM2039 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71420] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2039 folded precursor RNA into VGAM2039 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2039 RNA is designated SEQ ID:4750, and is provided hereinbelow with reference to the sequence listing part.

[71421] VGAM2039 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2039 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2039 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71422] VGAM2039 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2039 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2039 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2039 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2039 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71423] The complementary binding of VGAM2039 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2039 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2039 host target RNA into VGAM2039 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71424] It is appreciated that VGAM2039 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2039 host target genes. The mRNA of each one of this plurality of VGAM2039 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2039 RNA, herein designated VGAM RNA, and which when bound by VGAM2039 RNA causes inhibition of translation of respective one or more

VGAM2039 host target proteins.

[71425] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2039 gene, herein designated VGAM GENE, on one or more VGAM2039 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71426] It is yet further appreciated that a function of VGAM2039 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of viral infection by Marburg Virus. Specific

functions, and accordingly utilities, of VGAM2039 correlate with, and may be deduced from, the identity of the host target genes which VGAM2039 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71427] Nucleotide sequences of the VGAM2039 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2039 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2039 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2039 are further described hereinbelow with reference to Table 1.

[71428] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2039 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2039 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71429] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2039 gene, herein designated VGAM is inhibition of expression of VGAM2039 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2039 correlate with, and may be deduced from, the identity of the target genes which VGAM2039 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71430] ABH (Accession XM_007409) is a VGAM2039 host target gene. ABH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABH BINDING SITE, designated SEQ ID:30055, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71431] A function of VGAM2039 is therefore inhibition of ABH (Accession XM_007409). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABH. Attractin (ATRN, Accession NM_139321) is another VGAM2039 host target gene. ATRN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATRN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of ATRN BINDING SITE, designated SEQ ID:29299, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71432] Another function of VGAM2039 is therefore inhibition of Attractin (ATRN, Accession NM_139321), a gene which is involved in the initial immune cell clustering during inflammatory response. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATRN. The function of ATRN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM53.Cardiotrophin 1 (CTF1, Accession NM_001330) is another VGAM2039 host target gene. CTF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CTF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTF1 BINDING SITE, designated SEQ ID:7011, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71433] Another function of VGAM2039 is therefore inhibition of Cardiotrophin 1 (CTF1, Accession NM_001330), a gene which may play a role in cardiac hypertrophy. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTF1. The function of CTF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM71.Dystrobrevin, Alpha (DTNA, Accession NM_001390) is another VGAM2039 host target gene. DTNA BINDING SITE1 and DTNA BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DTNA, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DTNA BINDING SITE1 and DTNA BINDING SITE2, designated SEQ ID:7078 and SEQ ID:7081 respectively, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71434] Another function of VGAM2039 is therefore inhibition of Dystrobrevin, Alpha (DTNA, Accession NM_001390), a gene which may be involved in the formation and stability

of synapses. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DTNA. The function of DTNA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1021.Glucosamine-6-phosphate Isomerase (GNPI, Accession NM_005471) is another VGAM2039 host target gene. GNPI BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNPI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNPI BINDING SITE, designated SEQ ID:11966, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71435] Another function of VGAM2039 is therefore inhibition of Glucosamine-6-phosphate Isomerase (GNPI, Accession NM_005471), a gene which converts glucosamine-6-phosphate to fructose-6-phosphate. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNPI. The function of GNPI and its association with

various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM124.Inducible T-cell Co-stimulator (ICOS, Accession NM_012092) is another VGAM2039 host target gene. ICOS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICOS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ICOS BINDING SITE, designated SEQ ID:14388, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71436] Another function of VGAM2039 is therefore inhibition of Inducible T-cell Co-stimulator (ICOS, Accession NM_012092), a gene which forms homodimers and functions as an inducible T-cell co-stimulator. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICOS. The function of ICOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM18.Insulin Receptor (INSR, Accession

XM_048346) is another VGAM2039 host target gene. INSR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by INSR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of INSR BINDING SITE, designated SEQ ID:35155, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71437] Another function of VGAM2039 is therefore inhibition of Insulin Receptor (INSR, Accession XM_048346), a gene which binds insulin and has a tyrosine-protein kinase activity. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INSR. The function of INSR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Integrin, Alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4, Accession NM_000885) is another VGAM2039 host target gene. ITGA4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ITGA4, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA4 BINDING SITE, designated SEQ ID:6582, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71438] Another function of VGAM2039 is therefore inhibition of Integrin, Alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4, Accession NM_000885), a gene which recognizes one or more domains within the alternatively spliced cs-1 and cs-5 regions of fibronectin. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA4. The function of ITGA4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1096.LNK (Accession NM_005475) is another VGAM2039 host target gene. LNK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LNK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LNK BINDING

SITE, designated SEQ ID:11973, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71439] Another function of VGAM2039 is therefore inhibition of LNK (Accession NM_005475), a gene which links T-cell receptor activation signal to phospholipase c-gamma-1, grb-2 and phosphatidylinositol 3-kinase (by similarity). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LNK. The function of LNK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM115.V-maf Musculoaponeurotic Fibrosarcoma Oncogene Homolog (avian) (MAF, Accession NM_005360) is another VGAM2039 host target gene. MAF BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAF BINDING SITE, designated SEQ ID:11835, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ

ID:4750.

[71440] Another function of VGAM2039 is therefore inhibition of V-maf Musculoaponeurotic Fibrosarcoma Oncogene Homolog (avian) (MAF, Accession NM_005360), a gene which is a transcription factor; contains a leucine zipper motif. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAF. The function of MAF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM822.Mastermind-like 1 (Drosophila) (MAML1, Accession NM_014757) is another VGAM2039 host target gene. MAML1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAML1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAML1 BINDING SITE, designated SEQ ID:16498, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71441] Another function of VGAM2039 is therefore inhibition of Mastermind-like 1 (Drosophila) (MAML1, Accession

NM_014757), a gene which MAML1 functions as a transcriptional coactivator for Notch signaling. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAML1. The function of MAML1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM556.Matrix Metalloproteinase 13 (collagenase 3) (MMP13, Accession NM_002427) is another VGAM2039 host target gene. MMP13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MMP13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MMP13 BINDING SITE, designated SEQ ID:8260, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71442] Another function of VGAM2039 is therefore inhibition of Matrix Metalloproteinase 13 (collagenase 3) (MMP13, Accession NM_002427). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMP13. Neu-

rotrophic Tyrosine Kinase, Receptor, Type 2 (NTRK2, Accession NM_006180) is another VGAM2039 host target gene. NTRK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NTRK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NTRK2 BINDING SITE, designated SEQ ID:12842, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71443] Another function of VGAM2039 is therefore inhibition of Neurotrophic Tyrosine Kinase, Receptor, Type 2 (NTRK2, Accession NM_006180), a gene which is involved in the development and/or maintenance of the nervous system. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTRK2. The function of NTRK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM341.2'-5'-oligoadenylate Synthetase 3, 100kDa (OAS3, Accession NM_006187) is another VGAM2039 host

target gene. OAS3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OAS3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OAS3 BINDING SITE, designated SEQ ID:12861, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71444] Another function of VGAM2039 is therefore inhibition of 2'-5'-oligoadenylate Synthetase 3, 100kDa (OAS3, Accession NM_006187), a gene which may play a role in mediating resistance to virus infection, control of cell growth, differentiation, and apoptosis. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OAS3. The function of OAS3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM309.Prostaglandin F2 Receptor Negative Regulator (PTGFRN, Accession XM_040709) is another VGAM2039 host target gene. PTGFRN BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by PTGFRN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTGFRN BINDING SITE, designated SEQ ID:33364, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71445] Another function of VGAM2039 is therefore inhibition of Prostaglandin F2 Receptor Negative Regulator (PTGFRN, Accession XM_040709), a gene which inhibits the binding of prostaglandin f2-alpha (pgf2- alpha) to its specific fp receptor. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGFRN. The function of PTGFRN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM125.Regulator of G-protein Signalling 16 (RGS16, Accession NM_002928) is another VGAM2039 host target gene. RGS16 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RGS16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of RGS16 BINDING SITE, designated SEQ ID:8832, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71446] Another function of VGAM2039 is therefore inhibition of Regulator of G-protein Signalling 16 (RGS16, Accession NM_002928), a gene which inhibits signal transduction. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS16. The function of RGS16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1843.Regulator of G-protein Signalling 19 Interacting Protein 1 (RGS19IP1, Accession XM_031263) is another VGAM2039 host target gene. RGS19IP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RGS19IP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RGS19IP1 BINDING SITE, designated SEQ ID:31325, to the nucleotide

sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71447] Another function of VGAM2039 is therefore inhibition of Regulator of G-protein Signalling 19 Interacting Protein 1 (RGS19IP1, Accession XM_031263), a gene which is involved in g protein-linked signaling. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS19IP1. The function of RGS19IP1 has been established by previous studies. Northern blot analysis detected a 1.8-kb C19ORF3 transcript in all tissues tested, with strongest expression in pancreas, followed by skeletal muscle, brain, kidney, placenta, lung, liver, and lowest expression in heart. Expression levels did not correlate with those of GAIP. Immunoblot analysis demonstrated the presence of C19ORF3 primarily in cytosolic fractions but also in membrane fractions. Immunofluorescence analysis showed expression of endogenous C19ORF3 in both a diffuse and a punctate staining pattern throughout the cytoplasm. Using a yeast 2-hybrid system, Bunn et al. (1999) isolated a cDNA encoding C19ORF3, which they called GLUT1CBP (GLUT1 (SLC2A1; 138140) C-terminus-binding protein). SDS-PAGE and Western blot anal-

yses determined that C19ORF3 is expressed as a 39-kD protein in all tissues tested except small intestine. Yeast 2-hybrid analysis showed that C19ORF3 binds SLC2A1 through its PDZ domain. Northern blot analysis revealed similar expression patterns for C19ORF3 and SLC2A1, with both being expressed most strongly in brain. Using a yeast 2-hybrid screen for brain-interacting proteins, the authors determined that only SLC2A1, KIF1B, and alpha actinin-1 (ACTN1; 102575) bind C19ORF3 through its PDZ domain; myosin VI (MYO6; 600970) was shown to interact with C19ORF3 but not via the PDZ domain.

[71448] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[71449] Bunn, R. C.; Jensen, M. A.; Reed, B. C. : Protein interactions with the glucose transporter binding protein GLUT1CBP that provide a link between GLUT1 and the cytoskeleton. Molec. Biol. Cell 10: 819-832, 1999. ; and

[71450] Von Kap-Herr, C.; Kandala, G.; Mann, S. S.; Hart, T. C.; Pettenati, M. J.; Setaluri, V. : Assignment of PDZ domain-containing protein GIPC gene (C19orf3) to human chromosome band 19p13.1 b.

[71451] Further studies establishing the function and utilities of

RGS19IP1 are found in John Hopkins OMIM database record ID 605072, and in sited publications numbered 6953-6955 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.SRY (sex determining region Y)-box 12 (SOX12, Accession NM_006943) is another VGAM2039 host target gene. SOX12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX12 BINDING SITE, designated SEQ ID:13830, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71452] Another function of VGAM2039 is therefore inhibition of SRY (sex determining region Y)-box 12 (SOX12, Accession NM_006943). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX12. Transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM2, Accession NM_004613) is another VGAM2039 host target gene.

TGM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TGM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TGM2 BINDING SITE, designated SEQ ID:10954, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71453] Another function of VGAM2039 is therefore inhibition of Transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM2, Accession NM_004613), a gene which catalyzes the cross-linking of proteins and the conjugation of polyamines to proteins. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGM2. The function of TGM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM899.Tumor Protein P63 (TP63, Accession NM_003722) is another VGAM2039 host target gene. TP63 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TP63, corresponding to a HOST TARGET bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TP63 BINDING SITE, designated SEQ ID:9815, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71454] Another function of VGAM2039 is therefore inhibition of Tumor Protein P63 (TP63, Accession NM_003722). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP63. Vitamin D (1,25- dihydroxyvitamin D3) Receptor (VDR, Accession NM_000376) is another VGAM2039 host target gene. VDR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VDR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VDR BINDING SITE, designated SEQ ID:5947, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71455] Another function of VGAM2039 is therefore inhibition of Vitamin D (1,25- dihydroxyvitamin D3) Receptor (VDR,

Accession NM_000376). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VDR. Williams-Beuren Syndrome Chromosome Region 1 (WBSCR1, Accession NM_022170) is another VGAM2039 host target gene. WBSCR1 BINDING SITE1 and WBSCR1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WBSCR1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WBSCR1 BINDING SITE1 and WBSCR1 BINDING SITE2, designated SEQ ID:22722 and SEQ ID:25705 respectively, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71456] Another function of VGAM2039 is therefore inhibition of Williams-Beuren Syndrome Chromosome Region 1 (WBSCR1, Accession NM_022170), a gene which stimulates protein translation. Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR1. The function of WBSCR1 and its association with various diseases and clinical conditions, has been estab-

lished by previous studies, as described hereinabove with reference to VGAM110.Basic, Immunoglobulin-like Variable Motif Containing (BIVM, Accession NM_017693) is another VGAM2039 host target gene. BIVM BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BIVM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIVM BINDING SITE, designated SEQ ID:19252, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71457] Another function of VGAM2039 is therefore inhibition of Basic, Immunoglobulin-like Variable Motif Containing (BIVM, Accession NM_017693). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIVM. Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273) is another VGAM2039 host target gene. CHST3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHST3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of CHST3 BINDING SITE, designated SEQ ID:10480, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71458] Another function of VGAM2039 is therefore inhibition of Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHST3. CPR2 (Accession NM_030900) is another VGAM2039 host target gene. CPR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CPR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPR2 BINDING SITE, designated SEQ ID:25175, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71459] Another function of VGAM2039 is therefore inhibition of CPR2 (Accession NM_030900). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with CPR2. DCOHM (Accession NM_032151) is another VGAM2039 host target gene. DCOHM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCOHM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCOHM BINDING SITE, designated SEQ ID:25845, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71460] Another function of VGAM2039 is therefore inhibition of DCOHM (Accession NM_032151). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCOHM. FKSG44 (Accession NM_031904) is another VGAM2039 host target gene. FKSG44 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FKSG44, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FKSG44 BINDING SITE, designated SEQ ID:25648, to the nucleotide

sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71461] Another function of VGAM2039 is therefore inhibition of FKSG44 (Accession NM_031904). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKSG44. FLJ10932 (Accession NM_018277) is another VGAM2039 host target gene. FLJ10932 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10932, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10932 BINDING SITE, designated SEQ ID:20263, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71462] Another function of VGAM2039 is therefore inhibition of FLJ10932 (Accession NM_018277). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10932. FLJ20729 (Accession NM_017953) is another VGAM2039 host target gene. FLJ20729 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ20729, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20729 BINDING SITE, designated SEQ ID:19656, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71463] Another function of VGAM2039 is therefore inhibition of FLJ20729 (Accession NM_017953). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20729. FLJ21916 (Accession NM_023112) is another VGAM2039 host target gene. FLJ21916 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21916, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21916 BINDING SITE, designated SEQ ID:23380, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71464] Another function of VGAM2039 is therefore inhibition of FLJ21916 (Accession NM_023112). Accordingly, utilities of

VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21916. FLJ22202 (Accession NM_024883) is another VGAM2039 host target gene. FLJ22202 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22202, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22202 BINDING SITE, designated SEQ ID:24337, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71465] Another function of VGAM2039 is therefore inhibition of FLJ22202 (Accession NM_024883). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22202. FLJ23462 (Accession NM_024843) is another VGAM2039 host target gene. FLJ23462 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23462, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23462

BINDING SITE, designated SEQ ID:24266, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71466] Another function of VGAM2039 is therefore inhibition of FLJ23462 (Accession NM_024843). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23462. Glutamate Receptor, Ionotropic, Delta 1 (GRID1, Accession XM_043613) is another VGAM2039 host target gene. GRID1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRID1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRID1 BINDING SITE, designated SEQ ID:33980, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71467] Another function of VGAM2039 is therefore inhibition of Glutamate Receptor, Ionotropic, Delta 1 (GRID1, Accession XM_043613). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRID1. Hyaluronan Binding

Protein 2 (HABP2, Accession NM_004132) is another VGAM2039 host target gene. HABP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HABP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HABP2 BINDING SITE, designated SEQ ID:10344, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71468] Another function of VGAM2039 is therefore inhibition of Hyaluronan Binding Protein 2 (HABP2, Accession NM_004132). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HABP2. HEMK (Accession NM_016173) is another VGAM2039 host target gene. HEMK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HEMK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HEMK BINDING SITE, designated SEQ ID:18265, to the nucleotide sequence of VGAM2039 RNA, herein

designated VGAM RNA, also designated SEQ ID:4750.

[71469] Another function of VGAM2039 is therefore inhibition of HEMK (Accession NM_016173). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEMK. Interleukin 1 Receptor Accessory Protein-like 1 (IL1RAPL1, Accession NM_014271) is another VGAM2039 host target gene. IL1RAPL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IL1RAPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1RAPL1 BINDING SITE, designated SEQ ID:15552, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71470] Another function of VGAM2039 is therefore inhibition of Interleukin 1 Receptor Accessory Protein-like 1 (IL1RAPL1, Accession NM_014271). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1RAPL1. KIAA0459 (Accession XM_027862) is another VGAM2039 host target gene. KIAA0459 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:30575, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71471] Another function of VGAM2039 is therefore inhibition of KIAA0459 (Accession XM_027862). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459. KIAA0731 (Accession XM_039975) is another VGAM2039 host target gene. KIAA0731 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0731, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0731 BINDING SITE, designated SEQ ID:33241, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71472] Another function of VGAM2039 is therefore inhibition of

KIAA0731 (Accession XM_039975). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0731. KIAA0960 (Accession XM_166543) is another VGAM2039 host target gene. KIAA0960 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0960, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0960 BINDING SITE, designated SEQ ID:44517, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71473] Another function of VGAM2039 is therefore inhibition of KIAA0960 (Accession XM_166543). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0960. KIAA1045 (Accession XM_048592) is another VGAM2039 host target gene. KIAA1045 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1045, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1045 BINDING SITE, designated SEQ ID:35196, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71474] Another function of VGAM2039 is therefore inhibition of KIAA1045 (Accession XM_048592). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1045. KIAA1184 (Accession NM_022572) is another VGAM2039 host target gene. KIAA1184 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1184, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1184 BINDING SITE, designated SEQ ID:22897, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71475] Another function of VGAM2039 is therefore inhibition of KIAA1184 (Accession NM_022572). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1184. KIAA1323 (Accession XM_032146) is another

VGAM2039 host target gene. KIAA1323 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1323 BINDING SITE, designated SEQ ID:31561, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71476] Another function of VGAM2039 is therefore inhibition of KIAA1323 (Accession XM_032146). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1323. KIAA1908 (Accession XM_055834) is another VGAM2039 host target gene. KIAA1908 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1908, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1908 BINDING SITE, designated SEQ ID:36334, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71477] Another function of VGAM2039 is therefore inhibition of KIAA1908 (Accession XM_055834). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1908. MACMARCKS (Accession NM_023009) is another VGAM2039 host target gene. MACMARCKS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MACMARCKS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MACMARCKS BINDING SITE, designated SEQ ID:23272, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71478] Another function of VGAM2039 is therefore inhibition of MACMARCKS (Accession NM_023009). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MACMARCKS. MOST2 (Accession NM_020250) is another VGAM2039 host target gene. MOST2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MOST2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MOST2 BINDING SITE, designated SEQ ID:21551, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71479] Another function of VGAM2039 is therefore inhibition of MOST2 (Accession NM_020250). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOST2. MSTP028 (Accession NM_031954) is another VGAM2039 host target gene. MSTP028 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MSTP028, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MSTP028 BINDING SITE, designated SEQ ID:25694, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71480] Another function of VGAM2039 is therefore inhibition of MSTP028 (Accession NM_031954). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MSTP028. Nudix (nucleoside diphosphate linked moiety X)-type Motif 4 (NUDT4, Accession NM_019094) is another VGAM2039 host target gene. NUDT4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUDT4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUDT4 BINDING SITE, designated SEQ ID:21169, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71481] Another function of VGAM2039 is therefore inhibition of Nudix (nucleoside diphosphate linked moiety X)-type Motif 4 (NUDT4, Accession NM_019094). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUDT4. TACTILE (Accession NM_005816) is another VGAM2039 host target gene. TACTILE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TACTILE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TACTILE

BINDING SITE, designated SEQ ID:12411, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71482] Another function of VGAM2039 is therefore inhibition of TACTILE (Accession NM_005816). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TACTILE. U5-116KD (Accession NM_004247) is another VGAM2039 host target gene. U5-116KD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by U5-116KD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of U5-116KD BINDING SITE, designated SEQ ID:10438, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71483] Another function of VGAM2039 is therefore inhibition of U5-116KD (Accession NM_004247). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U5-116KD. UBE3B (Accession XM_084941) is another VGAM2039 host target gene. UBE3B BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by UBE3B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE3B BINDING SITE, designated SEQ ID:37773, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71484] Another function of VGAM2039 is therefore inhibition of UBE3B (Accession XM_084941). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE3B. Ubiquitin Specific Protease 10 (USP10, Accession XM_033922) is another VGAM2039 host target gene. USP10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP10 BINDING SITE, designated SEQ ID:31984, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71485] Another function of VGAM2039 is therefore inhibition of Ubiquitin Specific Protease 10 (USP10, Accession XM_033922). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP10. Zinc Finger, DHHC Domain Containing 2 (ZDHHC2, Accession NM_016353) is another VGAM2039 host target gene. ZDHHC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZDHHC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZDHHC2 BINDING SITE, designated SEQ ID:18488, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71486] Another function of VGAM2039 is therefore inhibition of Zinc Finger, DHHC Domain Containing 2 (ZDHHC2, Accession NM_016353). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZDHHC2. LOC138389 (Accession XM_072534) is another VGAM2039 host target gene. LOC138389 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded

by LOC138389, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC138389 BINDING SITE, designated SEQ ID:37506, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71487] Another function of VGAM2039 is therefore inhibition of LOC138389 (Accession XM_072534). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC138389. LOC144110 (Accession XM_084735) is another VGAM2039 host target gene. LOC144110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144110 BINDING SITE, designated SEQ ID:37679, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71488] Another function of VGAM2039 is therefore inhibition of LOC144110 (Accession XM_084735). Accordingly, utilities

of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144110. LOC144558 (Accession XM_096629) is another VGAM2039 host target gene. LOC144558 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144558, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144558 BINDING SITE, designated SEQ ID:40438, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71489] Another function of VGAM2039 is therefore inhibition of LOC144558 (Accession XM_096629). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144558. LOC144893 (Accession XM_096687) is another VGAM2039 host target gene. LOC144893 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144893, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC144893 BINDING SITE, designated SEQ ID:40459, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71490] Another function of VGAM2039 is therefore inhibition of LOC144893 (Accession XM_096687). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144893. LOC145368 (Accession XM_085112) is another VGAM2039 host target gene. LOC145368 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145368, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145368 BINDING SITE, designated SEQ ID:37828, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71491] Another function of VGAM2039 is therefore inhibition of LOC145368 (Accession XM_085112). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145368. LOC145719 (Accession XM_096848) is another VGAM2039 host target gene. LOC145719 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145719, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145719 BINDING SITE, designated SEQ ID:40576, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71492] Another function of VGAM2039 is therefore inhibition of LOC145719 (Accession XM_096848). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145719. LOC145720 (Accession XM_096846) is another VGAM2039 host target gene. LOC145720 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145720, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145720 BINDING SITE, designated SEQ ID:40565, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71493] Another function of VGAM2039 is therefore inhibition of

LOC145720 (Accession XM_096846). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145720. LOC146346 (Accession XM_085430) is another VGAM2039 host target gene. LOC146346 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146346, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146346 BINDING SITE, designated SEQ ID:38135, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71494] Another function of VGAM2039 is therefore inhibition of LOC146346 (Accession XM_085430). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146346. LOC148029 (Accession XM_086014) is another VGAM2039 host target gene. LOC148029 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148029, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC148029 BINDING SITE, designated SEQ ID:38445, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71495] Another function of VGAM2039 is therefore inhibition of LOC148029 (Accession XM_086014). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148029. LOC150423 (Accession XM_086912) is another VGAM2039 host target gene. LOC150423 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150423, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150423 BINDING SITE, designated SEQ ID:38968, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71496] Another function of VGAM2039 is therefore inhibition of LOC150423 (Accession XM_086912). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150423. LOC155072 (Accession XM_098661) is an-

other VGAM2039 host target gene. LOC155072 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155072, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155072 BINDING SITE, designated SEQ ID:41760, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71497] Another function of VGAM2039 is therefore inhibition of LOC155072 (Accession XM_098661). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155072. LOC158156 (Accession XM_088496) is another VGAM2039 host target gene. LOC158156 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158156, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158156 BINDING SITE, designated SEQ ID:39741, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71498] Another function of VGAM2039 is therefore inhibition of LOC158156 (Accession XM_088496). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158156. LOC169270 (Accession XM_095607) is another VGAM2039 host target gene. LOC169270 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC169270, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169270 BINDING SITE, designated SEQ ID:40274, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71499] Another function of VGAM2039 is therefore inhibition of LOC169270 (Accession XM_095607). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169270. LOC197114 (Accession XM_116987) is another VGAM2039 host target gene. LOC197114 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC197114, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197114 BINDING SITE, designated SEQ ID:43188, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71500] Another function of VGAM2039 is therefore inhibition of LOC197114 (Accession XM_116987). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197114. LOC201799 (Accession XM_114380) is another VGAM2039 host target gene. LOC201799 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201799, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201799 BINDING SITE, designated SEQ ID:42916, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71501] Another function of VGAM2039 is therefore inhibition of LOC201799 (Accession XM_114380). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC201799. LOC202868 (Accession XM_117477) is another VGAM2039 host target gene. LOC202868 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202868, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202868 BINDING SITE, designated SEQ ID:43447, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71502] Another function of VGAM2039 is therefore inhibition of LOC202868 (Accession XM_117477). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202868. LOC220758 (Accession XM_165466) is another VGAM2039 host target gene. LOC220758 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220758, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220758 BINDING SITE, designated SEQ ID:43642, to the nucleotide sequence of VGAM2039 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4750.

[71503] Another function of VGAM2039 is therefore inhibition of LOC220758 (Accession XM_165466). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220758. LOC221528 (Accession XM_166377) is another VGAM2039 host target gene. LOC221528 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221528, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221528 BINDING SITE, designated SEQ ID:44211, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71504] Another function of VGAM2039 is therefore inhibition of LOC221528 (Accession XM_166377). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221528. LOC221687 (Accession XM_166423) is another VGAM2039 host target gene. LOC221687 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221687, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221687 BINDING SITE, designated SEQ ID:44307, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71505] Another function of VGAM2039 is therefore inhibition of LOC221687 (Accession XM_166423). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221687. LOC221882 (Accession XM_166507) is another VGAM2039 host target gene. LOC221882 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221882, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221882 BINDING SITE, designated SEQ ID:44433, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71506] Another function of VGAM2039 is therefore inhibition of LOC221882 (Accession XM_166507). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC221882. LOC255461 (Accession XM_173207) is another VGAM2039 host target gene. LOC255461 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255461, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255461 BINDING SITE, designated SEQ ID:46465, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71507] Another function of VGAM2039 is therefore inhibition of LOC255461 (Accession XM_173207). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255461. LOC255516 (Accession XM_173212) is another VGAM2039 host target gene. LOC255516 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255516 BINDING SITE, designated SEQ ID:46471, to

the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71508] Another function of VGAM2039 is therefore inhibition of LOC255516 (Accession XM_173212). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255516. LOC256789 (Accession XM_173369) is another VGAM2039 host target gene. LOC256789 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256789, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256789 BINDING SITE, designated SEQ ID:46536, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71509] Another function of VGAM2039 is therefore inhibition of LOC256789 (Accession XM_173369). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256789. LOC257552 (Accession XM_175174) is another VGAM2039 host target gene. LOC257552 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC257552, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257552 BINDING SITE, designated SEQ ID:46670, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71510] Another function of VGAM2039 is therefore inhibition of LOC257552 (Accession XM_175174). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257552. LOC257602 (Accession XM_175246) is another VGAM2039 host target gene. LOC257602 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257602, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257602 BINDING SITE, designated SEQ ID:46700, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71511] Another function of VGAM2039 is therefore inhibition of LOC257602 (Accession XM_175246). Accordingly, utilities

of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257602. LOC90342 (Accession XM_031009) is another VGAM2039 host target gene. LOC90342 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90342, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90342 BINDING SITE, designated SEQ ID:31251, to the nucleotide sequence of VGAM2039 RNA, herein designated VGAM RNA, also designated SEQ ID:4750.

[71512] Another function of VGAM2039 is therefore inhibition of LOC90342 (Accession XM_031009). Accordingly, utilities of VGAM2039 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90342. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2040 (VGAM2040) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71513] VGAM2040 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2040 was detected is described hereinabove with reference to Figs. 1-8.

[71514] VGAM2040 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Marburg Virus. VGAM2040 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71515] VGAM2040 gene encodes a VGAM2040 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2040 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2040 precursor RNA is designated SEQ ID:2026, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2026 is located at position 5679 relative to the genome of Marburg Virus.

[71516] VGAM2040 precursor RNA folds onto itself, forming VGAM2040 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71517] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2040 folded precursor RNA into VGAM2040 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2040 RNA is designated SEQ ID:4751, and is provided hereinbelow with reference to the sequence listing part.

[71518] VGAM2040 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2040 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2040 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[71519] VGAM2040 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2040 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2040 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2040 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2040 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71520] The complementary binding of VGAM2040 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2040 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2040 host target RNA into VGAM2040 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71521] It is appreciated that VGAM2040 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2040 host target genes. The mRNA of each one of this plurality of VGAM2040 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2040 RNA, herein designated VGAM RNA, and which when bound by VGAM2040 RNA causes inhibition of translation of respective one or more VGAM2040 host target proteins.

[71522] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2040 gene, herein designated VGAM GENE, on one or more VGAM2040 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71523] It is yet further appreciated that a function of VGAM2040 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2040 include diagnosis, prevention and treatment of viral infection by Marburg Virus. Specific functions, and accordingly utilities, of VGAM2040 correlate with, and may be deduced from, the identity of the host target genes which VGAM2040 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71524] Nucleotide sequences of the VGAM2040 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2040 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2040 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2040 are further described hereinbelow with reference to Table 1.

[71525] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2040 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2040 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71526] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2040 gene, herein designated VGAM is inhibition of expression of VGAM2040 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2040 correlate with, and may be deduced from, the identity of the target genes which VGAM2040 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71527] A Disintegrin-like and Metalloprotease (reprolysin type) with Thrombospondin Type 1 Motif, 1 (ADAMTS1, Acces-

sion NM_006988) is a VGAM2040 host target gene. ADAMTS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADAMTS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAMTS1 BINDING SITE, designated SEQ ID:13852, to the nucleotide sequence of VGAM2040 RNA, herein designated VGAM RNA, also designated SEQ ID:4751.

[71528] A function of VGAM2040 is therefore inhibition of A Disintegrin-like and Metalloprotease (reprolysin type) with Thrombospondin Type 1 Motif, 1 (ADAMTS1, Accession NM_006988). Accordingly, utilities of VGAM2040 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAMTS1. EGF-containing Fibulin-like Extracellular Matrix Protein 1 (EFEMP1, Accession NM_004105) is another VGAM2040 host target gene. EFEMP1 BINDING SITE1 and EFEMP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by EFEMP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the comple-

mentarity of the nucleotide sequences of EFEMP1 BINDING SITE1 and EFEMP1 BINDING SITE2, designated SEQ ID:10319 and SEQ ID:20839 respectively, to the nucleotide sequence of VGAM2040 RNA, herein designated VGAM RNA, also designated SEQ ID:4751.

[71529] Another function of VGAM2040 is therefore inhibition of EGF-containing Fibulin-like Extracellular Matrix Protein 1 (EFEMP1, Accession NM_004105). Accordingly, utilities of VGAM2040 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFEMP1. Phosphoribosyl Pyrophosphate Amidotransferase (PPAT, Accession NM_002703) is another VGAM2040 host target gene. PPAT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPAT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPAT BINDING SITE, designated SEQ ID:8552, to the nucleotide sequence of VGAM2040 RNA, herein designated VGAM RNA, also designated SEQ ID:4751.

[71530] Another function of VGAM2040 is therefore inhibition of Phosphoribosyl Pyrophosphate Amidotransferase (PPAT, Accession NM_002703). Accordingly, utilities of

VGAM2040 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPAT. Secretogranin III (SCG3, Accession NM_013243) is another VGAM2040 host target gene. SCG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCG3 BINDING SITE, designated SEQ ID:14905, to the nucleotide sequence of VGAM2040 RNA, herein designated VGAM RNA, also designated SEQ ID:4751.

[71531] Another function of VGAM2040 is therefore inhibition of Secretogranin III (SCG3, Accession NM_013243). Accordingly, utilities of VGAM2040 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCG3. SH3-domain Binding Protein 2 (SH3BP2, Accession NM_003023) is another VGAM2040 host target gene. SH3BP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3BP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of SH3BP2 BINDING SITE, designated SEQ ID:8950, to the nucleotide sequence of VGAM2040 RNA, herein designated VGAM RNA, also designated SEQ ID:4751.

[71532] Another function of VGAM2040 is therefore inhibition of SH3-domain Binding Protein 2 (SH3BP2, Accession NM_003023). Accordingly, utilities of VGAM2040 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BP2. KIAA1795 (Accession XM_050988) is another VGAM2040 host target gene. KIAA1795 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1795, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1795 BINDING SITE, designated SEQ ID:35703, to the nucleotide sequence of VGAM2040 RNA, herein designated VGAM RNA, also designated SEQ ID:4751.

[71533] Another function of VGAM2040 is therefore inhibition of KIAA1795 (Accession XM_050988). Accordingly, utilities of VGAM2040 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1795. UBE3B (Accession XM_084941) is another VGAM2040 host target gene. UBE3B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UBE3B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE3B BINDING SITE, designated SEQ ID:37776, to the nucleotide sequence of VGAM2040 RNA, herein designated VGAM RNA, also designated SEQ ID:4751.

[71534] Another function of VGAM2040 is therefore inhibition of UBE3B (Accession XM_084941). Accordingly, utilities of VGAM2040 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE3B. LOC129446 (Accession XM_072203) is another VGAM2040 host target gene. LOC129446 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC129446, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC129446 BINDING SITE, designated SEQ ID:37467, to the nucleotide sequence of VGAM2040 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4751.

[71535] Another function of VGAM2040 is therefore inhibition of LOC129446 (Accession XM_072203). Accordingly, utilities of VGAM2040 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129446. LOC158549 (Accession XM_098963) is another VGAM2040 host target gene. LOC158549 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158549, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158549 BINDING SITE, designated SEQ ID:42010, to the nucleotide sequence of VGAM2040 RNA, herein designated VGAM RNA, also designated SEQ ID:4751.

[71536] Another function of VGAM2040 is therefore inhibition of LOC158549 (Accession XM_098963). Accordingly, utilities of VGAM2040 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158549. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2041 (VGAM2041) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71537] VGAM2041 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2041 was detected is described hereinabove with reference to Figs. 1-8.

[71538] VGAM2041 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Marburg Virus. VGAM2041 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71539] VGAM2041 gene encodes a VGAM2041 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2041 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2041 precursor RNA is designated SEQ ID:2027, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2027 is located at position 9817 relative to the genome of Marburg Virus.

[71540] VGAM2041 precursor RNA folds onto itself, forming

VGAM2041 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71541] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2041 folded precursor RNA into VGAM2041 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2041 RNA is designated SEQ ID:4752, and is provided hereinbelow with reference to the sequence listing part.

[71542] VGAM2041 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2041 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2041 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71543] VGAM2041 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2041 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2041 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2041 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2041 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71544] The complementary binding of VGAM2041 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2041 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2041 host target RNA into VGAM2041 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71545] It is appreciated that VGAM2041 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2041 host target genes. The mRNA of each one of this plurality of VGAM2041 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2041 RNA, herein designated VGAM RNA, and which when bound by VGAM2041 RNA causes inhibition of translation of respective one or more VGAM2041 host target proteins.

[71546] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2041 gene, herein designated VGAM GENE, on one or more VGAM2041 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71547] It is yet further appreciated that a function of VGAM2041 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2041 include diagnosis, prevention and treatment of viral infection by Marburg Virus. Specific functions, and accordingly utilities, of VGAM2041 correlate with, and may be deduced from, the identity of the host target genes which VGAM2041 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[71548] Nucleotide sequences of the VGAM2041 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2041 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2041 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2041 are further described hereinbelow with reference to Table 1.

[71549] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2041 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2041 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71550] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2041 gene, herein designated VGAM is inhibition of expression of VGAM2041 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2041 correlate with, and may be deduced from, the identity of the target genes which VGAM2041 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[71551] Cytoplasmic Linker Associated Protein 1 (CLASP1, Accession XM_037105) is a VGAM2041 host target gene. CLASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLASP1 BINDING SITE, designated SEQ ID:32541, to the nucleotide sequence of VGAM2041 RNA, herein designated VGAM RNA, also designated SEQ ID:4752.

[71552] A function of VGAM2041 is therefore inhibition of Cytoplasmic Linker Associated Protein 1 (CLASP1, Accession XM_037105), a gene which plays a role in the local regulation of microtubule dynamics . Accordingly, utilities of VGAM2041 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLASP1. The function of CLASP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM298.Histamine Receptor H1 (HRH1, Accession NM_000861) is another VGAM2041 host target

gene. HRH1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HRH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRH1 BINDING SITE, designated SEQ ID:6523, to the nucleotide sequence of VGAM2041 RNA, herein designated VGAM RNA, also designated SEQ ID:4752.

[71553] Another function of VGAM2041 is therefore inhibition of Histamine Receptor H1 (HRH1, Accession NM_000861), a gene which stimulates the synthesis of inositol phosphate. Accordingly, utilities of VGAM2041 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRH1. The function of HRH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM766.Protein Kinase, AMP-activated, Beta 1 Non-catalytic Subunit (PRKAB1, Accession NM_006253) is another VGAM2041 host target gene. PRKAB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKAB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of PRKAB1 BINDING SITE, designated SEQ ID:12933, to the nucleotide sequence of VGAM2041 RNA, herein designated VGAM RNA, also designated SEQ ID:4752.

[71554] Another function of VGAM2041 is therefore inhibition of Protein Kinase, AMP-activated, Beta 1 Non-catalytic Subunit (PRKAB1, Accession NM_006253), a gene which is responsible for the regulation of fatty acid synthesis by phosphorylation of acetyl-coa carboxylase. Accordingly, utilities of VGAM2041 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKAB1. The function of PRKAB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1384.TERA (Accession NM_021238) is another VGAM2041 host target gene. TERA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TERA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TERA BINDING SITE, designated SEQ ID:22204,

to the nucleotide sequence of VGAM2041 RNA, herein designated VGAM RNA, also designated SEQ ID:4752.

[71555] Another function of VGAM2041 is therefore inhibition of TERA (Accession NM_021238). Accordingly, utilities of VGAM2041 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERA. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2042 (VGAM2042) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71556] VGAM2042 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2042 was detected is described hereinabove with reference to Figs. 1-8.

[71557] VGAM2042 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 5. VGAM2042 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71558] VGAM2042 gene encodes a VGAM2042 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2042 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2042 precursor RNA is designated SEQ ID:2028, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2028 is located at position 207065 relative to the genome of Human Herpesvirus 5.

[71559] VGAM2042 precursor RNA folds onto itself, forming VGAM2042 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71560] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2042 folded precursor RNA into VGAM2042 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2042 RNA is designated SEQ ID:4753, and is provided hereinbelow with reference to the sequence listing part.

[71561] VGAM2042 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2042 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2042 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71562] VGAM2042 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2042 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2042 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2042 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2042 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71563] The complementary binding of VGAM2042 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2042 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2042 host target RNA into VGAM2042 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71564] It is appreciated that VGAM2042 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2042 host target genes. The mRNA of

each one of this plurality of VGAM2042 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2042 RNA, herein designated VGAM RNA, and which when bound by VGAM2042 RNA causes inhibition of translation of respective one or more VGAM2042 host target proteins.

[71565] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2042 gene, herein designated VGAM GENE, on one or more VGAM2042 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[71566] It is yet further appreciated that a function of VGAM2042 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2042 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2042 correlate with, and may be deduced from, the identity of the host target genes which VGAM2042 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71567] Nucleotide sequences of the VGAM2042 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2042 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2042 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2042 are further described hereinbelow with reference to Table 1.

[71568] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2042 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2042 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71569] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2042 gene, herein designated VGAM is inhibition of expression of VGAM2042 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2042 correlate with, and may be deduced from, the identity of the target genes which VGAM2042 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71570] Filamin B, Beta (actin binding protein 278) (FLNB, Accession XM_030806) is a VGAM2042 host target gene. FLNB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLNB BINDING SITE, designated SEQ ID:31148, to the nucleotide sequence of VGAM2042 RNA, herein designated VGAM RNA, also designated SEQ ID:4753.

[71571] A function of VGAM2042 is therefore inhibition of Filamin B, Beta (actin binding protein 278) (FLNB, Accession XM_030806), a gene which Filamin B, beta; binds actin,

interacts with cytoplasmic domain of Ibalpha. Accordingly, utilities of VGAM2042 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLNB. The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM416.Junctophilin 3 (JPH3, Accession NM_020655) is another VGAM2042 host target gene. JPH3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by JPH3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JPH3 BINDING SITE, designated SEQ ID:21826, to the nucleotide sequence of VGAM2042 RNA, herein designated VGAM RNA, also designated SEQ ID:4753.

[71572] Another function of VGAM2042 is therefore inhibition of Junctophilin 3 (JPH3, Accession NM_020655), a gene which is involved in cytoskeletal organization and cellular growth. Accordingly, utilities of VGAM2042 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JPH3. The function of JPH3 and its association with various diseases and clinical condi-

tions, has been established by previous studies, as described hereinabove with reference to VGAM254.FLJ23598 (Accession NM_024783) is another VGAM2042 host target gene. FLJ23598 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23598, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23598 BINDING SITE, designated SEQ ID:24157, to the nucleotide sequence of VGAM2042 RNA, herein designated VGAM RNA, also designated SEQ ID:4753.

[71573] Another function of VGAM2042 is therefore inhibition of FLJ23598 (Accession NM_024783). Accordingly, utilities of VGAM2042 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23598. KIAA0295 (Accession XM_042833) is another VGAM2042 host target gene. KIAA0295 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0295, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0295 BINDING SITE, designated SEQ ID:33785, to the nucleotide sequence of VGAM2042 RNA, herein designated VGAM RNA, also designated SEQ ID:4753.

[71574] Another function of VGAM2042 is therefore inhibition of KIAA0295 (Accession XM_042833). Accordingly, utilities of VGAM2042 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0295. LOC149372 (Accession XM_086509) is another VGAM2042 host target gene. LOC149372 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149372, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149372 BINDING SITE, designated SEQ ID:38725, to the nucleotide sequence of VGAM2042 RNA, herein designated VGAM RNA, also designated SEQ ID:4753.

[71575] Another function of VGAM2042 is therefore inhibition of LOC149372 (Accession XM_086509). Accordingly, utilities of VGAM2042 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149372. LOC150577 (Accession XM_097918) is another VGAM2042 host target gene. LOC150577 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150577 BINDING SITE, designated SEQ ID:41217, to the nucleotide sequence of VGAM2042 RNA, herein designated VGAM RNA, also designated SEQ ID:4753.

[71576] Another function of VGAM2042 is therefore inhibition of LOC150577 (Accession XM_097918). Accordingly, utilities of VGAM2042 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150577. LOC157627 (Accession XM_088347) is another VGAM2042 host target gene. LOC157627 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157627, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157627 BINDING SITE, designated SEQ ID:39619, to the nucleotide sequence of VGAM2042 RNA, herein designated VGAM RNA, also designated SEQ ID:4753.

[71577] Another function of VGAM2042 is therefore inhibition of

LOC157627 (Accession XM_088347). Accordingly, utilities of VGAM2042 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157627. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2043 (VGAM2043) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71578] VGAM2043 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2043 was detected is described hereinabove with reference to Figs. 1-8.

[71579] VGAM2043 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 5. VGAM2043 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71580] VGAM2043 gene encodes a VGAM2043 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2043 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2043 precursor RNA is designated SEQ ID:2029, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2029 is located at position 200386 relative to the genome of Human Herpesvirus 5.

[71581] VGAM2043 precursor RNA folds onto itself, forming VGAM2043 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71582] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2043 folded precursor RNA into VGAM2043 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide se-

quence of VGAM2043 RNA is designated SEQ ID:4754, and is provided hereinbelow with reference to the sequence listing part.

[71583] VGAM2043 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2043 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2043 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71584] VGAM2043 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2043 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2043 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2043 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2043 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71585] The complementary binding of VGAM2043 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2043 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2043 host target RNA into VGAM2043 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71586] It is appreciated that VGAM2043 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2043 host target genes. The mRNA of each one of this plurality of VGAM2043 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2043 RNA, herein designated VGAM RNA, and which when bound by VGAM2043 RNA causes inhibition of translation of respective one or more VGAM2043 host target proteins.

[71587] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2043 gene, herein designated VGAM GENE, on one or more VGAM2043 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71588] It is yet further appreciated that a function of VGAM2043

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2043 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2043 correlate with, and may be deduced from, the identity of the host target genes which VGAM2043 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71589] Nucleotide sequences of the VGAM2043 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2043 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2043 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2043 are further described hereinbelow with reference to Table 1.

[71590] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2043 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2043 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71591] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2043 gene, herein designated VGAM is inhibition of expression of VGAM2043 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2043 correlate with, and may be deduced from, the identity of the target genes which VGAM2043 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71592] Actinin, Alpha 2 (ACTN2, Accession NM_001103) is a VGAM2043 host target gene. ACTN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ACTN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACTN2 BINDING SITE, designated SEQ ID:6760, to the nucleotide sequence of VGAM2043 RNA, herein designated VGAM RNA, also designated SEQ ID:4754.

[71593] A function of VGAM2043 is therefore inhibition of Actinin, Alpha 2 (ACTN2, Accession NM_001103), a gene which an actin-binding protein with multiple roles in different cell types. Accordingly, utilities of VGAM2043 include diagnosis, prevention and treatment of diseases and clinical con-

ditions associated with ACTN2. The function of ACTN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM88.Protein Tyrosine Phosphatase, Receptor Type, G (PTPRG, Accession NM_002841) is another VGAM2043 host target gene. PTPRG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPRG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRG BINDING SITE, designated SEQ ID:8728, to the nucleotide sequence of VGAM2043 RNA, herein designated VGAM RNA, also designated SEQ ID:4754.

[71594] Another function of VGAM2043 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, G (PTPRG, Accession NM_002841), a gene which is a candidate tumor suppressor and represents a subfamily of receptor tyrosine phosphatases. Accordingly, utilities of VGAM2043 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRG. The function of PTPRG and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to VGAM1924.MIC2 Like 1 (MIC2L1, Accession NM_031462) is another VGAM2043 host target gene. MIC2L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MIC2L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MIC2L1 BINDING SITE, designated SEQ ID:25489, to the nucleotide sequence of VGAM2043 RNA, herein designated VGAM RNA, also designated SEQ ID:4754.

[71595] Another function of VGAM2043 is therefore inhibition of MIC2 Like 1 (MIC2L1, Accession NM_031462). Accordingly, utilities of VGAM2043 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIC2L1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2044 (VGAM2044) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71596] VGAM2044 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2044 was detected is described hereinabove with reference to Figs. 1-8.

[71597] VGAM2044 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 5. VGAM2044 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71598] VGAM2044 gene encodes a VGAM2044 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2044 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2044 precursor RNA is designated SEQ ID:2030, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2030 is located at position 212421 relative to the genome of Human Herpesvirus 5.

[71599] VGAM2044 precursor RNA folds onto itself, forming VGAM2044 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71600] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2044 folded precursor RNA into VGAM2044 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2044 RNA is designated SEQ ID:4755, and is provided hereinbelow with reference to the sequence listing part.

[71601] VGAM2044 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2044 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2044 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71602] VGAM2044 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2044 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2044 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2044 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2044 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71603] The complementary binding of VGAM2044 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2044 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2044 host target RNA into VGAM2044 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71604] It is appreciated that VGAM2044 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2044 host target genes. The mRNA of each one of this plurality of VGAM2044 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2044 RNA, herein designated VGAM RNA, and which when bound by VGAM2044 RNA causes inhibition of translation of respective one or more VGAM2044 host target proteins.

[71605] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2044 gene, herein designated VGAM GENE, on one or more VGAM2044 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71606] It is yet further appreciated that a function of VGAM2044 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2044 correlate with, and may be deduced from, the identity of the host target genes which VGAM2044 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71607] Nucleotide sequences of the VGAM2044 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2044 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2044 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2044 are further described hereinbelow with reference to Table 1.

[71608] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2044 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2044 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71609] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2044 gene, herein designated VGAM is inhibition of expression of VGAM2044 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2044 correlate with, and may be deduced from, the identity of the target genes which VGAM2044 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71610] Chromosome 8 Open Reading Frame 1 (C8orf1, Accession NM_004337) is a VGAM2044 host target gene. C8orf1 BINDING SITE is HOST TARGET binding site found in the

5` untranslated region of mRNA encoded by C8orf1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C8orf1 BINDING SITE, designated SEQ ID:10531, to the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, also designated SEQ ID:4755.

[71611] A function of VGAM2044 is therefore inhibition of Chromosome 8 Open Reading Frame 1 (C8orf1, Accession NM_004337). Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf1. Cullin 3 (CUL3, Accession NM_003590) is another VGAM2044 host target gene. CUL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CUL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CUL3 BINDING SITE, designated SEQ ID:9644, to the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, also designated SEQ ID:4755.

[71612] Another function of VGAM2044 is therefore inhibition of Cullin 3 (CUL3, Accession NM_003590), a gene which may

target other proteins for ubiquitin-dependent proteolysis. Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CUL3. The function of CUL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM143.5-hydroxytryptamine (serotonin) Receptor 4 (HTR4, Accession NM_000870) is another VGAM2044 host target gene. HTR4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HTR4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HTR4 BINDING SITE, designated SEQ ID:6542, to the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, also designated SEQ ID:4755.

[71613] Another function of VGAM2044 is therefore inhibition of 5-hydroxytryptamine (serotonin) Receptor 4 (HTR4, Accession NM_000870), a gene which mediates calcium channel currents. Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with HTR4. The function of HTR4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM65.RAB Interacting Factor (RABIF, Accession NM_002871) is another VGAM2044 host target gene. RABIF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RABIF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RABIF BINDING SITE, designated SEQ ID:8781, to the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, also designated SEQ ID:4755.

[71614] Another function of VGAM2044 is therefore inhibition of RAB Interacting Factor (RABIF, Accession NM_002871), a gene which is involved in the regulation of intracellular vesicular transport. Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RABIF. The function of RABIF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM1633.Transient Receptor Potential Cation Channel, Subfamily C, Member 6 (TRPC6, Accession NM_004621) is another VGAM2044 host target gene. TRPC6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TRPC6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPC6 BINDING SITE, designated SEQ ID:10976, to the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, also designated SEQ ID:4755.

[71615] Another function of VGAM2044 is therefore inhibition of Transient Receptor Potential Cation Channel, Subfamily C, Member 6 (TRPC6, Accession NM_004621), a gene which has calcium channel activity. Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPC6. The function of TRPC6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM25.Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_014919) is another VGAM2044 host target gene. WHSC1 BINDING SITE1 through WHSC1

BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WHSC1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE1 through WHSC1 BINDING SITE4, designated SEQ ID:17183, SEQ ID:28447, SEQ ID:28464 and SEQ ID:28475 respectively, to the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, also designated SEQ ID:4755.

[71616] Another function of VGAM2044 is therefore inhibition of Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_014919), a gene which binds covalently to and repairs g/t mismatches. Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WHSC1. The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.DKFZp434J1015 (Accession XM_166538) is another VGAM2044 host target gene. DKFZp434J1015 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DK-

FZp434J1015, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434J1015 BINDING SITE, designated SEQ ID:44506, to the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, also designated SEQ ID:4755.

[71617] Another function of VGAM2044 is therefore inhibition of DKFZp434J1015 (Accession XM_166538). Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434J1015. IMAGE:4907098 (Accession XM_166247) is another VGAM2044 host target gene. IMAGE:4907098 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IMAGE:4907098, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IMAGE:4907098 BINDING SITE, designated SEQ ID:44060, to the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, also designated SEQ ID:4755.

[71618] Another function of VGAM2044 is therefore inhibition of

IMAGE:4907098 (Accession XM_166247). Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMAGE:4907098. LOC123876 (Accession XM_058743) is another VGAM2044 host target gene. LOC123876 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC123876, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC123876 BINDING SITE, designated SEQ ID:36733, to the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, also designated SEQ ID:4755.

[71619] Another function of VGAM2044 is therefore inhibition of LOC123876 (Accession XM_058743). Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC123876. LOC146316 (Accession XM_027568) is another VGAM2044 host target gene. LOC146316 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146316, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146316 BINDING SITE, designated SEQ ID:30526, to the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, also designated SEQ ID:4755.

[71620] Another function of VGAM2044 is therefore inhibition of LOC146316 (Accession XM_027568). Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146316. LOC200470 (Accession XM_117235) is another VGAM2044 host target gene. LOC200470 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200470, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200470 BINDING SITE, designated SEQ ID:43309, to the nucleotide sequence of VGAM2044 RNA, herein designated VGAM RNA, also designated SEQ ID:4755.

[71621] Another function of VGAM2044 is therefore inhibition of LOC200470 (Accession XM_117235). Accordingly, utilities of VGAM2044 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC200470. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2045 (VGAM2045) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71622] VGAM2045 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2045 was detected is described hereinabove with reference to Figs. 1-8.

[71623] VGAM2045 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 5. VGAM2045 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71624] VGAM2045 gene encodes a VGAM2045 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2045 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2045 precursor RNA is designated SEQ ID:2031, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2031 is located at position 196544 relative to the genome of Human Herpesvirus 5.

[71625] VGAM2045 precursor RNA folds onto itself, forming VGAM2045 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71626] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2045 folded precursor RNA into VGAM2045 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2045 RNA is designated SEQ ID:4756, and is provided hereinbelow with reference to the sequence listing part.

[71627] VGAM2045 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2045 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2045 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71628] VGAM2045 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2045 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2045 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2045 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2045 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71629] The complementary binding of VGAM2045 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2045 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2045 host target RNA into VGAM2045 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71630] It is appreciated that VGAM2045 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2045 host target genes. The mRNA of each one of this plurality of VGAM2045 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2045 RNA, herein designated VGAM RNA, and which when bound by VGAM2045 RNA causes

inhibition of translation of respective one or more VGAM2045 host target proteins.

[71631] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2045 gene, herein designated VGAM GENE, on one or more VGAM2045 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71632] It is yet further appreciated that a function of VGAM2045 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2045 include diagnosis, prevention and

treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2045 correlate with, and may be deduced from, the identity of the host target genes which VGAM2045 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71633] Nucleotide sequences of the VGAM2045 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2045 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2045 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2045 are further described hereinbelow with reference to Table 1.

[71634] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2045 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2045 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71635] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2045 gene, herein designated VGAM is inhibition of expression of VGAM2045 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2045 correlate with, and may be deduced from, the identity of the target genes which VGAM2045 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71636] Interleukin 1 Receptor, Type I (IL1R1, Accession NM_000877) is a VGAM2045 host target gene. IL1R1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL1R1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1R1 BINDING SITE, designated SEQ ID:6564, to the nucleotide sequence of VGAM2045 RNA, herein designated VGAM RNA, also designated SEQ ID:4756.

[71637] A function of VGAM2045 is therefore inhibition of Interleukin 1 Receptor, Type I (IL1R1, Accession NM_000877), a gene which is a receptor for interleukin-1 alpha (il-1a), beta (il-1b), and interleukin-1 receptor antagonist protein (il-1ra). Accordingly, utilities of VGAM2045 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1R1. The function of IL1R1 and its association with various diseases and clinical con-

ditions, has been established by previous studies, as described hereinabove with reference to VGAM704.Tryptophan Rich Basic Protein (WRB, Accession NM_004627) is another VGAM2045 host target gene. WRB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WRB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WRB BINDING SITE, designated SEQ ID:10997, to the nucleotide sequence of VGAM2045 RNA, herein designated VGAM RNA, also designated SEQ ID:4756.

[71638] Another function of VGAM2045 is therefore inhibition of Tryptophan Rich Basic Protein (WRB, Accession NM_004627). Accordingly, utilities of VGAM2045 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WRB. C6orf5 (Accession NM_015524) is another VGAM2045 host target gene. C6orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C6orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of C6orf5 BINDING SITE, designated SEQ ID:17777, to the nucleotide sequence of VGAM2045 RNA, herein designated VGAM RNA, also designated SEQ ID:4756.

[71639] Another function of VGAM2045 is therefore inhibition of C6orf5 (Accession NM_015524). Accordingly, utilities of VGAM2045 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf5. LOC203595 (Accession XM_119962) is another VGAM2045 host target gene. LOC203595 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203595, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203595 BINDING SITE, designated SEQ ID:43606, to the nucleotide sequence of VGAM2045 RNA, herein designated VGAM RNA, also designated SEQ ID:4756.

[71640] Another function of VGAM2045 is therefore inhibition of LOC203595 (Accession XM_119962). Accordingly, utilities of VGAM2045 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203595. LOC51667 (Accession NM_016118) is an-

other VGAM2045 host target gene. LOC51667 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51667, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51667 BINDING SITE, designated SEQ ID:18196, to the nucleotide sequence of VGAM2045 RNA, herein designated VGAM RNA, also designated SEQ ID:4756.

[71641] Another function of VGAM2045 is therefore inhibition of LOC51667 (Accession NM_016118). Accordingly, utilities of VGAM2045 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51667. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2046 (VGAM2046) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71642] VGAM2046 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2046 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[71643] VGAM2046 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 5. VGAM2046 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71644] VGAM2046 gene encodes a VGAM2046 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2046 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2046 precursor RNA is designated SEQ ID:2032, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2032 is located at position 209917 relative to the genome of Human Herpesvirus 5.

[71645] VGAM2046 precursor RNA folds onto itself, forming VGAM2046 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71646] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2046 folded precursor RNA into VGAM2046 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2046 RNA is designated SEQ ID:4757, and is provided hereinbelow with reference to the sequence listing part.

[71647] VGAM2046 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2046 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2046 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71648] VGAM2046 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2046 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2046 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2046 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2046 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71649] The complementary binding of VGAM2046 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2046 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2046 host target RNA into VGAM2046 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71650] It is appreciated that VGAM2046 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2046 host target genes. The mRNA of each one of this plurality of VGAM2046 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2046 RNA, herein designated VGAM RNA, and which when bound by VGAM2046 RNA causes inhibition of translation of respective one or more VGAM2046 host target proteins.

[71651] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2046 gene, herein designated VGAM GENE, on one or more VGAM2046 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71652] It is yet further appreciated that a function of VGAM2046 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2046 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2046 correlate with, and may be deduced from, the identity of the host target genes which VGAM2046 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71653] Nucleotide sequences of the VGAM2046 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2046 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2046 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2046 are further described hereinbelow with reference to Table 1.

[71654] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2046 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2046 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71655] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2046 gene, herein designated VGAM is inhibition of expression of VGAM2046 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2046 correlate with, and may be deduced from, the identity of the target genes which VGAM2046 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71656] G2A (Accession NM_013345) is a VGAM2046 host target gene. G2A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by G2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Ta-

ble 2 illustrates the complementarity of the nucleotide sequences of G2A BINDING SITE, designated SEQ ID:14988, to the nucleotide sequence of VGAM2046 RNA, herein designated VGAM RNA, also designated SEQ ID:4757.

[71657] A function of VGAM2046 is therefore inhibition of G2A (Accession NM_013345), a gene which may mediate some of the effects of extracellular atp on insulin secretion. Accordingly, utilities of VGAM2046 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G2A. The function of G2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1965.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2047 (VGAM2047) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71658] VGAM2047 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2047 was detected is described hereinabove with reference to Figs. 1-8.

[71659] VGAM2047 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 5. VGAM2047 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71660] VGAM2047 gene encodes a VGAM2047 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2047 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2047 precursor RNA is designated SEQ ID:2033, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2033 is located at position 202249 relative to the genome of Human Herpesvirus 5.

[71661] VGAM2047 precursor RNA folds onto itself, forming VGAM2047 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[71662] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2047 folded precursor RNA into VGAM2047 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2047 RNA is designated SEQ ID:4758, and is provided hereinbelow with reference to the sequence listing part.

[71663] VGAM2047 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2047 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2047 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71664] VGAM2047 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2047 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2047 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2047 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2047 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71665] The complementary binding of VGAM2047 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2047 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2047 host target RNA into VGAM2047 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71666] It is appreciated that VGAM2047 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2047 host target genes. The mRNA of each one of this plurality of VGAM2047 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2047 RNA, herein designated VGAM RNA, and which when bound by VGAM2047 RNA causes inhibition of translation of respective one or more VGAM2047 host target proteins.

[71667] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2047 gene, herein designated VGAM GENE, on one or more VGAM2047 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71668] It is yet further appreciated that a function of VGAM2047 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2047 correlate with, and may be deduced from, the identity of the host target genes which VGAM2047 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71669] Nucleotide sequences of the VGAM2047 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2047 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2047 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2047 are further described hereinbelow with reference to Table 1.

[71670] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2047 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2047 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71671] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2047 gene, herein designated VGAM is inhibition of expression of VGAM2047 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2047 correlate with, and may be deduced from, the identity of the target genes which VGAM2047 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71672] CAAX Box 1 (CXX1, Accession NM_003928) is a VGAM2047 host target gene. CXX1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CXX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of CXX1 BINDING SITE, designated SEQ ID:10023, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71673] A function of VGAM2047 is therefore inhibition of CAAX Box 1 (CXX1, Accession NM_003928). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXX1. Death Effector Domain Containing (DEDD, Accession NM_032998) is another VGAM2047 host target gene. DEDD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DEDD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DEDD BINDING SITE, designated SEQ ID:26878, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71674] Another function of VGAM2047 is therefore inhibition of Death Effector Domain Containing (DEDD, Accession NM_032998), a gene which intervenes in apoptosis. Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with DEDD. The function of DEDD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1189.GDP Dissociation Inhibitor 1 (GDI1, Accession XM_010152) is another VGAM2047 host target gene. GDI1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GDI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GDI1 BINDING SITE, designated SEQ ID:30131, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71675] Another function of VGAM2047 is therefore inhibition of GDP Dissociation Inhibitor 1 (GDI1, Accession XM_010152). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GDI1. Homeo Box C11 (HOXC11, Accession XM_012215) is another VGAM2047 host target gene. HOXC11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HOXC11, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOXC11 BINDING SITE, designated SEQ ID:30210, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71676] Another function of VGAM2047 is therefore inhibition of Homeo Box C11 (HOXC11, Accession XM_012215), a gene which interacts with the lactase-phlorizin hydrolase promoter. Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXC11. The function of HOXC11 has been established by previous studies. See 142950 for general information on homeo box genes. HOXC11 is a member of the Hox C cluster on human chromosome 12 (Scott, 1992) and is homologous to the mouse Hoxc11 gene (previously called Hox3.7) which is located on chromosome 15. Using a yeast 1-hybrid screen designed to identify factors that bind to a portion of the lactase (LCT; 603202) gene promoter, Mitchelmore et al. (1998) identified a partial clone of HOXC11. They assembled the full-length HOXC11 cDNA using database searches and 5-prime RACE. The HOXC11 cDNA encodes

a 304-amino acid protein with a homeodomain and a C-terminal extension identical to those of mouse Hoxc11. The homeodomain of HOXC11 is most similar to the homeodomains of mouse Hoxa11, mouse Hoxd11, and Drosophila Abdominal-B genes. Using Northern blot analysis, Mitchelmore et al. (1998) detected a 2.1-kb HOXC11 transcript in HeLa cells. This expression was confirmed by ribonuclease protection assay. A second, 1.7-kb transcript, hypothesized to encode a protein lacking 114 amino acids at the HOXC11 N-terminal end, was detected in HeLa cells and Caco-2 intestinal cells. This smaller transcript becomes more abundant in Caco-2 cells after differentiation. Using RT-PCR, Mitchelmore et al. (1998) showed that HOXC11 is expressed in fetal tissues, including kidney, skeletal muscle, and small intestine. The expression in fetal small intestine was higher than that in small intestine from a 15-year old. Transfection studies using the C-terminal 190 amino acids of HOXC11 in HeLa cells demonstrated binding with similar affinity to the LCT promoter and an optimized Abdominal-B binding site. Both the long and short transcript forms of HOXC11 stimulated HNF1-alpha (OMIM Ref. No. 142410)-dependent transcription of LCT in cotransfection experiments.

[71677] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[71678] Mitchelmore, C.; Troelsen, J. T.; Sjostrom, H.; Noren, O. : The HOXC11 homeodomain protein interacts with the lactose-phlorizin hydrolase promoter and stimulates HNF1-alpha-dependent transcription. J. Biol. Chem. 273: 13297-13306, 1998. ; and

[71679] Scott, M. P. : Vertebrate homeobox gene nomenclature. Cell 71: 551-553, 1992.

[71680] Further studies establishing the function and utilities of HOXC11 are found in John Hopkins OMIM database record ID 605559, and in sited publications numbered 97 and 4377 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.PCTAIRE Protein Kinase 3 (PCTK3, Accession XM_053746) is another VGAM2047 host target gene. PCTK3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PCTK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCTK3 BINDING SITE, designated SEQ ID:36124, to the nucleotide sequence of

VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71681] Another function of VGAM2047 is therefore inhibition of PCTAIRE Protein Kinase 3 (PCTK3, Accession XM_053746), a gene which may play a role in signal transduction cascades in terminally differentiated cells. Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCTK3. The function of PCTK3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM132.Transcription Factor 19 (SC1) (TCF19, Accession XM_175167) is another VGAM2047 host target gene. TCF19 BINDING SITE1 and TCF19 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TCF19, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF19 BINDING SITE1 and TCF19 BINDING SITE2, designated SEQ ID:46659 and SEQ ID:46708 respectively, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71682] Another function of VGAM2047 is therefore inhibition of Transcription Factor 19 (SC1) (TCF19, Accession XM_175167), a gene which plays an important role in the transcription of genes required for the later stages of cell cycle progression. Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF19. The function of TCF19 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM299.Ubiquitin-conjugating Enzyme E2L 6 (UBE2L6, Accession NM_004223) is another VGAM2047 host target gene. UBE2L6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UBE2L6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE2L6 BINDING SITE, designated SEQ ID:10419, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71683] Another function of VGAM2047 is therefore inhibition of Ubiquitin-conjugating Enzyme E2L 6 (UBE2L6, Accession

NM_004223), a gene which catalyzes the covalent attachment of ubiquitin to other proteins. Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE2L6. The function of UBE2L6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1059.Zinc Finger Protein 236 (ZNF236, Accession NM_007345) is another VGAM2047 host target gene. ZNF236 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF236, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF236 BINDING SITE, designated SEQ ID:14274, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71684] Another function of VGAM2047 is therefore inhibition of Zinc Finger Protein 236 (ZNF236, Accession NM_007345). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF236. DKFZP564B147 (Accession

XM_088745) is another VGAM2047 host target gene. DKFZP564B147 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP564B147, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564B147 BINDING SITE, designated SEQ ID:39934, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71685] Another function of VGAM2047 is therefore inhibition of DKFZP564B147 (Accession XM_088745). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564B147. FLJ10352 (Accession NM_032142) is another VGAM2047 host target gene. FLJ10352 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10352, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10352 BINDING SITE, designated SEQ ID:25827, to the nucleotide sequence of VGAM2047 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4758.

[71686] Another function of VGAM2047 is therefore inhibition of FLJ10352 (Accession NM_032142). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10352. KIAA0140 (Accession NM_014661) is another VGAM2047 host target gene. KIAA0140 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0140 BINDING SITE, designated SEQ ID:16109, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71687] Another function of VGAM2047 is therefore inhibition of KIAA0140 (Accession NM_014661). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0140. KIAA0329 (Accession NM_014844) is another VGAM2047 host target gene. KIAA0329 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0329, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0329 BINDING SITE, designated SEQ ID:16879, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71688] Another function of VGAM2047 is therefore inhibition of KIAA0329 (Accession NM_014844). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0329. KIAA0863 (Accession NM_014913) is another VGAM2047 host target gene. KIAA0863 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0863, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0863 BINDING SITE, designated SEQ ID:17154, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71689] Another function of VGAM2047 is therefore inhibition of KIAA0863 (Accession NM_014913). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0863. Ras and Rab Interactor 3 (RIN3, Accession NM_024832) is another VGAM2047 host target gene. RIN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RIN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RIN3 BINDING SITE, designated SEQ ID:24233, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71690] Another function of VGAM2047 is therefore inhibition of Ras and Rab Interactor 3 (RIN3, Accession NM_024832). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RIN3. LOC144305 (Accession XM_096572) is another VGAM2047 host target gene. LOC144305 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144305, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144305 BINDING SITE, desig-

nated SEQ ID:40401, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71691] Another function of VGAM2047 is therefore inhibition of LOC144305 (Accession XM_096572). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144305. LOC154877 (Accession XM_098626) is another VGAM2047 host target gene. LOC154877 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154877, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE, designated SEQ ID:41740, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71692] Another function of VGAM2047 is therefore inhibition of LOC154877 (Accession XM_098626). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154877. LOC157983 (Accession XM_088433) is another VGAM2047 host target gene. LOC157983 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157983, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157983 BINDING SITE, designated SEQ ID:39686, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71693] Another function of VGAM2047 is therefore inhibition of LOC157983 (Accession XM_088433). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157983. LOC203289 (Accession XM_114672) is another VGAM2047 host target gene. LOC203289 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203289, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203289 BINDING SITE, designated SEQ ID:43028, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71694] Another function of VGAM2047 is therefore inhibition of

LOC203289 (Accession XM_114672). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203289. LOC256544 (Accession XM_171228) is another VGAM2047 host target gene. LOC256544 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256544, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256544 BINDING SITE, designated SEQ ID:46015, to the nucleotide sequence of VGAM2047 RNA, herein designated VGAM RNA, also designated SEQ ID:4758.

[71695] Another function of VGAM2047 is therefore inhibition of LOC256544 (Accession XM_171228). Accordingly, utilities of VGAM2047 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256544. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2048 (VGAM2048) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[71696] VGAM2048 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2048 was detected is described hereinabove with reference to Figs. 1-8.

[71697] VGAM2048 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 5. VGAM2048 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71698] VGAM2048 gene encodes a VGAM2048 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2048 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2048 precursor RNA is designated SEQ ID:2034, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2034 is located at position 207766 relative to the genome of Human Herpesvirus 5.

[71699] VGAM2048 precursor RNA folds onto itself, forming VGAM2048 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71700] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2048 folded precursor RNA into VGAM2048 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2048 RNA is designated SEQ ID:4759, and is provided hereinbelow with reference to the sequence listing part.

[71701] VGAM2048 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2048 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2048 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71702] VGAM2048 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2048 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2048 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2048 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2048 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[71703] The complementary binding of VGAM2048 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2048 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2048 host target RNA into VGAM2048 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71704] It is appreciated that VGAM2048 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2048 host target genes. The mRNA of each one of this plurality of VGAM2048 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2048 RNA, herein designated VGAM RNA, and which when bound by VGAM2048 RNA causes inhibition of translation of respective one or more VGAM2048 host target proteins.

[71705] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2048 gene, herein designated VGAM GENE, on one

or more VGAM2048 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71706] It is yet further appreciated that a function of VGAM2048 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2048 correlate with, and may be deduced from, the identity of the host target genes which VGAM2048 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71707] Nucleotide sequences of the VGAM2048 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2048 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2048 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2048 are further described hereinbelow with reference to Table 1.

[71708] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2048 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2048 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71709] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2048 gene, herein designated VGAM is inhibition of expression of VGAM2048 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2048 correlate with, and may be deduced from, the identity of the target genes which VGAM2048 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71710] Coagulation Factor II (thrombin) Receptor-like 3 (F2RL3,

Accession NM_003950) is a VGAM2048 host target gene. F2RL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by F2RL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of F2RL3 BINDING SITE, designated SEQ ID:10079, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71711] A function of VGAM2048 is therefore inhibition of Coagulation Factor II (thrombin) Receptor-like 3 (F2RL3, Accession NM_003950), a gene which Protease-activated receptor 4; G protein-coupled receptor that increases phosphoinositide hydrolysis. Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F2RL3. The function of F2RL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM193.Mannose-6-phosphate Receptor (cation dependent) (M6PR, Accession NM_002355) is another VGAM2048 host target gene. M6PR BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by M6PR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of M6PR BINDING SITE, designated SEQ ID:8163, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71712] Another function of VGAM2048 is therefore inhibition of Mannose-6-phosphate Receptor (cation dependent) (M6PR, Accession NM_002355), a gene which is nvolved in intracellular sorting and transport of acid hydrolases. Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with M6PR. The function of M6PR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1924.Nescient Helix Loop Helix 1 (NHLH1, Accession NM_005598) is another VGAM2048 host target gene. NHLH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NHLH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NHLH1 BINDING SITE, designated SEQ ID:12123, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71713] Another function of VGAM2048 is therefore inhibition of Nescient Helix Loop Helix 1 (NHLH1, Accession NM_005598), a gene which may have a role in development of the nervous system. Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NHLH1. The function of NHLH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1923.CCR4-NOT Transcription Complex, Subunit 4 (CNOT4, Accession NM_013316) is another VGAM2048 host target gene. CNOT4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNOT4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNOT4 BINDING SITE, designated SEQ ID:14964, to the nucleotide sequence of

VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71714] Another function of VGAM2048 is therefore inhibition of CCR4-NOT Transcription Complex, Subunit 4 (CNOT4, Accession NM_013316). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNOT4. EFA6R (Accession NM_015310) is another VGAM2048 host target gene. EFA6R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EFA6R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFA6R BINDING SITE, designated SEQ ID:17621, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71715] Another function of VGAM2048 is therefore inhibition of EFA6R (Accession NM_015310). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFA6R. FLJ20220 (Accession NM_017718) is another VGAM2048 host target gene. FLJ20220 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by FLJ20220, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20220 BINDING SITE, designated SEQ ID:19303, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71716] Another function of VGAM2048 is therefore inhibition of FLJ20220 (Accession NM_017718). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20220. FLJ20392 (Accession NM_017799) is another VGAM2048 host target gene. FLJ20392 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20392, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20392 BINDING SITE, designated SEQ ID:19444, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71717] Another function of VGAM2048 is therefore inhibition of

FLJ20392 (Accession NM_017799). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20392. FLJ20445 (Accession NM_017824) is another VGAM2048 host target gene. FLJ20445 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20445 BINDING SITE, designated SEQ ID:19477, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71718] Another function of VGAM2048 is therefore inhibition of FLJ20445 (Accession NM_017824). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20445. FLJ22596 (Accession NM_025086) is another VGAM2048 host target gene. FLJ22596 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22596, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ22596 BINDING SITE, designated SEQ ID:24701, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71719] Another function of VGAM2048 is therefore inhibition of FLJ22596 (Accession NM_025086). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22596. KIAA1046 (Accession NM_014928) is another VGAM2048 host target gene. KIAA1046 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1046, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1046 BINDING SITE, designated SEQ ID:17216, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71720] Another function of VGAM2048 is therefore inhibition of KIAA1046 (Accession NM_014928). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1046. Musculin (activated B-cell factor-1) (MSC, Ac-

cession XM_084266) is another VGAM2048 host target gene. MSC BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MSC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MSC BINDING SITE, designated SEQ ID:37532, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71721] Another function of VGAM2048 is therefore inhibition of Musculin (activated B-cell factor-1) (MSC, Accession XM_084266). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSC. PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335) is another VGAM2048 host target gene. PRPF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRPF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRPF8 BINDING SITE, designated SEQ ID:30678, to the nucleotide sequence of VGAM2048 RNA,

herein designated VGAM RNA, also designated SEQ ID:4759.

[71722] Another function of VGAM2048 is therefore inhibition of PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRPF8. TBP-like 1 (TBPL1, Accession NM_004865) is another VGAM2048 host target gene. TBPL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TBPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBPL1 BINDING SITE, designated SEQ ID:11289, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71723] Another function of VGAM2048 is therefore inhibition of TBP-like 1 (TBPL1, Accession NM_004865). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBPL1. VPS39 (Accession XM_031720) is another VGAM2048 host target gene. VPS39 BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by VPS39, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS39 BINDING SITE, designated SEQ ID:31468, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71724] Another function of VGAM2048 is therefore inhibition of VPS39 (Accession XM_031720). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS39. ZTL1 (Accession NM_024055) is another VGAM2048 host target gene. ZTL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZTL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZTL1 BINDING SITE, designated SEQ ID:23490, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71725] Another function of VGAM2048 is therefore inhibition of

ZTL1 (Accession NM_024055). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZTL1. LOC150067 (Accession XM_016411) is another VGAM2048 host target gene. LOC150067 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150067, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150067 BINDING SITE, designated SEQ ID:30258, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71726] Another function of VGAM2048 is therefore inhibition of LOC150067 (Accession XM_016411). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150067. LOC151057 (Accession XM_097998) is another VGAM2048 host target gene. LOC151057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC151057 BINDING SITE, designated SEQ ID:41292, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71727] Another function of VGAM2048 is therefore inhibition of LOC151057 (Accession XM_097998). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151057. LOC153443 (Accession XM_087669) is another VGAM2048 host target gene. LOC153443 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153443, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153443 BINDING SITE, designated SEQ ID:39373, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71728] Another function of VGAM2048 is therefore inhibition of LOC153443 (Accession XM_087669). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153443. LOC197003 (Accession XM_113798) is an-

other VGAM2048 host target gene. LOC197003 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197003, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197003 BINDING SITE, designated SEQ ID:42442, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71729] Another function of VGAM2048 is therefore inhibition of LOC197003 (Accession XM_113798). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197003. LOC200205 (Accession XM_114152) is another VGAM2048 host target gene. LOC200205 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200205, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200205 BINDING SITE, designated SEQ ID:42734, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71730] Another function of VGAM2048 is therefore inhibition of LOC200205 (Accession XM_114152). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200205. LOC219401 (Accession XM_166706) is another VGAM2048 host target gene. LOC219401 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219401, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219401 BINDING SITE, designated SEQ ID:44592, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71731] Another function of VGAM2048 is therefore inhibition of LOC219401 (Accession XM_166706). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219401. LOC255126 (Accession XM_173585) is another VGAM2048 host target gene. LOC255126 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255126, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255126 BINDING SITE, designated SEQ ID:46550, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71732] Another function of VGAM2048 is therefore inhibition of LOC255126 (Accession XM_173585). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255126. LOC51072 (Accession NM_015955) is another VGAM2048 host target gene. LOC51072 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51072, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51072 BINDING SITE, designated SEQ ID:18067, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71733] Another function of VGAM2048 is therefore inhibition of LOC51072 (Accession NM_015955). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC51072. LOC90139 (Accession NM_130783) is another VGAM2048 host target gene. LOC90139 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90139 BINDING SITE, designated SEQ ID:28273, to the nucleotide sequence of VGAM2048 RNA, herein designated VGAM RNA, also designated SEQ ID:4759.

[71734] Another function of VGAM2048 is therefore inhibition of LOC90139 (Accession NM_130783). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90139. LOC91373 (Accession XM_038063) is another VGAM2048 host target gene. LOC91373 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91373, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91373 BINDING SITE, designated SEQ ID:32750, to the nucleotide sequence of VGAM2048 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4759.

[71735] Another function of VGAM2048 is therefore inhibition of LOC91373 (Accession XM_038063). Accordingly, utilities of VGAM2048 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91373. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2049 (VGAM2049) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71736] VGAM2049 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2049 was detected is described hereinabove with reference to Figs. 1-8.

[71737] VGAM2049 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 5. VGAM2049 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71738] VGAM2049 gene encodes a VGAM2049 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2049 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2049 precursor RNA is designated SEQ ID:2035, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2035 is located at position 196060 relative to the genome of Human Herpesvirus 5.

[71739] VGAM2049 precursor RNA folds onto itself, forming VGAM2049 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71740] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2049 folded precursor RNA into VGAM2049 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2049 RNA is designated SEQ ID:4760, and is provided hereinbelow with reference to the sequence listing part.

[71741] VGAM2049 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2049 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2049 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71742] VGAM2049 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2049 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2049 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2049 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2049 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71743] The complementary binding of VGAM2049 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2049 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2049 host target RNA into VGAM2049 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71744] It is appreciated that VGAM2049 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2049 host target genes. The mRNA of

each one of this plurality of VGAM2049 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2049 RNA, herein designated VGAM RNA, and which when bound by VGAM2049 RNA causes inhibition of translation of respective one or more VGAM2049 host target proteins.

[71745] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2049 gene, herein designated VGAM GENE, on one or more VGAM2049 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[71746] It is yet further appreciated that a function of VGAM2049 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2049 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 5. Specific functions, and accordingly utilities, of VGAM2049 correlate with, and may be deduced from, the identity of the host target genes which VGAM2049 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71747] Nucleotide sequences of the VGAM2049 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2049 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2049 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2049 are further described hereinbelow with reference to Table 1.

[71748] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2049 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2049 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71749] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2049 gene, herein designated VGAM is inhibition of expression of VGAM2049 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2049 correlate with, and may be deduced from, the identity of the target genes which VGAM2049 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71750] Complement Component 7 (C7, Accession NM_000587) is a VGAM2049 host target gene. C7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C7 BINDING SITE, designated SEQ ID:6192, to the nucleotide sequence of VGAM2049 RNA, herein designated VGAM RNA, also designated SEQ ID:4760.

[71751] A function of VGAM2049 is therefore inhibition of Complement Component 7 (C7, Accession NM_000587). Accordingly, utilities of VGAM2049 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with C7. Dual Specificity Phosphatase 5 (DUSP5, Accession NM_004419) is another VGAM2049 host target gene. DUSP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DUSP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DUSP5 BINDING SITE, designated SEQ ID:10686, to the nucleotide sequence of VGAM2049 RNA, herein designated VGAM RNA, also designated SEQ ID:4760.

[71752] Another function of VGAM2049 is therefore inhibition of Dual Specificity Phosphatase 5 (DUSP5, Accession NM_004419), a gene which displays phosphatase activity toward several substrates. Accordingly, utilities of VGAM2049 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP5. The function of DUSP5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM538.DKFZP564C103 (Accession NM_015654) is another VGAM2049 host target gene. DKFZP564C103

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564C103, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564C103 BINDING SITE, designated SEQ ID:17901, to the nucleotide sequence of VGAM2049 RNA, herein designated VGAM RNA, also designated SEQ ID:4760.

[71753] Another function of VGAM2049 is therefore inhibition of DKFZP564C103 (Accession NM_015654). Accordingly, utilities of VGAM2049 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564C103. KIAA0561 (Accession XM_038150) is another VGAM2049 host target gene. KIAA0561 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0561, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0561 BINDING SITE, designated SEQ ID:32762, to the nucleotide sequence of VGAM2049 RNA, herein designated VGAM RNA, also designated SEQ ID:4760.

[71754] Another function of VGAM2049 is therefore inhibition of KIAA0561 (Accession XM_038150). Accordingly, utilities of VGAM2049 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0561. KIAA0935 (Accession XM_052620) is another VGAM2049 host target gene. KIAA0935 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0935, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0935 BINDING SITE, designated SEQ ID:36012, to the nucleotide sequence of VGAM2049 RNA, herein designated VGAM RNA, also designated SEQ ID:4760.

[71755] Another function of VGAM2049 is therefore inhibition of KIAA0935 (Accession XM_052620). Accordingly, utilities of VGAM2049 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0935. Protein Phosphatase 4, Regulatory Subunit 1-like (PPP4R1L, Accession XM_086650) is another VGAM2049 host target gene. PPP4R1L BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PPP4R1L, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP4R1L BINDING SITE, designated SEQ ID:38816, to the nucleotide sequence of VGAM2049 RNA, herein designated VGAM RNA, also designated SEQ ID:4760.

[71756] Another function of VGAM2049 is therefore inhibition of Protein Phosphatase 4, Regulatory Subunit 1-like (PPP4R1L, Accession XM_086650). Accordingly, utilities of VGAM2049 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP4R1L. ZAK (Accession NM_016653) is another VGAM2049 host target gene. ZAK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZAK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZAK BINDING SITE, designated SEQ ID:18778, to the nucleotide sequence of VGAM2049 RNA, herein designated VGAM RNA, also designated SEQ ID:4760.

[71757] Another function of VGAM2049 is therefore inhibition of ZAK (Accession NM_016653). Accordingly, utilities of

VGAM2049 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAK. LOC149566 (Accession XM_097670) is another VGAM2049 host target gene. LOC149566 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149566, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149566 BINDING SITE, designated SEQ ID:41012, to the nucleotide sequence of VGAM2049 RNA, herein designated VGAM RNA, also designated SEQ ID:4760.

[71758] Another function of VGAM2049 is therefore inhibition of LOC149566 (Accession XM_097670). Accordingly, utilities of VGAM2049 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149566. LOC150368 (Accession XM_086826) is another VGAM2049 host target gene. LOC150368 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150368, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC150368 BINDING SITE, designated SEQ ID:38911, to the nucleotide sequence of VGAM2049 RNA, herein designated VGAM RNA, also designated SEQ ID:4760.

[71759] Another function of VGAM2049 is therefore inhibition of LOC150368 (Accession XM_086826). Accordingly, utilities of VGAM2049 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150368. LOC255718 (Accession XM_174148) is another VGAM2049 host target gene. LOC255718 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255718, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255718 BINDING SITE, designated SEQ ID:46582, to the nucleotide sequence of VGAM2049 RNA, herein designated VGAM RNA, also designated SEQ ID:4760.

[71760] Another function of VGAM2049 is therefore inhibition of LOC255718 (Accession XM_174148). Accordingly, utilities of VGAM2049 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255718. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2050 (VGAM2050) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71761] VGAM2050 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2050 was detected is described hereinabove with reference to Figs. 1-8.

[71762] VGAM2050 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ovine Adenovirus A. VGAM2050 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71763] VGAM2050 gene encodes a VGAM2050 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2050 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2050 precursor RNA is designated SEQ ID:2036, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2036 is located at position 13096 relative to the

genome of Ovine Adenovirus A.

[71764] VGAM2050 precursor RNA folds onto itself, forming VGAM2050 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71765] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2050 folded precursor RNA into VGAM2050 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2050 RNA is designated SEQ ID:4761, and is provided hereinbelow with reference to the sequence listing part.

[71766] VGAM2050 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2050 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2050 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71767] VGAM2050 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2050 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2050 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2050 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2050 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71768] The complementary binding of VGAM2050 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2050 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2050 host target RNA into VGAM2050 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71769] It is appreciated that VGAM2050 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2050 host target genes. The mRNA of each one of this plurality of VGAM2050 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2050 RNA, herein designated VGAM RNA, and which when bound by VGAM2050 RNA causes inhibition of translation of respective one or more VGAM2050 host target proteins.

[71770] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2050 gene, herein designated VGAM GENE, on one or more VGAM2050 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71771] It is yet further appreciated that a function of VGAM2050 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2050 include diagnosis, prevention and treatment of viral infection by Ovine Adenovirus A. Specific functions, and accordingly utilities, of VGAM2050

correlate with, and may be deduced from, the identity of the host target genes which VGAM2050 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71772] Nucleotide sequences of the VGAM2050 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2050 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2050 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2050 are further described hereinbelow with reference to Table 1.

[71773] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2050 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2050 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71774] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2050 gene, herein designated VGAM is inhibition of expression of VGAM2050 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2050 correlate with, and may be deduced

from, the identity of the target genes which VGAM2050 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71775] KIAA0820 (Accession XM_044463) is a VGAM2050 host target gene. KIAA0820 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0820, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0820 BINDING SITE, designated SEQ ID:34215, to the nucleotide sequence of VGAM2050 RNA, herein designated VGAM RNA, also designated SEQ ID:4761.

[71776] A function of VGAM2050 is therefore inhibition of KIAA0820 (Accession XM_044463). Accordingly, utilities of VGAM2050 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0820. LOC205327 (Accession XM_115788) is another VGAM2050 host target gene. LOC205327 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC205327, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC205327 BINDING SITE, designated SEQ ID:43103, to the nucleotide sequence of VGAM2050 RNA, herein designated VGAM RNA, also designated SEQ ID:4761.

[71777] Another function of VGAM2050 is therefore inhibition of LOC205327 (Accession XM_115788). Accordingly, utilities of VGAM2050 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC205327. LOC222681 (Accession XM_167116) is another VGAM2050 host target gene. LOC222681 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222681, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222681 BINDING SITE, designated SEQ ID:44607, to the nucleotide sequence of VGAM2050 RNA, herein designated VGAM RNA, also designated SEQ ID:4761.

[71778] Another function of VGAM2050 is therefore inhibition of LOC222681 (Accession XM_167116). Accordingly, utilities of VGAM2050 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222681. LOC257507 (Accession XM_175204) is an-

other VGAM2050 host target gene. LOC257507 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257507, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257507 BINDING SITE, designated SEQ ID:46673, to the nucleotide sequence of VGAM2050 RNA, herein designated VGAM RNA, also designated SEQ ID:4761.

[71779] Another function of VGAM2050 is therefore inhibition of LOC257507 (Accession XM_175204). Accordingly, utilities of VGAM2050 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257507. LOC257625 (Accession XM_175267) is another VGAM2050 host target gene. LOC257625 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257625, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257625 BINDING SITE, designated SEQ ID:46729, to the nucleotide sequence of VGAM2050 RNA, herein designated VGAM RNA, also designated SEQ ID:4761.

[71780] Another function of VGAM2050 is therefore inhibition of LOC257625 (Accession XM_175267). Accordingly, utilities of VGAM2050 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257625. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2051 (VGAM2051) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71781] VGAM2051 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2051 was detected is described hereinabove with reference to Figs. 1-8.

[71782] VGAM2051 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ovine Adenovirus A. VGAM2051 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71783] VGAM2051 gene encodes a VGAM2051 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2051 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2051 precursor RNA is designated SEQ ID:2037, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2037 is located at position 24505 relative to the genome of Ovine Adenovirus A.

[71784] VGAM2051 precursor RNA folds onto itself, forming VGAM2051 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71785] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2051 folded precursor RNA into VGAM2051 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2051 RNA is designated SEQ ID:4762, and is provided hereinbelow with reference to the sequence listing part.

[71786] VGAM2051 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2051 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2051 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71787] VGAM2051 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2051 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2051 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2051 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2051 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71788] The complementary binding of VGAM2051 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2051 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2051 host target RNA into VGAM2051 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71789] It is appreciated that VGAM2051 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2051 host target genes. The mRNA of each one of this plurality of VGAM2051 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2051 RNA, herein designated VGAM RNA, and which when bound by VGAM2051 RNA causes inhibition of translation of respective one or more VGAM2051 host target proteins.

[71790] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2051 gene, herein designated VGAM GENE, on one or more VGAM2051 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71791] It is yet further appreciated that a function of VGAM2051 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of viral infection by Ovine Adenovirus A. Specific functions, and accordingly utilities, of VGAM2051 correlate with, and may be deduced from, the identity of the host target genes which VGAM2051 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71792] Nucleotide sequences of the VGAM2051 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2051 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2051 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2051 are further described hereinbelow with reference to Table 1.

[71793] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2051 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2051 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[71794] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2051 gene, herein designated VGAM is inhibition of expression of VGAM2051 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2051 correlate with, and may be deduced from, the identity of the target genes which VGAM2051 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71795] Mitogen-activated Protein Kinase Kinase Kinase 14 (MAP3K14, Accession NM_003954) is a VGAM2051 host target gene. MAP3K14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K14 BINDING SITE, designated SEQ ID:10089, to the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, also designated SEQ ID:4762.

[71796] A function of VGAM2051 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 14 (MAP3K14, Accession NM_003954), a gene which is involved in the

activation of nf-kappa-b and its transcriptional activity. induces the processing of nf-kappa-b 2/p100. could act in a receptor-selective manner (by similarity). Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K14. The function of MAP3K14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Methionine Adenosyltransferase II, Alpha (MAT2A, Accession NM_005911) is another VGAM2051 host target gene. MAT2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAT2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAT2A BINDING SITE, designated SEQ ID:12543, to the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, also designated SEQ ID:4762.

[71797] Another function of VGAM2051 is therefore inhibition of Methionine Adenosyltransferase II, Alpha (MAT2A, Accession NM_005911), a gene which catalyzes the biosynthesis of S-adenosylmethionine (AdoMet) from methionine

and ATP. Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAT2A. The function of MAT2A has been established by previous studies. Methionine adenosyltransferase (EC 2.5.1.6) catalyzes the biosynthesis of S-adenosylmethionine (OMIM Ref. No. AdoMet) from methionine and ATP. AdoMet is the major methyl donor for many of the transmethylation reactions in the body. Chamberlin et al. (1996) noted that AdoMet also participates in the transsulfuration pathway and, after decarboxylation, serves as a propylamine group donor in the biosynthesis of polyamines. Three forms of MAT have been identified in mammalian tissues. MAT I and MAT III, which are encoded by the single-copy MAT1A gene (OMIM Ref. No. 250850), represent tetramers and dimers, respectively, formed from identical alpha-1 subunits and are synthesized primarily in the liver. MAT II, encoded by a separate gene, which was cloned by Horikawa and Tsukada (1992), is found in fetal liver (and to a lesser extent in adult liver) as well as in kidney, brain, testis, and lymphocytes. Horikawa and Tsukada (1992) showed that the 395-amino acid MAT II shares 84% amino acid similarity with the human liver MAT I/III protein. Mao et al.

(1998) cloned the 5-prime flanking region of the MAT2A gene. They identified 2 major transcriptional start sites, one located within 10 nucleotides downstream and the other 158 nucleotides upstream from the TATA box. The MAT2A promoter is highly GC rich, especially in the first 300 bp. The promoter contains several potential SP1-, v-myb-, and GATA-binding sites, as well as potential binding sites for C/EBP, HSF2, c-myb, and STATx. Mao et al. (1998) showed that the MAT2A promoter can efficiently drive expression from a reporter gene in both Jurkat and 293 cells. The authors identified regions of the promoter that are important for cell-specific MAT2A expression. By in situ hybridization, De La Rosa et al. (1995) mapped the MATA2 gene to 2p11.2.

[71798] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[71799] Chamberlin, M. E.; Ubagai, T.; Mudd, S. H.; Wilson, W. G.; Leonard, J. V.; Chou, J. Y. : Demyelination of the brain is associated with methionine adenosyltransferase I/III deficiency. J. Clin. Invest. 98: 1021-1027, 1996. ; and

[71800] De La Rosa, J.; Ostrowski, J.; Hryniewicz, M. M.; Kredich, N. M.; Kotb, M.; LeGros, H. L., Jr.; Valentine, M.; Geller, A. M.

: Chromosomal localization and catalytic properties of the r.

[71801] Further studies establishing the function and utilities of MAT2A are found in John Hopkins OMIM database record ID 601468, and in sited publications numbered 907 and 6689-6690 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.N-ethylmaleimide-sensitive Factor (NSF, Accession XM_032173) is another VGAM2051 host target gene. NSF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NSF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NSF BINDING SITE, designated SEQ ID:31587, to the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, also designated SEQ ID:4762.

[71802] Another function of VGAM2051 is therefore inhibition of N-ethylmaleimide-sensitive Factor (NSF, Accession XM_032173), a gene which catalyzes the fusion of transport vesicles within the golgi cisternae. Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with NSF. The function of NSF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM370.Pyrimidinergic Receptor P2Y, G-protein Coupled, 6 (P2RY6, Accession NM_004154) is another VGAM2051 host target gene. P2RY6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by P2RY6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P2RY6 BINDING SITE, designated SEQ ID:10353, to the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, also designated SEQ ID:4762.

[71803] Another function of VGAM2051 is therefore inhibition of Pyrimidinergic Receptor P2Y, G-protein Coupled, 6 (P2RY6, Accession NM_004154), a gene which mediates cellular responses to nucleotides. Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RY6. The function of P2RY6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM445.Ring Finger Protein 26 (RNF26, Accession NM_032015) is another VGAM2051 host target gene. RNF26 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNF26, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF26 BINDING SITE, designated SEQ ID:25727, to the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, also designated SEQ ID:4762.

[71804] Another function of VGAM2051 is therefore inhibition of Ring Finger Protein 26 (RNF26, Accession NM_032015). Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF26. Carboxylesterase 2 (intestine, liver) (CES2, Accession NM_003869) is another VGAM2051 host target gene. CES2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CES2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CES2 BINDING SITE,

designated SEQ ID:9956, to the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, also designated SEQ ID:4762.

[71805] Another function of VGAM2051 is therefore inhibition of Carboxylesterase 2 (intestine, liver) (CES2, Accession NM_003869). Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CES2. FLJ14642 (Accession NM_032818) is another VGAM2051 host target gene. FLJ14642 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14642, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14642 BINDING SITE, designated SEQ ID:26594, to the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, also designated SEQ ID:4762.

[71806] Another function of VGAM2051 is therefore inhibition of FLJ14642 (Accession NM_032818). Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14642. HSNOV1 (Accession NM_017515) is another

VGAM2051 host target gene. HSNOV1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSNOV1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSNOV1 BINDING SITE, designated SEQ ID:18964, to the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, also designated SEQ ID:4762.

[71807] Another function of VGAM2051 is therefore inhibition of HSNOV1 (Accession NM_017515). Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSNOV1. KIAA0757 (Accession NM_006038) is another VGAM2051 host target gene. KIAA0757 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0757, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0757 BINDING SITE, designated SEQ ID:12670, to the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, also designated SEQ ID:4762.

[71808] Another function of VGAM2051 is therefore inhibition of KIAA0757 (Accession NM_006038). Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0757. NDRG Family Member 4 (NDRG4, Accession NM_020465) is another VGAM2051 host target gene. NDRG4 BINDING SITE1 and NDRG4 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NDRG4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDRG4 BINDING SITE1 and NDRG4 BINDING SITE2, designated SEQ ID:21696 and SEQ ID:23211 respectively, to the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, also designated SEQ ID:4762.

[71809] Another function of VGAM2051 is therefore inhibition of NDRG Family Member 4 (NDRG4, Accession NM_020465). Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG4. LOC145497 (Accession XM_085150) is another VGAM2051 host target gene. LOC145497 BINDING SITE is HOST TARGET binding site

found in the 5` untranslated region of mRNA encoded by LOC145497, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145497 BINDING SITE, designated SEQ ID:37872, to the nucleotide sequence of VGAM2051 RNA, herein designated VGAM RNA, also designated SEQ ID:4762.

[71810] Another function of VGAM2051 is therefore inhibition of LOC145497 (Accession XM_085150). Accordingly, utilities of VGAM2051 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145497. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2052 (VGAM2052) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71811] VGAM2052 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2052 was detected is described hereinabove with reference to Figs. 1-8.

[71812] VGAM2052 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ovine Adenovirus A. VGAM2052 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71813] VGAM2052 gene encodes a VGAM2052 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2052 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2052 precursor RNA is designated SEQ ID:2038, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2038 is located at position 28963 relative to the genome of Ovine Adenovirus A.

[71814] VGAM2052 precursor RNA folds onto itself, forming VGAM2052 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[71815] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2052 folded precursor RNA into VGAM2052 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2052 RNA is designated SEQ ID:4763, and is provided hereinbelow with reference to the sequence listing part.

[71816] VGAM2052 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2052 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2052 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71817] VGAM2052 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2052 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2052 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2052 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2052 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71818] The complementary binding of VGAM2052 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2052 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2052 host target RNA into VGAM2052 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71819] It is appreciated that VGAM2052 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2052 host target genes. The mRNA of each one of this plurality of VGAM2052 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2052 RNA, herein designated VGAM RNA, and which when bound by VGAM2052 RNA causes inhibition of translation of respective one or more VGAM2052 host target proteins.

[71820] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2052 gene, herein designated VGAM GENE, on one or more VGAM2052 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71821] It is yet further appreciated that a function of VGAM2052 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of viral infection by Ovine Adenovirus A. Specific functions, and accordingly utilities, of VGAM2052 correlate with, and may be deduced from, the identity of the host target genes which VGAM2052 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71822] Nucleotide sequences of the VGAM2052 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2052 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2052 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2052 are further described hereinbelow with reference to Table 1.

[71823] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2052 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2052 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71824] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2052 gene, herein designated VGAM is inhibition of expression of VGAM2052 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2052 correlate with, and may be deduced from, the identity of the target genes which VGAM2052 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71825] Adaptor-related Protein Complex 2, Beta 1 Subunit (AP2B1, Accession NM_001282) is a VGAM2052 host target gene. AP2B1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AP2B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of AP2B1 BINDING SITE, designated SEQ ID:6951, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71826] A function of VGAM2052 is therefore inhibition of Adaptor-related Protein Complex 2, Beta 1 Subunit (AP2B1, Accession NM_001282), a gene which links clathrin to receptors in coated vesicles. Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP2B1. The function of AP2B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1126.Cadherin 1, Type 1, E-cadherin (epithelial) (CDH1, Accession NM_004360) is another VGAM2052 host target gene. CDH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDH1 BINDING SITE, designated SEQ ID:10565, to the nucleotide sequence of VGAM2052 RNA,

herein designated VGAM RNA, also designated SEQ ID:4763.

[71827] Another function of VGAM2052 is therefore inhibition of Cadherin 1, Type 1, E-cadherin (epithelial) (CDH1, Accession NM_004360). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH1. Decorin (DCN, Accession NM_001920) is another VGAM2052 host target gene. DCN BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DCN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCN BINDING SITE, designated SEQ ID:7635, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71828] Another function of VGAM2052 is therefore inhibition of Decorin (DCN, Accession NM_001920), a gene which may mediate in epithelial/mesenchymal interactions . Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCN. The function of DCN and its association with various diseases and clinical conditions, has been es-

tablished by previous studies, as described hereinabove with reference to VGAM1326.High Mobility Group AT-hook 2 (HMGA2, Accession NM_003483) is another VGAM2052 host target gene. HMGA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HMGA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMGA2 BINDING SITE, designated SEQ ID:9571, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71829] Another function of VGAM2052 is therefore inhibition of High Mobility Group AT-hook 2 (HMGA2, Accession NM_003483), a gene which may affect transcription and cell differentiation; shares common DNA-binding motif with other HMG HMG I/Y family members. Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMGA2. The function of HMGA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM552.Interferon (alpha, beta and

omega) Receptor 2 (IFNAR2, Accession NM_000874) is another VGAM2052 host target gene. IFNAR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IFNAR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IFNAR2 BINDING SITE, designated SEQ ID:6553, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71830] Another function of VGAM2052 is therefore inhibition of Interferon (alpha, beta and omega) Receptor 2 (IFNAR2, Accession NM_000874), a gene which is a receptor for interferons alpha and beta. Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IFNAR2. The function of IFNAR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM487.Integrin, Beta-like 1 (with EGF-like repeat domains) (ITGBL1, Accession NM_004791) is another VGAM2052 host target gene. ITGBL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by ITGBL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGBL1 BINDING SITE, designated SEQ ID:11200, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71831] Another function of VGAM2052 is therefore inhibition of Integrin, Beta-like 1 (with EGF-like repeat domains) (ITGBL1, Accession NM_004791). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGBL1. MLL Septin-like Fusion (MSF, Accession XM_113892) is another VGAM2052 host target gene. MSF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MSF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MSF BINDING SITE, designated SEQ ID:42524, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71832] Another function of VGAM2052 is therefore inhibition of

MLL Septin-like Fusion (MSF, Accession XM_113892), a gene which plays a role in the cell cycle. Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSF. The function of MSF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM514.Protocadherin Alpha 9 (PCDHA9, Accession NM_014005) is another VGAM2052 host target gene. PCDHA9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHA9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA9 BINDING SITE, designated SEQ ID:15212, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71833] Another function of VGAM2052 is therefore inhibition of Protocadherin Alpha 9 (PCDHA9, Accession NM_014005), a gene which is a calcium-dependent cell-adhesion protein. Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical con-

ditions associated with PCDHA9. The function of PCDHA9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM71.Protease, Serine, 16 (thymus) (PRSS16, Accession NM_005865) is another VGAM2052 host target gene. PRSS16 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRSS16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRSS16 BINDING SITE, designated SEQ ID:12481, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71834] Another function of VGAM2052 is therefore inhibition of Protease, Serine, 16 (thymus) (PRSS16, Accession NM_005865). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRSS16. Protein Tyrosine Phosphatase, Receptor Type, F (PTPRF, Accession NM_130440) is another VGAM2052 host target gene. PTPRF BINDING SITE1 and PTPRF BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of

mRNA encoded by PTPRF, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRF BINDING SITE1 and PTPRF BINDING SITE2, designated SEQ ID:28197 and SEQ ID:8723 respectively, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71835] Another function of VGAM2052 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, F (PTPRF, Accession NM_130440), a gene which negatively regulates the insulin signaling pathway. Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRF. The function of PTPRF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1105.SON DNA Binding Protein (SON, Accession NM_138926) is another VGAM2052 host target gene. SON BINDING SITE1 through SON BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SON, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SON BINDING SITE1 through SON BINDING SITE3, designated SEQ ID:29042, SEQ ID:29046 and SEQ ID:27746 respectively, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71836] Another function of VGAM2052 is therefore inhibition of SON DNA Binding Protein (SON, Accession NM_138926). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SON. TAF7-like RNA Polymerase II, TATA Box Binding Protein (TBP)-associated Factor, 50kDa (TAF7L, Accession NM_024885) is another VGAM2052 host target gene. TAF7L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAF7L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAF7L BINDING SITE, designated SEQ ID:24338, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71837] Another function of VGAM2052 is therefore inhibition of

TAF7-like RNA Polymerase II, TATA Box Binding Protein (TBP)-associated Factor, 50kDa (TAF7L, Accession NM_024885). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAF7L. Transcription Factor AP-4 (activating enhancer binding protein 4) (TFAP4, Accession NM_003223) is another VGAM2052 host target gene. TFAP4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TFAP4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TFAP4 BINDING SITE, designated SEQ ID:9226, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71838] Another function of VGAM2052 is therefore inhibition of Transcription Factor AP-4 (activating enhancer binding protein 4) (TFAP4, Accession NM_003223), a gene which activates both viral and cellular genes by binding to the symmetrical dna sequence 5'-cagctg-3'. Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with TFAP4. The function of TFAP4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM175.WWP2 (Accession XM_028151) is another VGAM2052 host target gene. WWP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WWP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WWP2 BINDING SITE, designated SEQ ID:30624, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71839] Another function of VGAM2052 is therefore inhibition of WWP2 (Accession XM_028151), a gene which exhibits ubiquitin-protein ligase activity and contains WW and HECT domains. Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WWP2. The function of WWP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.Apolipoprotein A-V (APOA5, Accession

NM_052968) is another VGAM2052 host target gene. APOA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APOA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APOA5 BINDING SITE, designated SEQ ID:27538, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71840] Another function of VGAM2052 is therefore inhibition of Apolipoprotein A-V (APOA5, Accession NM_052968). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOA5. Destrin (actin depolymerizing factor) (DSTN, Accession NM_006870) is another VGAM2052 host target gene. DSTN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DSTN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DSTN BINDING SITE, designated SEQ ID:13741, to the nucleotide sequence of

VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71841] Another function of VGAM2052 is therefore inhibition of Destrin (actin depolymerizing factor) (DSTN, Accession NM_006870). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSTN. FLJ10081 (Accession NM_017991) is another VGAM2052 host target gene. FLJ10081 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10081, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10081 BINDING SITE, designated SEQ ID:19722, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71842] Another function of VGAM2052 is therefore inhibition of FLJ10081 (Accession NM_017991). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10081. FLJ11726 (Accession NM_024971) is another VGAM2052 host target gene. FLJ11726 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11726, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11726 BINDING SITE, designated SEQ ID:24525, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71843] Another function of VGAM2052 is therefore inhibition of FLJ11726 (Accession NM_024971). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11726. FLJ14327 (Accession NM_024912) is another VGAM2052 host target gene. FLJ14327 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14327, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14327 BINDING SITE, designated SEQ ID:24423, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71844] Another function of VGAM2052 is therefore inhibition of

FLJ14327 (Accession NM_024912). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14327. ICK (Accession NM_014920) is another VGAM2052 host target gene. ICK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:17194, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71845] Another function of VGAM2052 is therefore inhibition of ICK (Accession NM_014920). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICK. KIAA0532 (Accession XM_047659) is another VGAM2052 host target gene. KIAA0532 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0532, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of KIAA0532 BINDING SITE, designated SEQ ID:35022, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71846] Another function of VGAM2052 is therefore inhibition of KIAA0532 (Accession XM_047659). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0532. KIAA0682 (Accession NM_014852) is another VGAM2052 host target gene. KIAA0682 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0682, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0682 BINDING SITE, designated SEQ ID:16901, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71847] Another function of VGAM2052 is therefore inhibition of KIAA0682 (Accession NM_014852). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0682. KIAA0766 (Accession NM_014805) is another

VGAM2052 host target gene. KIAA0766 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0766, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0766 BINDING SITE, designated SEQ ID:16744, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71848] Another function of VGAM2052 is therefore inhibition of KIAA0766 (Accession NM_014805). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0766. KIAA1045 (Accession XM_048592) is another VGAM2052 host target gene. KIAA1045 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1045, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1045 BINDING SITE, designated SEQ ID:35199, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71849] Another function of VGAM2052 is therefore inhibition of KIAA1045 (Accession XM_048592). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1045. KIAA1184 (Accession NM_022572) is another VGAM2052 host target gene. KIAA1184 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1184, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1184 BINDING SITE, designated SEQ ID:22894, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71850] Another function of VGAM2052 is therefore inhibition of KIAA1184 (Accession NM_022572). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1184. KIAA1579 (Accession NM_018211) is another VGAM2052 host target gene. KIAA1579 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1579, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1579 BINDING SITE, designated SEQ ID:20119, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71851] Another function of VGAM2052 is therefore inhibition of KIAA1579 (Accession NM_018211). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1579. KIAA1908 (Accession XM_055834) is another VGAM2052 host target gene. KIAA1908 BINDING SITE1 and KIAA1908 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1908, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1908 BINDING SITE1 and KIAA1908 BINDING SITE2, designated SEQ ID:36328 and SEQ ID:36338 respectively, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71852] Another function of VGAM2052 is therefore inhibition of KIAA1908 (Accession XM_055834). Accordingly, utilities

of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1908. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840) is another VGAM2052 host target gene. PPP1R16B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R16B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R16B BINDING SITE, designated SEQ ID:30776, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71853] Another function of VGAM2052 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R16B. Syndecan Binding Protein (syntenin) (SDCBP, Accession NM_005625) is another VGAM2052 host target gene. SDCBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SDCBP, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDCBP BINDING SITE, designated SEQ ID:12135, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71854] Another function of VGAM2052 is therefore inhibition of Syndecan Binding Protein (syntenin) (SDCBP, Accession NM_005625). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDCBP. SE70-2 (Accession NM_022118) is another VGAM2052 host target gene. SE70-2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SE70-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SE70-2 BINDING SITE, designated SEQ ID:22663, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71855] Another function of VGAM2052 is therefore inhibition of SE70-2 (Accession NM_022118). Accordingly, utilities of

VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SE70-2. LOC112476 (Accession NM_145239) is another VGAM2052 host target gene. LOC112476 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC112476, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112476 BINDING SITE, designated SEQ ID:29752, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71856] Another function of VGAM2052 is therefore inhibition of LOC112476 (Accession NM_145239). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112476. LOC115399 (Accession XM_055874) is another VGAM2052 host target gene. LOC115399 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC115399, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC115399 BINDING SITE, designated SEQ ID:36345, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71857] Another function of VGAM2052 is therefore inhibition of LOC115399 (Accession XM_055874). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115399. LOC130595 (Accession XM_065793) is another VGAM2052 host target gene. LOC130595 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC130595, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130595 BINDING SITE, designated SEQ ID:37299, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71858] Another function of VGAM2052 is therefore inhibition of LOC130595 (Accession XM_065793). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130595. LOC134266 (Accession XM_059701) is another VGAM2052 host target gene. LOC134266 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC134266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC134266 BINDING SITE, designated SEQ ID:37071, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71859] Another function of VGAM2052 is therefore inhibition of LOC134266 (Accession XM_059701). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC134266. LOC149103 (Accession XM_086434) is another VGAM2052 host target gene. LOC149103 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149103, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149103 BINDING SITE, designated SEQ ID:38653, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71860] Another function of VGAM2052 is therefore inhibition of

LOC149103 (Accession XM_086434). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149103. LOC150577 (Accession XM_097918) is another VGAM2052 host target gene. LOC150577 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150577 BINDING SITE, designated SEQ ID:41226, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71861] Another function of VGAM2052 is therefore inhibition of LOC150577 (Accession XM_097918). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150577. LOC158572 (Accession XM_088608) is another VGAM2052 host target gene. LOC158572 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158572, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC158572 BINDING SITE, designated SEQ ID:39872, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71862] Another function of VGAM2052 is therefore inhibition of LOC158572 (Accession XM_088608). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158572. LOC199704 (Accession XM_113994) is another VGAM2052 host target gene. LOC199704 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199704, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199704 BINDING SITE, designated SEQ ID:42603, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71863] Another function of VGAM2052 is therefore inhibition of LOC199704 (Accession XM_113994). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199704. LOC220573 (Accession XM_045569) is an-

other VGAM2052 host target gene. LOC220573 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220573, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220573 BINDING SITE, designated SEQ ID:34483, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71864] Another function of VGAM2052 is therefore inhibition of LOC220573 (Accession XM_045569). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220573. LOC255098 (Accession XM_170912) is another VGAM2052 host target gene. LOC255098 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255098, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255098 BINDING SITE, designated SEQ ID:45690, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71865] Another function of VGAM2052 is therefore inhibition of LOC255098 (Accession XM_170912). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255098. LOC257000 (Accession XM_172999) is another VGAM2052 host target gene. LOC257000 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257000, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257000 BINDING SITE, designated SEQ ID:46272, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71866] Another function of VGAM2052 is therefore inhibition of LOC257000 (Accession XM_172999). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257000. LOC257465 (Accession XM_088384) is another VGAM2052 host target gene. LOC257465 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257465, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257465 BINDING SITE, designated SEQ ID:39665, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71867] Another function of VGAM2052 is therefore inhibition of LOC257465 (Accession XM_088384). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257465. LOC57105 (Accession NM_020377) is another VGAM2052 host target gene. LOC57105 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57105, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57105 BINDING SITE, designated SEQ ID:21636, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71868] Another function of VGAM2052 is therefore inhibition of LOC57105 (Accession NM_020377). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC57105. LOC90333 (Accession XM_030958) is another VGAM2052 host target gene. LOC90333 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90333 BINDING SITE, designated SEQ ID:31222, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71869] Another function of VGAM2052 is therefore inhibition of LOC90333 (Accession XM_030958). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90333. LOC90494 (Accession XM_032161) is another VGAM2052 host target gene. LOC90494 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90494, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90494 BINDING SITE, designated SEQ ID:31576, to the nucleotide sequence of VGAM2052 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4763.

[71870] Another function of VGAM2052 is therefore inhibition of LOC90494 (Accession XM_032161). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90494. LOC92299 (Accession XM_044075) is another VGAM2052 host target gene. LOC92299 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92299, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92299 BINDING SITE, designated SEQ ID:34132, to the nucleotide sequence of VGAM2052 RNA, herein designated VGAM RNA, also designated SEQ ID:4763.

[71871] Another function of VGAM2052 is therefore inhibition of LOC92299 (Accession XM_044075). Accordingly, utilities of VGAM2052 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92299. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2053 (VGAM2053) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71872] VGAM2053 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2053 was detected is described hereinabove with reference to Figs. 1-8.

[71873] VGAM2053 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ovine Adenovirus A. VGAM2053 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71874] VGAM2053 gene encodes a VGAM2053 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2053 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2053 precursor RNA is designated SEQ ID:2039, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2039 is located at position 25948 relative to the genome of Ovine Adenovirus A.

[71875] VGAM2053 precursor RNA folds onto itself, forming

VGAM2053 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71876] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2053 folded precursor RNA into VGAM2053 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2053 RNA is designated SEQ ID:4764, and is provided hereinbelow with reference to the sequence listing part.

[71877] VGAM2053 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2053 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2053 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71878] VGAM2053 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2053 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2053 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2053 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2053 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71879] The complementary binding of VGAM2053 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2053 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2053 host target RNA into VGAM2053 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71880] It is appreciated that VGAM2053 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2053 host target genes. The mRNA of each one of this plurality of VGAM2053 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2053 RNA, herein designated VGAM RNA, and which when bound by VGAM2053 RNA causes inhibition of translation of respective one or more VGAM2053 host target proteins.

[71881] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2053 gene, herein designated VGAM GENE, on one or more VGAM2053 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71882] It is yet further appreciated that a function of VGAM2053 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2053 include diagnosis, prevention and treatment of viral infection by Ovine Adenovirus A. Specific functions, and accordingly utilities, of VGAM2053 correlate with, and may be deduced from, the identity of the host target genes which VGAM2053 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[71883] Nucleotide sequences of the VGAM2053 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2053 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2053 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2053 are further described hereinbelow with reference to Table 1.

[71884] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2053 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2053 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71885] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2053 gene, herein designated VGAM is inhibition of expression of VGAM2053 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2053 correlate with, and may be deduced from, the identity of the target genes which VGAM2053 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[71886] Fatty Acid Binding Protein 2, Intestinal (FABP2, Accession NM_000134) is a VGAM2053 host target gene. FABP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FABP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FABP2 BINDING SITE, designated SEQ ID:5620, to the nucleotide sequence of VGAM2053 RNA, herein designated VGAM RNA, also designated SEQ ID:4764.

[71887] A function of VGAM2053 is therefore inhibition of Fatty Acid Binding Protein 2, Intestinal (FABP2, Accession NM_000134), a gene which may have a role in dietary fat uptake or processing. Accordingly, utilities of VGAM2053 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FABP2. The function of FABP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM951.High-mobility Group Box 3 (HMGB3, Accession NM_005342) is another VGAM2053 host target gene. HMGB3 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by HMGB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMGB3 BINDING SITE, designated SEQ ID:11818, to the nucleotide sequence of VGAM2053 RNA, herein designated VGAM RNA, also designated SEQ ID:4764.

[71888] Another function of VGAM2053 is therefore inhibition of High-mobility Group Box 3 (HMGB3, Accession NM_005342), a gene which plays a fundamental role in DNA replication, nucleosome assembly, and transcription. Accordingly, utilities of VGAM2053 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMGB3. The function of HMGB3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1272.HN1L (Accession NM_144570) is another VGAM2053 host target gene. HN1L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HN1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Ta-

ble 2 illustrates the complementarity of the nucleotide sequences of HN1L BINDING SITE, designated SEQ ID:29378, to the nucleotide sequence of VGAM2053 RNA, herein designated VGAM RNA, also designated SEQ ID:4764.

[71889] Another function of VGAM2053 is therefore inhibition of HN1L (Accession NM_144570). Accordingly, utilities of VGAM2053 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HN1L. poly(A) Polymerase Gamma (PAPOLG, Accession NM_022894) is another VGAM2053 host target gene. PAPOLG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAPOLG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAPOLG BINDING SITE, designated SEQ ID:23153, to the nucleotide sequence of VGAM2053 RNA, herein designated VGAM RNA, also designated SEQ ID:4764.

[71890] Another function of VGAM2053 is therefore inhibition of poly(A) Polymerase Gamma (PAPOLG, Accession NM_022894). Accordingly, utilities of VGAM2053 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PAPOLG. LOC145790 (Accession XM_085234) is another VGAM2053 host target gene. LOC145790 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145790, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145790 BINDING SITE, designated SEQ ID:37977, to the nucleotide sequence of VGAM2053 RNA, herein designated VGAM RNA, also designated SEQ ID:4764.

[71891] Another function of VGAM2053 is therefore inhibition of LOC145790 (Accession XM_085234). Accordingly, utilities of VGAM2053 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145790. LOC219654 (Accession XM_166095) is another VGAM2053 host target gene. LOC219654 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219654, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219654 BINDING SITE, designated SEQ ID:43876, to

the nucleotide sequence of VGAM2053 RNA, herein designated VGAM RNA, also designated SEQ ID:4764.

[71892] Another function of VGAM2053 is therefore inhibition of LOC219654 (Accession XM_166095). Accordingly, utilities of VGAM2053 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219654. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2054 (VGAM2054) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71893] VGAM2054 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2054 was detected is described hereinabove with reference to Figs. 1-8.

[71894] VGAM2054 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2054 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71895] VGAM2054 gene encodes a VGAM2054 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2054 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2054 precursor RNA is designated SEQ ID:2040, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2040 is located at position 2713 relative to the genome of Ectromelia Virus.

[71896] VGAM2054 precursor RNA folds onto itself, forming VGAM2054 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71897] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2054 folded precursor RNA into VGAM2054 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2054 RNA is designated SEQ ID:4765, and is provided hereinbelow with reference to the sequence listing part.

[71898] VGAM2054 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2054 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2054 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71899] VGAM2054 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2054 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2054 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2054 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2054 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71900] The complementary binding of VGAM2054 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2054 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2054 host target RNA into VGAM2054 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71901] It is appreciated that VGAM2054 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2054 host target genes. The mRNA of each one of this plurality of VGAM2054 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2054 RNA, herein designated VGAM RNA, and which when bound by VGAM2054 RNA causes inhibition of translation of respective one or more VGAM2054 host target proteins.

[71902] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2054 gene, herein designated VGAM GENE, on one or more VGAM2054 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71903] It is yet further appreciated that a function of VGAM2054 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2054 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2054 correlate with, and may be deduced from, the identity of the host target genes which VGAM2054 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71904] Nucleotide sequences of the VGAM2054 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2054 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2054 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2054 are further described hereinbelow with reference to Table 1.

[71905] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2054 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2054 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71906] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2054 gene, herein designated VGAM is inhibition of expression of VGAM2054 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2054 correlate with, and may be deduced from, the identity of the target genes which VGAM2054 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71907] Cyclin-dependent Kinase Inhibitor 2C (p18, inhibits CDK4) (CDKN2C, Accession NM_001262) is a VGAM2054 host target gene. CDKN2C BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CDKN2C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDKN2C BINDING SITE, designated SEQ ID:6927, to the nucleotide sequence of VGAM2054 RNA, herein designated VGAM RNA, also designated SEQ ID:4765.

[71908] A function of VGAM2054 is therefore inhibition of Cyclin-

dependent Kinase Inhibitor 2C (p18, inhibits CDK4) (CDKN2C, Accession NM_001262), a gene which associate with cyclin-CDK complexes or CDKs alone and inhibit their activity. Accordingly, utilities of VGAM2054 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKN2C. The function of CDKN2C has been established by previous studies. Cyclin-dependent kinase inhibitors (CKIs) are a group of low molecular weight proteins that associate with cyclin-CDK complexes or CDKs alone and inhibit their activity. Members of the INK4 family of CKIs specifically bind and inhibit CDK4 (OMIM Ref. No. 123829) and CDK6 (OMIM Ref. No. 603368), thereby preventing cyclin D-dependent phosphorylation of RB1 (OMIM Ref. No. 180200). See INK4D (OMIM Ref. No. 600927). By using a yeast 2-hybrid screen to search for CDK6-interacting proteins, Guan et al. (1994) isolated a partial cDNA encoding a protein that they designated p18 based on its molecular mass of 18 kD. They used the partial cDNA to screen a HeLa cell library and recovered additional cDNAs corresponding to the entire p18 coding region. Sequence analysis revealed that the predicted 168-amino acid p18 protein shares 38% and 42% sequence identity with p16/INK4A (OMIM Ref.

No. 600160) and p14/INK4B (OMIM Ref. No. 600431), respectively. Like p14 and p16, p18 contains an ankyrin repeat domain. Both in vivo and in vitro, p18 interacted strongly with CDK6 and weakly with CDK4, but not with the other CDKs tested. Recombinant p18 inhibited the kinase activity of cyclin D-CDK6 in vitro. Ectopic expression of either p16 or p18 suppressed the growth of human cells in a manner that appears to correlate with the presence of a wildtype RB1 function. Using Northern blot analysis, Guan et al. (1994) found that p18 is expressed as multiple transcripts in various human tissues, with the strongest expression in skeletal muscle. Blais et al. (1998) determined that the p18, or INK4C, gene contains 3 exons and spans more than 7.5 kb. Lapointe et al. (1996) identified a single amino acid substitution (ala72 to pro; A72P) in BT-20 human breast cancer cells that abrogated the ability of p18 to interact with CDK6 and to suppress cell growth. These authors suggested that p18 inactivation by point mutations may contribute to deregulated growth control in certain cell lines and/or tumors. Blais et al. (1998) found this p18 variant in 3 of 35 breast tumors examined, and suggested that it may be a polymorphism.

[71909] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[71910] Blais, A.; Labrie, Y.; Pouliot, F.; Lachance, Y.; Labrie, C. : Structure of the gene encoding the human cyclin-dependent kinase inhibitor p18 and mutational analysis in breast cancer. Biochem. Biophys. Res. Commun. 247: 146-153, 1998. ; and

[71911] Lapointe, J.; Lachance, Y.; Labrie, Y.; Labrie, C. : A p18 mutant defective in CDK6 binding in human breast cancer cells. Cancer Res. 56: 4586-4589, 1996.

[71912] Further studies establishing the function and utilities of CDKN2C are found in John Hopkins OMIM database record ID 603369, and in sited publications numbered 851 and 8511 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.DKFZp761N0624 (Accession NM_032295) is another VGAM2054 host target gene. DKFZp761N0624 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761N0624, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761N0624 BINDING SITE, designated

SEQ ID:26071, to the nucleotide sequence of VGAM2054 RNA, herein designated VGAM RNA, also designated SEQ ID:4765.

[71913] Another function of VGAM2054 is therefore inhibition of DKFZp761N0624 (Accession NM_032295). Accordingly, utilities of VGAM2054 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761N0624. Nuclear Receptor Subfamily 4, Group A, Member 3 (NR4A3, Accession NM_006981) is another VGAM2054 host target gene. NR4A3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NR4A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR4A3 BINDING SITE, designated SEQ ID:13843, to the nucleotide sequence of VGAM2054 RNA, herein designated VGAM RNA, also designated SEQ ID:4765.

[71914] Another function of VGAM2054 is therefore inhibition of Nuclear Receptor Subfamily 4, Group A, Member 3 (NR4A3, Accession NM_006981). Accordingly, utilities of VGAM2054 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR4A3.

LOC149073 (Accession XM_097577) is another VGAM2054 host target gene. LOC149073 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149073, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149073 BINDING SITE, designated SEQ ID:40943, to the nucleotide sequence of VGAM2054 RNA, herein designated VGAM RNA, also designated SEQ ID:4765.

[71915] Another function of VGAM2054 is therefore inhibition of LOC149073 (Accession XM_097577). Accordingly, utilities of VGAM2054 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149073. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2055 (VGAM2055) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71916] VGAM2055 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2055 was detected is described hereinabove with reference to Figs. 1-8.

[71917] VGAM2055 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Peanut Bud Necrosis Virus. VGAM2055 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71918] VGAM2055 gene encodes a VGAM2055 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2055 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2055 precursor RNA is designated SEQ ID:2041, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2041 is located at position 6690 relative to the genome of Peanut Bud Necrosis Virus.

[71919] VGAM2055 precursor RNA folds onto itself, forming VGAM2055 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71920] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2055 folded precursor RNA into VGAM2055 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2055 RNA is designated SEQ ID:4766, and is provided hereinbelow with reference to the sequence listing part.

[71921] VGAM2055 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2055 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2055 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71922] VGAM2055 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2055 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2055 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2055 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2055 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71923] The complementary binding of VGAM2055 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2055 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2055 host target RNA into VGAM2055 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71924] It is appreciated that VGAM2055 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2055 host target genes. The mRNA of each one of this plurality of VGAM2055 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2055 RNA, herein designated VGAM RNA, and which when bound by VGAM2055 RNA causes inhibition of translation of respective one or more VGAM2055 host target proteins.

[71925] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2055 gene, herein designated VGAM GENE, on one or more VGAM2055 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71926] It is yet further appreciated that a function of VGAM2055 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of viral infection by Peanut Bud Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2055 correlate with, and may be deduced from, the identity of the host target genes which VGAM2055 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71927] Nucleotide sequences of the VGAM2055 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2055 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2055 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2055 are further described hereinbelow with reference to Table 1.

[71928] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2055 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2055 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71929] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2055 gene, herein designated VGAM is inhibition of expression of VGAM2055 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2055 correlate with, and may be deduced from, the identity of the target genes which VGAM2055 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71930] BIG1 (Accession NM_006421) is a VGAM2055 host target gene. BIG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BIG1, corresponding to a HOST TARGET binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIG1 BINDING SITE, designated SEQ ID:13140, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71931] A function of VGAM2055 is therefore inhibition of BIG1 (Accession NM_006421), a gene which is a guanine nucleotide-exchange protein, has a role in vesicular transport. Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIG1. The function of BIG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1190.Fukuyama Type Congenital Muscular Dystrophy (fukutin) (FCMD, Accession NM_006731) is another VGAM2055 host target gene. FCMD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FCMD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FCMD BINDING SITE, designated SEQ ID:13578, to the nucleotide sequence of VGAM2055 RNA, herein

designated VGAM RNA, also designated SEQ ID:4766.

[71932] Another function of VGAM2055 is therefore inhibition of Fukuyama Type Congenital Muscular Dystrophy (fukutin) (FCMD, Accession NM_006731). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCMD. FtsJ Homolog 2 (E. coli) (FTSJ2, Accession NM_013393) is another VGAM2055 host target gene. FTSJ2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FTSJ2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FTSJ2 BINDING SITE, designated SEQ ID:15045, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71933] Another function of VGAM2055 is therefore inhibition of FtsJ Homolog 2 (E. coli) (FTSJ2, Accession NM_013393). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FTSJ2. Prostatic Binding Protein (PBP, Accession NM_002567) is another VGAM2055 host target gene. PBP BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by PBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PBP BINDING SITE, designated SEQ ID:8417, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71934] Another function of VGAM2055 is therefore inhibition of Prostatic Binding Protein (PBP, Accession NM_002567), a gene which regulates the activity of the Raf/MEK/ERK module. Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PBP. The function of PBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1332.Serine/threonine Kinase 10 (STK10, Accession NM_005990) is another VGAM2055 host target gene. STK10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STK10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of STK10 BINDING SITE, designated SEQ ID:12615, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71935] Another function of VGAM2055 is therefore inhibition of Serine/threonine Kinase 10 (STK10, Accession NM_005990), a gene which can act on substrates such as myelin basic protein and histone iia on serine and threonine residues. Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK10. The function of STK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Rho GTPase Activating Protein 5 (ARHGAP5, Accession XM_085082) is another VGAM2055 host target gene. ARHGAP5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARHGAP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGAP5 BINDING SITE, designated SEQ ID:37824, to the nucleotide sequence of VGAM2055

RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71936] Another function of VGAM2055 is therefore inhibition of Rho GTPase Activating Protein 5 (ARHGAP5, Accession XM_085082). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP5. Chromosome 1 Open Reading Frame 22 (C1orf22, Accession NM_025191) is another VGAM2055 host target gene. C1orf22 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf22, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf22 BINDING SITE, designated SEQ ID:24842, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71937] Another function of VGAM2055 is therefore inhibition of Chromosome 1 Open Reading Frame 22 (C1orf22, Accession NM_025191). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf22. Chromobox Homolog 6 (CBX6, Accession NM_014292) is another

VGAM2055 host target gene. CBX6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CBX6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBX6 BINDING SITE, designated SEQ ID:15580, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71938] Another function of VGAM2055 is therefore inhibition of Chromobox Homolog 6 (CBX6, Accession NM_014292). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBX6. DKFZP434A043 (Accession NM_015396) is another VGAM2055 host target gene. DKFZP434A043 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434A043, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434A043 BINDING SITE, designated SEQ ID:17704, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4766.

[71939] Another function of VGAM2055 is therefore inhibition of DKFZP434A043 (Accession NM_015396). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434A043. DKFZP434C212 (Accession XM_044196) is another VGAM2055 host target gene. DKFZP434C212 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434C212, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434C212 BINDING SITE, designated SEQ ID:34172, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71940] Another function of VGAM2055 is therefore inhibition of DKFZP434C212 (Accession XM_044196). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434C212. DKFZP434J037 (Accession NM_030952) is another VGAM2055 host target gene. DKFZP434J037 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by DKFZP434J037, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434J037 BINDING SITE, designated SEQ ID:25221, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71941] Another function of VGAM2055 is therefore inhibition of DKFZP434J037 (Accession NM_030952). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434J037. FLJ23129 (Accession NM_024763) is another VGAM2055 host target gene. FLJ23129 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23129, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23129 BINDING SITE, designated SEQ ID:24122, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71942] Another function of VGAM2055 is therefore inhibition of

FLJ23129 (Accession NM_024763). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23129. HEMK (Accession NM_016173) is another VGAM2055 host target gene. HEMK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HEMK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HEMK BINDING SITE, designated SEQ ID:18275, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71943] Another function of VGAM2055 is therefore inhibition of HEMK (Accession NM_016173). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEMK. KIAA0781 (Accession XM_041314) is another VGAM2055 host target gene. KIAA0781 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0781, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of KIAA0781 BINDING SITE, designated SEQ ID:33500, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71944] Another function of VGAM2055 is therefore inhibition of KIAA0781 (Accession XM_041314). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0781. KIAA1034 (Accession XM_031223) is another VGAM2055 host target gene. KIAA1034 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1034 BINDING SITE, designated SEQ ID:31313, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71945] Another function of VGAM2055 is therefore inhibition of KIAA1034 (Accession XM_031223). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1034. KIAA1508 (Accession XM_030209) is another

VGAM2055 host target gene. KIAA1508 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1508, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1508 BINDING SITE, designated SEQ ID:30997, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71946] Another function of VGAM2055 is therefore inhibition of KIAA1508 (Accession XM_030209). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1508. KIAA1804 (Accession XM_045864) is another VGAM2055 host target gene. KIAA1804 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1804, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1804 BINDING SITE, designated SEQ ID:34589, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71947] Another function of VGAM2055 is therefore inhibition of KIAA1804 (Accession XM_045864). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1804. Ornithine Decarboxylase Antizyme 3 (OAZ3, Accession NM_016178) is another VGAM2055 host target gene. OAZ3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by OAZ3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OAZ3 BINDING SITE, designated SEQ ID:18281, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71948] Another function of VGAM2055 is therefore inhibition of Ornithine Decarboxylase Antizyme 3 (OAZ3, Accession NM_016178). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OAZ3. PI4KII (Accession NM_018425) is another VGAM2055 host target gene. PI4KII BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PI4KII, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PI4KII BINDING SITE, designated SEQ ID:20485, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71949] Another function of VGAM2055 is therefore inhibition of PI4KII (Accession NM_018425). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PI4KII. Rho-related BTB Domain Containing 1 (RHOBTB1, Accession XM_166144) is another VGAM2055 host target gene. RHOBTB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RHOBTB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RHOBTB1 BINDING SITE, designated SEQ ID:43953, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71950] Another function of VGAM2055 is therefore inhibition of Rho-related BTB Domain Containing 1 (RHOBTB1, Accession XM_166144). Accordingly, utilities of VGAM2055 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with RHOBTB1. VEZATIN (Accession NM_017599) is another VGAM2055 host target gene. VEZATIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VEZATIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VEZATIN BINDING SITE, designated SEQ ID:19071, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71951] Another function of VGAM2055 is therefore inhibition of VEZATIN (Accession NM_017599). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VEZATIN. ZFP106 (Accession NM_022473) is another VGAM2055 host target gene. ZFP106 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZFP106, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZFP106 BIND-

ING SITE, designated SEQ ID:22836, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71952] Another function of VGAM2055 is therefore inhibition of ZFP106 (Accession NM_022473). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP106. Zinc Finger Protein 363 (ZNF363, Accession XM_055989) is another VGAM2055 host target gene. ZNF363 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF363, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF363 BINDING SITE, designated SEQ ID:36357, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71953] Another function of VGAM2055 is therefore inhibition of Zinc Finger Protein 363 (ZNF363, Accession XM_055989). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF363. LOC149821 (Accession

XM_097751) is another VGAM2055 host target gene. LOC149821 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149821, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149821 BINDING SITE, designated SEQ ID:41110, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71954] Another function of VGAM2055 is therefore inhibition of LOC149821 (Accession XM_097751). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149821. LOC150271 (Accession XM_097859) is another VGAM2055 host target gene. LOC150271 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150271 BINDING SITE, designated SEQ ID:41176, to the nucleotide sequence of VGAM2055 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4766.

[71955] Another function of VGAM2055 is therefore inhibition of LOC150271 (Accession XM_097859). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150271. LOC150445 (Accession XM_086916) is another VGAM2055 host target gene. LOC150445 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150445 BINDING SITE, designated SEQ ID:38972, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71956] Another function of VGAM2055 is therefore inhibition of LOC150445 (Accession XM_086916). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150445. LOC90736 (Accession XM_033811) is another VGAM2055 host target gene. LOC90736 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90736, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90736 BINDING SITE, designated SEQ ID:31958, to the nucleotide sequence of VGAM2055 RNA, herein designated VGAM RNA, also designated SEQ ID:4766.

[71957] Another function of VGAM2055 is therefore inhibition of LOC90736 (Accession XM_033811). Accordingly, utilities of VGAM2055 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90736. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2056 (VGAM2056) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71958] VGAM2056 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2056 was detected is described hereinabove with reference to Figs. 1-8.

[71959] VGAM2056 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Peanut Bud Necrosis

Virus. VGAM2056 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71960] VGAM2056 gene encodes a VGAM2056 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2056 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2056 precursor RNA is designated SEQ ID:2042, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2042 is located at position 5281 relative to the genome of Peanut Bud Necrosis Virus.

[71961] VGAM2056 precursor RNA folds onto itself, forming VGAM2056 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71962] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2056 folded precursor RNA into VGAM2056 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2056 RNA is designated SEQ ID:4767, and is provided hereinbelow with reference to the sequence listing part.

[71963] VGAM2056 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2056 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2056 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71964] VGAM2056 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2056 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2056 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2056 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2056 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71965] The complementary binding of VGAM2056 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2056 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2056 host target RNA into VGAM2056 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71966] It is appreciated that VGAM2056 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2056 host target genes. The mRNA of each one of this plurality of VGAM2056 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2056 RNA, herein designated VGAM RNA, and which when bound by VGAM2056 RNA causes inhibition of translation of respective one or more VGAM2056 host target proteins.

[71967] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2056 gene, herein designated VGAM GENE, on one or more VGAM2056 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71968] It is yet further appreciated that a function of VGAM2056 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2056 include diagnosis, prevention and treatment of viral infection by Peanut Bud Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2056 correlate with, and may be deduced from, the identity of the host target genes which VGAM2056 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71969] Nucleotide sequences of the VGAM2056 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2056 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2056 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2056 are further described hereinbelow with reference to Table 1.

[71970] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2056 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2056 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71971] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2056 gene, herein designated VGAM is inhibition of expression of VGAM2056 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2056 correlate with, and may be deduced from, the identity of the target genes which VGAM2056 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71972] Amyotrophic Lateral Sclerosis 2 (juvenile) (ALS2, Accession NM_020919) is a VGAM2056 host target gene. ALS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALS2 BINDING SITE, designated SEQ ID:21930, to the nu-

cleotide sequence of VGAM2056 RNA, herein designated VGAM RNA, also designated SEQ ID:4767.

[71973] A function of VGAM2056 is therefore inhibition of Amyotrophic Lateral Sclerosis 2 (juvenile) (ALS2, Accession NM_020919). Accordingly, utilities of VGAM2056 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALS2. UDP-Gal:betaGlcNAc Beta 1,3-galactosyltransferase, Polypeptide 2 (B3GALT2, Accession NM_003783) is another VGAM2056 host target gene. B3GALT2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by B3GALT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B3GALT2 BINDING SITE, designated SEQ ID:9873, to the nucleotide sequence of VGAM2056 RNA, herein designated VGAM RNA, also designated SEQ ID:4767.

[71974] Another function of VGAM2056 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,3-galactosyltransferase, Polypeptide 2 (B3GALT2, Accession NM_003783). Accordingly, utilities of VGAM2056 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with B3GALT2. Nuclear RNA Export Factor 2 (NXF2, Accession NM_017809) is another VGAM2056 host target gene. NXF2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NXF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NXF2 BINDING SITE, designated SEQ ID:19456, to the nucleotide sequence of VGAM2056 RNA, herein designated VGAM RNA, also designated SEQ ID:4767.

[71975] Another function of VGAM2056 is therefore inhibition of Nuclear RNA Export Factor 2 (NXF2, Accession NM_017809), a gene which is involved in the export of mrna from the nucleus to the cytoplasm. Accordingly, utilities of VGAM2056 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXF2. The function of NXF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM595.DKFZP434C1715 (Accession XM_098421) is another VGAM2056 host target gene. DKFZP434C1715 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

DKFZP434C1715, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434C1715 BINDING SITE, designated SEQ ID:41678, to the nucleotide sequence of VGAM2056 RNA, herein designated VGAM RNA, also designated SEQ ID:4767.

[71976] Another function of VGAM2056 is therefore inhibition of DKFZP434C1715 (Accession XM_098421). Accordingly, utilities of VGAM2056 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434C1715. KIAA1831 (Accession XM_033366) is another VGAM2056 host target gene. KIAA1831 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1831, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1831 BINDING SITE, designated SEQ ID:31900, to the nucleotide sequence of VGAM2056 RNA, herein designated VGAM RNA, also designated SEQ ID:4767.

[71977] Another function of VGAM2056 is therefore inhibition of KIAA1831 (Accession XM_033366). Accordingly, utilities

of VGAM2056 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1831. MGC16824 (Accession NM_020314) is another VGAM2056 host target gene. MGC16824 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC16824, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16824 BINDING SITE, designated SEQ ID:21571, to the nucleotide sequence of VGAM2056 RNA, herein designated VGAM RNA, also designated SEQ ID:4767.

[71978] Another function of VGAM2056 is therefore inhibition of MGC16824 (Accession NM_020314). Accordingly, utilities of VGAM2056 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16824. MGC4562 (Accession NM_133375) is another VGAM2056 host target gene. MGC4562 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC4562, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4562

BINDING SITE, designated SEQ ID:28498, to the nucleotide sequence of VGAM2056 RNA, herein designated VGAM RNA, also designated SEQ ID:4767.

[71979] Another function of VGAM2056 is therefore inhibition of MGC4562 (Accession NM_133375). Accordingly, utilities of VGAM2056 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4562. RAB10, Member RAS Oncogene Family (RAB10, Accession XM_097979) is another VGAM2056 host target gene. RAB10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB10 BINDING SITE, designated SEQ ID:41284, to the nucleotide sequence of VGAM2056 RNA, herein designated VGAM RNA, also designated SEQ ID:4767.

[71980] Another function of VGAM2056 is therefore inhibition of RAB10, Member RAS Oncogene Family (RAB10, Accession XM_097979). Accordingly, utilities of VGAM2056 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB10. LOC221362

(Accession XM_168093) is another VGAM2056 host target gene. LOC221362 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221362, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221362 BINDING SITE, designated SEQ ID:45024, to the nucleotide sequence of VGAM2056 RNA, herein designated VGAM RNA, also designated SEQ ID:4767.

[71981] Another function of VGAM2056 is therefore inhibition of LOC221362 (Accession XM_168093). Accordingly, utilities of VGAM2056 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221362. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2057 (VGAM2057) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71982] VGAM2057 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2057 was detected is described hereinabove with reference to Figs. 1-8.

[71983] VGAM2057 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2057 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[71984] VGAM2057 gene encodes a VGAM2057 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2057 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2057 precursor RNA is designated SEQ ID:2043, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2043 is located at position 3968 relative to the genome of Ectromelia Virus.

[71985] VGAM2057 precursor RNA folds onto itself, forming VGAM2057 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[71986] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2057 folded precursor RNA into VGAM2057 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide sequence of VGAM2057 RNA is designated SEQ ID:4768, and is provided hereinbelow with reference to the sequence listing part.

[71987] VGAM2057 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2057 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2057 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[71988] VGAM2057 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2057 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2057 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2057 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2057 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[71989] The complementary binding of VGAM2057 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2057 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2057 host target RNA into VGAM2057 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[71990] It is appreciated that VGAM2057 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2057 host target genes. The mRNA of each one of this plurality of VGAM2057 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2057 RNA, herein designated VGAM RNA, and which when bound by VGAM2057 RNA causes inhibition of translation of respective one or more VGAM2057 host target proteins.

[71991] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2057 gene, herein designated VGAM GENE, on one or more VGAM2057 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[71992] It is yet further appreciated that a function of VGAM2057 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2057 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2057 correlate with, and may be deduced from, the identity of the host target genes which VGAM2057 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[71993] Nucleotide sequences of the VGAM2057 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2057 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2057 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2057 are further described hereinbelow with reference to Table 1.

[71994] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2057 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2057 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[71995] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2057 gene, herein designated VGAM is inhibition of expression of VGAM2057 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2057 correlate with, and may be deduced from, the identity of the target genes which VGAM2057 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[71996] FYVE and Coiled-coil Domain Containing 1 (FYCO1, Accession NM_024513) is a VGAM2057 host target gene. FYCO1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

FYCO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FYCO1 BINDING SITE, designated SEQ ID:23712, to the nucleotide sequence of VGAM2057 RNA, herein designated VGAM RNA, also designated SEQ ID:4768.

[71997] A function of VGAM2057 is therefore inhibition of FYVE and Coiled-coil Domain Containing 1 (FYCO1, Accession NM_024513). Accordingly, utilities of VGAM2057 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FYCO1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2058 (VGAM2058) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[71998] VGAM2058 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2058 was detected is described hereinabove with reference to Figs. 1-8.

[71999] VGAM2058 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Peanut Bud Necrosis Virus. VGAM2058 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72000] VGAM2058 gene encodes a VGAM2058 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2058 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2058 precursor RNA is designated SEQ ID:2044, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2044 is located at position 4967 relative to the genome of Peanut Bud Necrosis Virus.

[72001] VGAM2058 precursor RNA folds onto itself, forming VGAM2058 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72002] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2058 folded precursor RNA into VGAM2058 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2058 RNA is designated SEQ ID:4769, and is provided hereinbelow with reference to the sequence listing part.

[72003] VGAM2058 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2058 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2058 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72004] VGAM2058 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2058 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2058 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2058 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2058 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72005] The complementary binding of VGAM2058 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2058 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2058

host target RNA into VGAM2058 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72006] It is appreciated that VGAM2058 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2058 host target genes. The mRNA of each one of this plurality of VGAM2058 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2058 RNA, herein designated VGAM RNA, and which when bound by VGAM2058 RNA causes inhibition of translation of respective one or more VGAM2058 host target proteins.

[72007] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2058 gene, herein designated VGAM GENE, on one or more VGAM2058 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72008] It is yet further appreciated that a function of VGAM2058 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of viral infection by Peanut Bud Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2058 correlate with, and may be deduced from, the identity of the host target genes which VGAM2058 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72009] Nucleotide sequences of the VGAM2058 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2058 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2058 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2058 are further

described hereinbelow with reference to Table 1.

[72010] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2058 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2058 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72011] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2058 gene, herein designated VGAM is inhibition of expression of VGAM2058 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2058 correlate with, and may be deduced from, the identity of the target genes which VGAM2058 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72012] Adenosine Deaminase, RNA-specific (ADAR, Accession NM_001111) is a VGAM2058 host target gene. ADAR BINDING SITE1 through ADAR BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ADAR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of ADAR BINDING SITE1 through ADAR BINDING SITE3, designated SEQ ID:6770, SEQ ID:17956 and SEQ ID:17963 respectively, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72013] A function of VGAM2058 is therefore inhibition of Adenosine Deaminase, RNA-specific (ADAR, Accession NM_001111), a gene which converts adenosine to inosine in double-stranded RNA. Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAR. The function of ADAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM323.Collagen, Type IV, Alpha 3 (Goodpasture antigen) (COL4A3, Accession NM_031363) is another VGAM2058 host target gene. COL4A3 BINDING SITE1 through COL4A3 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by COL4A3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL4A3 BINDING SITE1 through COL4A3

BINDING SITE3, designated SEQ ID:25353, SEQ ID:5546 and SEQ ID:35916 respectively, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72014] Another function of VGAM2058 is therefore inhibition of Collagen, Type IV, Alpha 3 (Goodpasture antigen) (COL4A3, Accession NM_031363). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A3. Nuclear Receptor Subfamily 1, Group I, Member 2 (NR1I2, Accession NM_022002) is another VGAM2058 host target gene. NR1I2 BINDING SITE1 and NR1I2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NR1I2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR1I2 BINDING SITE1 and NR1I2 BINDING SITE2, designated SEQ ID:22545 and SEQ ID:9972 respectively, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72015] Another function of VGAM2058 is therefore inhibition of Nuclear Receptor Subfamily 1, Group I, Member 2 (NR1I2,

Accession NM_022002), a gene which binds to a response element in the cyp3a4 gene promoter and activates its expression in response to a wide variety of endobiotics and xenobiotics. Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR1I2. The function of NR1I2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM336.Solute Carrier Family 9 (sodium/hydrogen exchanger), Isoform 6 (SLC9A6, Accession NM_006359) is another VGAM2058 host target gene. SLC9A6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC9A6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC9A6 BINDING SITE, designated SEQ ID:13053, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72016] Another function of VGAM2058 is therefore inhibition of Solute Carrier Family 9 (sodium/hydrogen exchanger), Isoform 6 (SLC9A6, Accession NM_006359), a gene which

is involved electroneutral exchange of protons for na+ and k+ across the mitochondrial inner membrane. Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC9A6. The function of SLC9A6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM493.Tumor Necrosis Factor (ligand) Superfamily, Member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF4, Accession NM_003326) is another VGAM2058 host target gene. TNFSF4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFSF4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFSF4 BINDING SITE, designated SEQ ID:9334, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72017] Another function of VGAM2058 is therefore inhibition of Tumor Necrosis Factor (ligand) Superfamily, Member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa)

(TNFSF4, Accession NM_003326), a gene which co-stimulates t cell proliferation and cytokine production. Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFSF4. The function of TNFSF4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM463.Agmatine Ureohydrolase (agmatinase) (AGMAT, Accession NM_024758) is another VGAM2058 host target gene. AGMAT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AGMAT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AGMAT BINDING SITE, designated SEQ ID:24105, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72018] Another function of VGAM2058 is therefore inhibition of Agmatine Ureohydrolase (agmatinase) (AGMAT, Accession NM_024758). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with AGMAT. ATPase, H+ Transporting, Lysosomal V0 Subunit A Isoform 1 (ATP6V0A1, Accession NM_005177) is another VGAM2058 host target gene. ATP6V0A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP6V0A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP6V0A1 BINDING SITE, designated SEQ ID:11675, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72019] Another function of VGAM2058 is therefore inhibition of ATPase, H+ Transporting, Lysosomal V0 Subunit A Isoform 1 (ATP6V0A1, Accession NM_005177). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V0A1. Cat Eye Syndrome Chromosome Region, Candidate 6 (CECR6, Accession NM_031890) is another VGAM2058 host target gene. CECR6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CECR6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CECR6 BINDING SITE, designated SEQ ID:25638, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72020] Another function of VGAM2058 is therefore inhibition of Cat Eye Syndrome Chromosome Region, Candidate 6 (CECR6, Accession NM_031890). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR6. Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_013989) is another VGAM2058 host target gene. DIO2 BINDING SITE1 and DIO2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DIO2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DIO2 BINDING SITE1 and DIO2 BINDING SITE2, designated SEQ ID:15166 and SEQ ID:6456 respectively, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72021] Another function of VGAM2058 is therefore inhibition of

Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_013989). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIO2. ERG-1 (Accession NM_022034) is another VGAM2058 host target gene. ERG-1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ERG-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERG-1 BINDING SITE, designated SEQ ID:22556, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72022] Another function of VGAM2058 is therefore inhibition of ERG-1 (Accession NM_022034). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERG-1. FLJ14437 (Accession NM_032578) is another VGAM2058 host target gene. FLJ14437 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ14437, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14437 BINDING SITE, designated SEQ ID:26307, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72023] Another function of VGAM2058 is therefore inhibition of FLJ14437 (Accession NM_032578). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14437. HCAP-G (Accession NM_022346) is another VGAM2058 host target gene. HCAP-G BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HCAP-G, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCAP-G BINDING SITE, designated SEQ ID:22746, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72024] Another function of VGAM2058 is therefore inhibition of HCAP-G (Accession NM_022346). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCAP-

G. KIAA0205 (Accession NM_014873) is another VGAM2058 host target gene. KIAA0205 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0205, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0205 BINDING SITE, designated SEQ ID:17003, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72025] Another function of VGAM2058 is therefore inhibition of KIAA0205 (Accession NM_014873). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0205. MGC4737 (Accession NM_031466) is another VGAM2058 host target gene. MGC4737 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4737, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4737 BINDING SITE, designated SEQ ID:25504, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM

RNA, also designated SEQ ID:4769.

[72026] Another function of VGAM2058 is therefore inhibition of MGC4737 (Accession NM_031466). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4737. START Domain Containing 7 (STARD7, Accession NM_139267) is another VGAM2058 host target gene. STARD7 BINDING SITE1 and STARD7 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by STARD7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STARD7 BINDING SITE1 and STARD7 BINDING SITE2, designated SEQ ID:29263 and SEQ ID:21361 respectively, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72027] Another function of VGAM2058 is therefore inhibition of START Domain Containing 7 (STARD7, Accession NM_139267). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STARD7. LOC131368 (Accession XM_067347) is another VGAM2058 host target

gene. LOC131368 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC131368, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC131368 BINDING SITE, designated SEQ ID:37354, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72028] Another function of VGAM2058 is therefore inhibition of LOC131368 (Accession XM_067347). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC131368. LOC148930 (Accession XM_086369) is another VGAM2058 host target gene. LOC148930 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148930, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148930 BINDING SITE, designated SEQ ID:38617, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72029] Another function of VGAM2058 is therefore inhibition of LOC148930 (Accession XM_086369). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148930. LOC149506 (Accession XM_097661) is another VGAM2058 host target gene. LOC149506 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149506, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149506 BINDING SITE, designated SEQ ID:41001, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72030] Another function of VGAM2058 is therefore inhibition of LOC149506 (Accession XM_097661). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149506. LOC158434 (Accession XM_098939) is another VGAM2058 host target gene. LOC158434 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158434, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158434 BINDING SITE, designated SEQ ID:41983, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72031] Another function of VGAM2058 is therefore inhibition of LOC158434 (Accession XM_098939). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158434. LOC196955 (Accession XM_085210) is another VGAM2058 host target gene. LOC196955 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196955 BINDING SITE, designated SEQ ID:37930, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72032] Another function of VGAM2058 is therefore inhibition of LOC196955 (Accession XM_085210). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC196955. LOC256789 (Accession XM_173369) is another VGAM2058 host target gene. LOC256789 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256789, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256789 BINDING SITE, designated SEQ ID:46538, to the nucleotide sequence of VGAM2058 RNA, herein designated VGAM RNA, also designated SEQ ID:4769.

[72033] Another function of VGAM2058 is therefore inhibition of LOC256789 (Accession XM_173369). Accordingly, utilities of VGAM2058 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256789. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2059 (VGAM2059) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72034] VGAM2059 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2059 was detected is described hereinabove with reference to Figs. 1-8.

[72035] VGAM2059 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2059 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72036] VGAM2059 gene encodes a VGAM2059 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2059 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2059 precursor RNA is designated SEQ ID:2045, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2045 is located at position 15250 relative to the genome of Ectromelia Virus.

[72037] VGAM2059 precursor RNA folds onto itself, forming VGAM2059 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72038] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2059 folded precursor RNA into VGAM2059 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2059 RNA is designated SEQ ID:4770, and is provided hereinbelow with reference to the sequence listing part.

[72039] VGAM2059 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2059 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2059 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72040] VGAM2059 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2059 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2059 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2059 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2059 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72041] The complementary binding of VGAM2059 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2059 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2059 host target RNA into VGAM2059 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72042] It is appreciated that VGAM2059 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2059 host target genes. The mRNA of each one of this plurality of VGAM2059 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2059 RNA, herein designated VGAM RNA, and which when bound by VGAM2059 RNA causes inhibition of translation of respective one or more VGAM2059 host target proteins.

[72043] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2059 gene, herein designated VGAM GENE, on one or more VGAM2059 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72044] It is yet further appreciated that a function of VGAM2059 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2059 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2059 correlate with, and may be deduced from, the identity of the host target genes which VGAM2059 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72045] Nucleotide sequences of the VGAM2059 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2059 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2059 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2059 are further described hereinbelow with reference to Table 1.

[72046] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2059 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2059 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72047] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2059 gene, herein designated VGAM is inhibition of expression of VGAM2059 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2059 correlate with, and may be deduced from, the identity of the target genes which VGAM2059 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72048] Deleted In Azoospermia (DAZ, Accession NM_004081) is a VGAM2059 host target gene. DAZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DAZ, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAZ BINDING SITE, designated SEQ ID:10282, to the nucleotide sequence of VGAM2059 RNA, herein designated VGAM RNA, also designated SEQ ID:4770.

[72049] A function of VGAM2059 is therefore inhibition of Deleted In Azoospermia (DAZ, Accession NM_004081), a gene which may play a role in the germ-cell-specific patterns of RNA splicing and storage. Accordingly, utilities of VGAM2059 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAZ. The function of DAZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Deleted In Azoospermia-like (DAZL, Accession XM_042839) is another VGAM2059 host target gene. DAZL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DAZL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAZL BINDING SITE, designated SEQ ID:33801,

to the nucleotide sequence of VGAM2059 RNA, herein designated VGAM RNA, also designated SEQ ID:4770.

[72050] Another function of VGAM2059 is therefore inhibition of Deleted In Azoospermia-like (DAZL, Accession XM_042839), a gene which may be essential for gametogenesis. Accordingly, utilities of VGAM2059 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAZL. The function of DAZL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.FLJ20330 (Accession NM_018988) is another VGAM2059 host target gene. FLJ20330 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20330, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20330 BINDING SITE, designated SEQ ID:21060, to the nucleotide sequence of VGAM2059 RNA, herein designated VGAM RNA, also designated SEQ ID:4770.

[72051] Another function of VGAM2059 is therefore inhibition of FLJ20330 (Accession NM_018988). Accordingly, utilities of

VGAM2059 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20330. KIAA1908 (Accession XM_055834) is another VGAM2059 host target gene. KIAA1908 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1908, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1908 BINDING SITE, designated SEQ ID:36336, to the nucleotide sequence of VGAM2059 RNA, herein designated VGAM RNA, also designated SEQ ID:4770.

[72052] Another function of VGAM2059 is therefore inhibition of KIAA1908 (Accession XM_055834). Accordingly, utilities of VGAM2059 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1908. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2060 (VGAM2060) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72053] VGAM2060 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2060 was detected is described hereinabove with reference to Figs. 1-8.

[72054] VGAM2060 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2060 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72055] VGAM2060 gene encodes a VGAM2060 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2060 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2060 precursor RNA is designated SEQ ID:2046, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2046 is located at position 3202 relative to the genome of Ectromelia Virus.

[72056] VGAM2060 precursor RNA folds onto itself, forming VGAM2060 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72057] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2060 folded precursor RNA into VGAM2060 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2060 RNA is designated SEQ ID:4771, and is provided hereinbelow with reference to the sequence listing part.

[72058] VGAM2060 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2060 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2060 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[72059] VGAM2060 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2060 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2060 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2060 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2060 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72060] The complementary binding of VGAM2060 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2060 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2060 host target RNA into VGAM2060 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72061] It is appreciated that VGAM2060 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2060 host target genes. The mRNA of each one of this plurality of VGAM2060 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2060 RNA, herein designated VGAM RNA, and which when bound by VGAM2060 RNA causes inhibition of translation of respective one or more VGAM2060 host target proteins.

[72062] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2060 gene, herein designated VGAM GENE, on one or more VGAM2060 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72063] It is yet further appreciated that a function of VGAM2060 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2060 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2060 correlate with, and may be deduced from, the identity of the host target genes which VGAM2060 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72064] Nucleotide sequences of the VGAM2060 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2060 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2060 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2060 are further described hereinbelow with reference to Table 1.

[72065] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2060 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2060 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72066] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2060 gene, herein designated VGAM is inhibition of expression of VGAM2060 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2060 correlate with, and may be deduced from, the identity of the target genes which VGAM2060 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72067] Chromosome 1 Open Reading Frame 24 (C1orf24, Accession NM_052966) is a VGAM2060 host target gene.

C1orf24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:27531, to the nucleotide sequence of VGAM2060 RNA, herein designated VGAM RNA, also designated SEQ ID:4771.

[72068] A function of VGAM2060 is therefore inhibition of Chromosome 1 Open Reading Frame 24 (C1orf24, Accession NM_052966). Accordingly, utilities of VGAM2060 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24. FLJ12761 (Accession NM_024545) is another VGAM2060 host target gene. FLJ12761 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12761, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12761 BINDING SITE, designated SEQ ID:23757, to the nucleotide sequence of VGAM2060 RNA, herein designated VGAM RNA, also designated SEQ

ID:4771.

[72069] Another function of VGAM2060 is therefore inhibition of FLJ12761 (Accession NM_024545). Accordingly, utilities of VGAM2060 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12761. KIAA0574 (Accession XM_045076) is another VGAM2060 host target gene. KIAA0574 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0574, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0574 BINDING SITE, designated SEQ ID:34343, to the nucleotide sequence of VGAM2060 RNA, herein designated VGAM RNA, also designated SEQ ID:4771.

[72070] Another function of VGAM2060 is therefore inhibition of KIAA0574 (Accession XM_045076). Accordingly, utilities of VGAM2060 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0574. KIAA1766 (Accession XM_049218) is another VGAM2060 host target gene. KIAA1766 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1766, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1766 BINDING SITE, designated SEQ ID:35352, to the nucleotide sequence of VGAM2060 RNA, herein designated VGAM RNA, also designated SEQ ID:4771.

[72071] Another function of VGAM2060 is therefore inhibition of KIAA1766 (Accession XM_049218). Accordingly, utilities of VGAM2060 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1766. NIBAN (Accession NM_022083) is another VGAM2060 host target gene. NIBAN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NIBAN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NIBAN BINDING SITE, designated SEQ ID:22628, to the nucleotide sequence of VGAM2060 RNA, herein designated VGAM RNA, also designated SEQ ID:4771.

[72072] Another function of VGAM2060 is therefore inhibition of NIBAN (Accession NM_022083). Accordingly, utilities of VGAM2060 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with NIBAN. LOC90381 (Accession XM_031334) is another VGAM2060 host target gene. LOC90381 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90381, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90381 BINDING SITE, designated SEQ ID:31344, to the nucleotide sequence of VGAM2060 RNA, herein designated VGAM RNA, also designated SEQ ID:4771.

[72073] Another function of VGAM2060 is therefore inhibition of LOC90381 (Accession XM_031334). Accordingly, utilities of VGAM2060 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90381. LOC91960 (Accession XM_041872) is another VGAM2060 host target gene. LOC91960 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91960, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91960 BINDING SITE, designated SEQ ID:33609, to the

nucleotide sequence of VGAM2060 RNA, herein designated VGAM RNA, also designated SEQ ID:4771.

[72074] Another function of VGAM2060 is therefore inhibition of LOC91960 (Accession XM_041872). Accordingly, utilities of VGAM2060 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91960. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2061 (VGAM2061) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72075] VGAM2061 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2061 was detected is described hereinabove with reference to Figs. 1-8.

[72076] VGAM2061 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2061 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72077] VGAM2061 gene encodes a VGAM2061 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2061 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2061 precursor RNA is designated SEQ ID:2047, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2047 is located at position 132 relative to the genome of Ectromelia Virus.

[72078] VGAM2061 precursor RNA folds onto itself, forming VGAM2061 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72079] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2061 folded precursor RNA into VGAM2061 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2061 RNA is designated SEQ ID:4772, and is provided hereinbelow with reference to the sequence listing part.

[72080] VGAM2061 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2061 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2061 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72081] VGAM2061 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2061 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2061 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2061 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2061 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72082] The complementary binding of VGAM2061 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2061 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2061 host target RNA into VGAM2061 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72083] It is appreciated that VGAM2061 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2061 host target genes. The mRNA of each one of this plurality of VGAM2061 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2061 RNA, herein designated VGAM RNA, and which when bound by VGAM2061 RNA causes inhibition of translation of respective one or more VGAM2061 host target proteins.

[72084] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2061 gene, herein designated VGAM GENE, on one or more VGAM2061 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72085] It is yet further appreciated that a function of VGAM2061 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2061 correlate with, and may be deduced from, the identity of the host target genes which VGAM2061 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72086] Nucleotide sequences of the VGAM2061 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2061 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2061 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2061 are further described hereinbelow with reference to Table 1.

[72087] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2061 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2061 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72088] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2061 gene, herein designated VGAM is inhibition of expression of VGAM2061 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2061 correlate with, and may be deduced from, the identity of the target genes which VGAM2061 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72089] ATP-binding Cassette, Sub-family D (ALD), Member 2 (ABCD2, Accession NM_005164) is a VGAM2061 host target gene. ABCD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCD2 BINDING SITE, designated SEQ ID:11660, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72090] A function of VGAM2061 is therefore inhibition of ATP-

binding Cassette, Sub-family D (ALD), Member 2 (ABCD2, Accession NM_005164), a gene which probable transporter. Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCD2. The function of ABCD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM229.DNA2 DNA Replication Helicase 2-like (yeast) (DNA2L, Accession XM_166103) is another VGAM2061 host target gene. DNA2L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DNA2L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNA2L BINDING SITE, designated SEQ ID:43881, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72091] Another function of VGAM2061 is therefore inhibition of DNA2 DNA Replication Helicase 2-like (yeast) (DNA2L, Accession XM_166103), a gene which acts as a template for DNA polymerization during the process of DNA replica-

tion. Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNA2L. The function of DNA2L has been established by previous studies. While sequencing random cDNAs from the myeloid cell line KG-1, Nagase et al. (1995) found a partial sequence, KIAA0083, whose predicted polypeptide sequence had 41% identity to yeast Dna2 helicase. In yeast, Dna2 helicase is a DNA-dependent ATPase which unwinds duplex DNA to generate single-stranded DNA which then acts as a template for DNA polymerization during the process of DNA replication. Eki et al. (1996) used human-rodent PCR panels and fluorescence in situ hybridization to map the human DNA2L gene to human chromosome 10q21.3-q22.1.

[72092] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[72093] Eki, T; Okumura, K.; Shiratori, A.; Abe, M.; Nogami, M.; Taguchi, H.; Shibata, T.; Murakami, Y.; Hanaoka, F. : Assignment of the closest human homologue (DNA2L; KIAA0083) of the yeast Dna2 helicase gene to chromosome band 10q21.3-q22.1 Genomics 37: 408-410, 1996. ; and

[72094] Nagase, T; Miyajima, N; Tanaka, A.; Sazuka, T.; Seki, N.; Sato, S.; Tabata, S.; Ishikawa, K.; Kawarabayashi, Y.; Kotani, H.; Nomura, N. : Prediction of the coding sequences of unidentif.

[72095] Further studies establishing the function and utilities of DNA2L are found in John Hopkins OMIM database record ID 601810, and in sited publications numbered 6725-6726 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Ribosomal Protein L10 (RPL10, Accession NM_006013) is another VGAM2061 host target gene. RPL10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPL10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPL10 BINDING SITE, designated SEQ ID:12622, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72096] Another function of VGAM2061 is therefore inhibition of Ribosomal Protein L10 (RPL10, Accession NM_006013), a gene which may be a component of the 60S ribosomal

subunit. Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPL10. The function of RPL10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM476.DKFZP566M114 (Accession NM_032128) is another VGAM2061 host target gene. DKFZP566M114 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP566M114, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566M114 BINDING SITE, designated SEQ ID:25813, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72097] Another function of VGAM2061 is therefore inhibition of DKFZP566M114 (Accession NM_032128). Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566M114. FLJ20519 (Accession NM_017860) is another VGAM2061 host target gene. FLJ20519 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20519, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20519 BINDING SITE, designated SEQ ID:19539, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72098] Another function of VGAM2061 is therefore inhibition of FLJ20519 (Accession NM_017860). Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20519. FLJ21369 (Accession NM_024802) is another VGAM2061 host target gene. FLJ21369 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21369, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21369 BINDING SITE, designated SEQ ID:24182, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72099] Another function of VGAM2061 is therefore inhibition of

FLJ21369 (Accession NM_024802). Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21369. FLJ23462 (Accession NM_024843) is another VGAM2061 host target gene. FLJ23462 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23462, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23462 BINDING SITE, designated SEQ ID:24259, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72100] Another function of VGAM2061 is therefore inhibition of FLJ23462 (Accession NM_024843). Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23462. KIAA1237 (Accession XM_087386) is another VGAM2061 host target gene. KIAA1237 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1237, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1237 BINDING SITE, designated SEQ ID:39214, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72101] Another function of VGAM2061 is therefore inhibition of KIAA1237 (Accession XM_087386). Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1237. KIAA1554 (Accession XM_170834) is another VGAM2061 host target gene. KIAA1554 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1554, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1554 BINDING SITE, designated SEQ ID:45613, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72102] Another function of VGAM2061 is therefore inhibition of KIAA1554 (Accession XM_170834). Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1554. Ornithine Decarboxylase Antizyme Inhibitor

(OAZIN, Accession NM_015878) is another VGAM2061 host target gene. OAZIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OAZIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OAZIN BINDING SITE, designated SEQ ID:18022, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72103] Another function of VGAM2061 is therefore inhibition of Ornithine Decarboxylase Antizyme Inhibitor (OAZIN, Accession NM_015878). Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OAZIN. LOC147072 (Accession XM_017121) is another VGAM2061 host target gene. LOC147072 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147072, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147072 BINDING SITE, designated SEQ ID:30300, to the nucleotide sequence of

VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72104] Another function of VGAM2061 is therefore inhibition of LOC147072 (Accession XM_017121). Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147072. LOC147093 (Accession XM_097184) is another VGAM2061 host target gene. LOC147093 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147093, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147093 BINDING SITE, designated SEQ ID:40803, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72105] Another function of VGAM2061 is therefore inhibition of LOC147093 (Accession XM_097184). Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147093. LOC201626 (Accession XM_114349) is another VGAM2061 host target gene. LOC201626 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC201626, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201626 BINDING SITE, designated SEQ ID:42889, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72106] Another function of VGAM2061 is therefore inhibition of LOC201626 (Accession XM_114349). Accordingly, utilities of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201626. LOC93097 (Accession XM_049221) is another VGAM2061 host target gene. LOC93097 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93097, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93097 BINDING SITE, designated SEQ ID:35356, to the nucleotide sequence of VGAM2061 RNA, herein designated VGAM RNA, also designated SEQ ID:4772.

[72107] Another function of VGAM2061 is therefore inhibition of LOC93097 (Accession XM_049221). Accordingly, utilities

of VGAM2061 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93097. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2062 (VGAM2062) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72108] VGAM2062 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2062 was detected is described hereinabove with reference to Figs. 1-8.

[72109] VGAM2062 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Peanut Bud Necrosis Virus. VGAM2062 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72110] VGAM2062 gene encodes a VGAM2062 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2062 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2062 precursor RNA is designated SEQ ID:2048, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2048 is located at position 345 relative to the genome of Peanut Bud Necrosis Virus.

[72111] VGAM2062 precursor RNA folds onto itself, forming VGAM2062 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72112] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2062 folded precursor RNA into VGAM2062 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2062 RNA is designated SEQ ID:4773, and

is provided hereinbelow with reference to the sequence listing part.

[72113] VGAM2062 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2062 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2062 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72114] VGAM2062 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2062 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2062 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2062 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2062 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72115] The complementary binding of VGAM2062 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2062 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2062 host target RNA into VGAM2062 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72116] It is appreciated that VGAM2062 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2062 host target genes. The mRNA of each one of this plurality of VGAM2062 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2062 RNA, herein designated VGAM RNA, and which when bound by VGAM2062 RNA causes inhibition of translation of respective one or more VGAM2062 host target proteins.

[72117] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2062 gene, herein designated VGAM GENE, on one or more VGAM2062 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72118] It is yet further appreciated that a function of VGAM2062 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of viral infection by Peanut Bud Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2062 correlate with, and may be deduced from, the identity of the host target genes which VGAM2062 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72119] Nucleotide sequences of the VGAM2062 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2062 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2062 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2062 are further described hereinbelow with reference to Table 1.

[72120] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2062 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2062 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72121] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2062 gene, herein designated VGAM is inhibition of expression of VGAM2062 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2062 correlate with, and may be deduced from, the identity of the target genes which VGAM2062 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72122] Bassoon (presynaptic cytomatrix protein) (BSN, Accession NM_003458) is a VGAM2062 host target gene. BSN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BSN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BSN BINDING SITE, designated SEQ ID:9516, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72123] A function of VGAM2062 is therefore inhibition of Bassoon (presynaptic cytomatrix protein) (BSN, Accession NM_003458), a gene which may be involved in cytomatrix organization at the site of neurotransmitter release. Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with BSN. The function of BSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM638.DXS1283E (Accession XM_047871) is another VGAM2062 host target gene. DXS1283E BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DXS1283E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DXS1283E BINDING SITE, designated SEQ ID:35067, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72124] Another function of VGAM2062 is therefore inhibition of DXS1283E (Accession XM_047871). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DXS1283E. IL2-inducible T-cell Kinase (ITK, Accession NM_005546) is another VGAM2062 host target gene. ITK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITK, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITK BINDING SITE, designated SEQ ID:12078, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72125] Another function of VGAM2062 is therefore inhibition of IL2-inducible T-cell Kinase (ITK, Accession NM_005546), a gene which plays a role in t cell proliferation and differentiation. Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITK. The function of ITK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM288.Protocadherin 11 X-linked (PCDH11X, Accession NM_032969) is another VGAM2062 host target gene. PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDH11X, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2, designated SEQ ID:26805 and SEQ

ID:26790 respectively, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72126] Another function of VGAM2062 is therefore inhibition of Protocadherin 11 X-linked (PCDH11X, Accession NM_032969), a gene which is thought to play a fundamental role in cell-cell recognition essential for the segmental development and function of the central nervous system. Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11X. The function of PCDH11X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Replication Protein A1, 70kDa (RPA1, Accession NM_002945) is another VGAM2062 host target gene. RPA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPA1 BINDING SITE, designated SEQ ID:8855, to the nucleotide sequence of VGAM2062 RNA, herein

designated VGAM RNA, also designated SEQ ID:4773.

[72127] Another function of VGAM2062 is therefore inhibition of Replication Protein A1, 70kDa (RPA1, Accession NM_002945), a gene which is required for simian virus 40 dna replication in vitro. it participates in a very early step in initiation. rp-a is a single-stranded dna-binding protein. Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPA1. The function of RPA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM180.Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha-1 antiproteinase, antitrypsin), Member 5 (SERPINA5, Accession NM_000624) is another VGAM2062 host target gene. SERPINA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SERPINA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERPINA5 BINDING SITE, designated SEQ ID:6241, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ

ID:4773.

[72128] Another function of VGAM2062 is therefore inhibition of Serine (or cysteine) Proteinase Inhibitor, Clade A (alpha-1 antiproteinase, antitrypsin), Member 5 (SERPINA5, Accession NM_000624), a gene which inhibits activated protein c as well as plasminogen activators. Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINA5. The function of SERPINA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1233.ARL8 (Accession XM_167671) is another VGAM2062 host target gene. ARL8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARL8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARL8 BINDING SITE, designated SEQ ID:44766, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72129] Another function of VGAM2062 is therefore inhibition of ARL8 (Accession XM_167671). Accordingly, utilities of

VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARL8. Chromosome 1 Open Reading Frame 22 (C1orf22, Accession NM_025191) is another VGAM2062 host target gene. C1orf22 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf22, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf22 BINDING SITE, designated SEQ ID:24841, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72130] Another function of VGAM2062 is therefore inhibition of Chromosome 1 Open Reading Frame 22 (C1orf22, Accession NM_025191). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf22. Chromosome 20 Open Reading Frame 20 (C20orf20, Accession NM_018270) is another VGAM2062 host target gene. C20orf20 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf20, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf20 BINDING SITE, designated SEQ ID:20244, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72131] Another function of VGAM2062 is therefore inhibition of Chromosome 20 Open Reading Frame 20 (C20orf20, Accession NM_018270). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf20. Chromosome 9 Open Reading Frame 12 (C9orf12, Accession NM_022755) is another VGAM2062 host target gene. C9orf12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C9orf12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C9orf12 BINDING SITE, designated SEQ ID:22992, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72132] Another function of VGAM2062 is therefore inhibition of

Chromosome 9 Open Reading Frame 12 (C9orf12, Accession NM_022755). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf12. CDC14 Cell Division Cycle 14 Homolog B (S. cerevisiae) (CDC14B, Accession NM_003671) is another VGAM2062 host target gene. CDC14B BINDING SITE1 and CDC14B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CDC14B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDC14B BINDING SITE1 and CDC14B BINDING SITE2, designated SEQ ID:9762 and SEQ ID:27165 respectively, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72133] Another function of VGAM2062 is therefore inhibition of CDC14 Cell Division Cycle 14 Homolog B (S. cerevisiae) (CDC14B, Accession NM_003671). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC14B. Ephrin-A5 (EFNA5, Accession NM_001962) is another VGAM2062 host target gene. EFNA5 BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EFNA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFNA5 BINDING SITE, designated SEQ ID:7686, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72134] Another function of VGAM2062 is therefore inhibition of Ephrin-A5 (EFNA5, Accession NM_001962). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFNA5. FLJ12409 (Accession NM_025105) is another VGAM2062 host target gene. FLJ12409 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12409, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12409 BINDING SITE, designated SEQ ID:24753, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72135] Another function of VGAM2062 is therefore inhibition of

FLJ12409 (Accession NM_025105). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12409. FLJ12604 (Accession XM_035022) is another VGAM2062 host target gene. FLJ12604 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12604, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12604 BINDING SITE, designated SEQ ID:32191, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72136] Another function of VGAM2062 is therefore inhibition of FLJ12604 (Accession XM_035022). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12604. FLJ14640 (Accession NM_032816) is another VGAM2062 host target gene. FLJ14640 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ14640, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ14640 BINDING SITE, designated SEQ ID:26586, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72137] Another function of VGAM2062 is therefore inhibition of FLJ14640 (Accession NM_032816). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14640. FLJ20413 (Accession NM_017808) is another VGAM2062 host target gene. FLJ20413 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20413, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20413 BINDING SITE, designated SEQ ID:19453, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72138] Another function of VGAM2062 is therefore inhibition of FLJ20413 (Accession NM_017808). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20413. H_GS165L15.1 (Accession NM_004904) is an-

other VGAM2062 host target gene. H_GS165L15.1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by H_GS165L15.1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H_GS165L15.1 BINDING SITE, designated SEQ ID:11339, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72139] Another function of VGAM2062 is therefore inhibition of H_GS165L15.1 (Accession NM_004904). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H_GS165L15.1. HN1L (Accession NM_144570) is another VGAM2062 host target gene. HN1L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HN1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HN1L BINDING SITE, designated SEQ ID:29375, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA,

also designated SEQ ID:4773.

[72140] Another function of VGAM2062 is therefore inhibition of HN1L (Accession NM_144570). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HN1L. KIAA0379 (Accession XM_042860) is another VGAM2062 host target gene. KIAA0379 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0379, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0379 BINDING SITE, designated SEQ ID:33813, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72141] Another function of VGAM2062 is therefore inhibition of KIAA0379 (Accession XM_042860). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0379. KIAA0560 (Accession XM_029045) is another VGAM2062 host target gene. KIAA0560 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0560, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0560 BINDING SITE, designated SEQ ID:30838, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72142] Another function of VGAM2062 is therefore inhibition of KIAA0560 (Accession XM_029045). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0560. KIAA0916 (Accession NM_015057) is another VGAM2062 host target gene. KIAA0916 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0916, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0916 BINDING SITE, designated SEQ ID:17417, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72143] Another function of VGAM2062 is therefore inhibition of KIAA0916 (Accession NM_015057). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0916. KIAA1211 (Accession XM_044178) is another VGAM2062 host target gene. KIAA1211 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1211, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1211 BINDING SITE, designated SEQ ID:34163, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72144] Another function of VGAM2062 is therefore inhibition of KIAA1211 (Accession XM_044178). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1211. KIAA1376 (Accession XM_033042) is another VGAM2062 host target gene. KIAA1376 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1376, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1376 BINDING SITE, designated SEQ ID:31823, to the

nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72145] Another function of VGAM2062 is therefore inhibition of KIAA1376 (Accession XM_033042). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1376. MBLL39 (Accession NM_144778) is another VGAM2062 host target gene. MBLL39 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MBLL39, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MBLL39 BINDING SITE, designated SEQ ID:29570, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72146] Another function of VGAM2062 is therefore inhibition of MBLL39 (Accession NM_144778). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBLL39. N-ethylmaleimide-sensitive Factor Attachment Protein, Gamma (NAPG, Accession XM_172983) is another VGAM2062 host target gene. NAPG BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by NAPG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAPG BINDING SITE, designated SEQ ID:46254, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72147] Another function of VGAM2062 is therefore inhibition of N-ethylmaleimide-sensitive Factor Attachment Protein, Gamma (NAPG, Accession XM_172983). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAPG. Pellino Homolog 2 (Drosophila) (PELI2, Accession NM_021255) is another VGAM2062 host target gene. PELI2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PELI2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PELI2 BINDING SITE, designated SEQ ID:22231, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72148] Another function of VGAM2062 is therefore inhibition of Pellino Homolog 2 (Drosophila) (PELI2, Accession NM_021255). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PELI2. Protein Serine Kinase H1 (PSKH1, Accession XM_043047) is another VGAM2062 host target gene. PSKH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSKH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSKH1 BINDING SITE, designated SEQ ID:33868, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72149] Another function of VGAM2062 is therefore inhibition of Protein Serine Kinase H1 (PSKH1, Accession XM_043047). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSKH1. SEC14-like 2 (S. cerevisiae) (SEC14L2, Accession NM_012429) is another VGAM2062 host target gene. SEC14L2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA

encoded by SEC14L2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC14L2 BINDING SITE, designated SEQ ID:14806, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72150] Another function of VGAM2062 is therefore inhibition of SEC14-like 2 (S. cerevisiae) (SEC14L2, Accession NM_012429). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC14L2. Zinc Finger Protein 339 (ZNF339, Accession NM_021220) is another VGAM2062 host target gene. ZNF339 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF339, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF339 BINDING SITE, designated SEQ ID:22200, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72151] Another function of VGAM2062 is therefore inhibition of

Zinc Finger Protein 339 (ZNF339, Accession NM_021220). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF339. LOC138654 (Accession XM_071015) is another VGAM2062 host target gene. LOC138654 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC138654, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC138654 BINDING SITE, designated SEQ ID:37397, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72152] Another function of VGAM2062 is therefore inhibition of LOC138654 (Accession XM_071015). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC138654. LOC142948 (Accession XM_096364) is another VGAM2062 host target gene. LOC142948 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC142948, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC142948 BINDING SITE, designated SEQ ID:40326, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72153] Another function of VGAM2062 is therefore inhibition of LOC142948 (Accession XM_096364). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142948. LOC143916 (Accession XM_084664) is another VGAM2062 host target gene. LOC143916 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143916, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143916 BINDING SITE, designated SEQ ID:37654, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72154] Another function of VGAM2062 is therefore inhibition of LOC143916 (Accession XM_084664). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC143916. LOC145439 (Accession XM_085144) is another VGAM2062 host target gene. LOC145439 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145439, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145439 BINDING SITE, designated SEQ ID:37866, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72155] Another function of VGAM2062 is therefore inhibition of LOC145439 (Accession XM_085144). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145439. LOC147178 (Accession XM_028755) is another VGAM2062 host target gene. LOC147178 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147178 BINDING SITE, designated SEQ ID:30744, to the nucleotide sequence of VGAM2062 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4773.

[72156] Another function of VGAM2062 is therefore inhibition of LOC147178 (Accession XM_028755). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147178. LOC151194 (Accession NM_145280) is another VGAM2062 host target gene. LOC151194 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151194, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151194 BINDING SITE, designated SEQ ID:29798, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72157] Another function of VGAM2062 is therefore inhibition of LOC151194 (Accession NM_145280). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151194. LOC153416 (Accession XM_018473) is another VGAM2062 host target gene. LOC153416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153416, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153416 BINDING SITE, designated SEQ ID:30361, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72158] Another function of VGAM2062 is therefore inhibition of LOC153416 (Accession XM_018473). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153416. LOC157450 (Accession XM_048209) is another VGAM2062 host target gene. LOC157450 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157450, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157450 BINDING SITE, designated SEQ ID:35146, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72159] Another function of VGAM2062 is therefore inhibition of LOC157450 (Accession XM_048209). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC157450. LOC157556 (Accession XM_098783) is another VGAM2062 host target gene. LOC157556 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157556, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157556 BINDING SITE, designated SEQ ID:41823, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72160] Another function of VGAM2062 is therefore inhibition of LOC157556 (Accession XM_098783). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157556. LOC158629 (Accession XM_098972) is another VGAM2062 host target gene. LOC158629 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158629, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158629 BINDING SITE, designated SEQ ID:42020, to

the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72161] Another function of VGAM2062 is therefore inhibition of LOC158629 (Accession XM_098972). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158629. LOC200301 (Accession XM_114197) is another VGAM2062 host target gene. LOC200301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200301 BINDING SITE, designated SEQ ID:42784, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72162] Another function of VGAM2062 is therefore inhibition of LOC200301 (Accession XM_114197). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200301. LOC220790 (Accession XM_166037) is another VGAM2062 host target gene. LOC220790 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC220790, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220790 BINDING SITE, designated SEQ ID:43838, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72163] Another function of VGAM2062 is therefore inhibition of LOC220790 (Accession XM_166037). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220790. LOC221795 (Accession XM_166491) is another VGAM2062 host target gene. LOC221795 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221795, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221795 BINDING SITE, designated SEQ ID:44424, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72164] Another function of VGAM2062 is therefore inhibition of LOC221795 (Accession XM_166491). Accordingly, utilities

of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221795. LOC257019 (Accession XM_171208) is another VGAM2062 host target gene. LOC257019 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257019, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257019 BINDING SITE, designated SEQ ID:45995, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72165] Another function of VGAM2062 is therefore inhibition of LOC257019 (Accession XM_171208). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257019. LOC91664 (Accession XM_039908) is another VGAM2062 host target gene. LOC91664 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91664, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC91664 BINDING SITE, designated SEQ ID:33213, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72166] Another function of VGAM2062 is therefore inhibition of LOC91664 (Accession XM_039908). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91664. LOC93320 (Accession XM_050534) is another VGAM2062 host target gene. LOC93320 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93320, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93320 BINDING SITE, designated SEQ ID:35655, to the nucleotide sequence of VGAM2062 RNA, herein designated VGAM RNA, also designated SEQ ID:4773.

[72167] Another function of VGAM2062 is therefore inhibition of LOC93320 (Accession XM_050534). Accordingly, utilities of VGAM2062 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93320. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2063 (VGAM2063) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72168] VGAM2063 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2063 was detected is described hereinabove with reference to Figs. 1-8.

[72169] VGAM2063 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2063 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72170] VGAM2063 gene encodes a VGAM2063 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2063 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2063 precursor RNA is designated SEQ ID:2049, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2049 is located at position 7074 relative to the

genome of Ectromelia Virus.

[72171] VGAM2063 precursor RNA folds onto itself, forming VGAM2063 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72172] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2063 folded precursor RNA into VGAM2063 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2063 RNA is designated SEQ ID:4774, and is provided hereinbelow with reference to the sequence listing part.

[72173] VGAM2063 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2063 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2063 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72174] VGAM2063 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2063 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2063 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2063 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2063 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72175] The complementary binding of VGAM2063 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2063 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2063 host target RNA into VGAM2063 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72176] It is appreciated that VGAM2063 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2063 host target genes. The mRNA of each one of this plurality of VGAM2063 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2063 RNA, herein designated VGAM RNA, and which when bound by VGAM2063 RNA causes inhibition of translation of respective one or more VGAM2063 host target proteins.

[72177] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2063 gene, herein designated VGAM GENE, on one or more VGAM2063 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72178] It is yet further appreciated that a function of VGAM2063 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2063 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2063 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2063 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72179] Nucleotide sequences of the VGAM2063 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2063 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2063 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2063 are further described hereinbelow with reference to Table 1.

[72180] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2063 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2063 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72181] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2063 gene, herein designated VGAM is inhibition of expression of VGAM2063 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2063 correlate with, and may be deduced

from, the identity of the target genes which VGAM2063 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72182] Diacylglycerol Kinase, Beta 90kDa (DGKB, Accession XM_166516) is a VGAM2063 host target gene. DGKB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DGKB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGKB BINDING SITE, designated SEQ ID:44447, to the nucleotide sequence of VGAM2063 RNA, herein designated VGAM RNA, also designated SEQ ID:4774.

[72183] A function of VGAM2063 is therefore inhibition of Diacylglycerol Kinase, Beta 90kDa (DGKB, Accession XM_166516), a gene which regulates the intracellular concentration of the second messenger diacylglycerol (DAG). Accordingly, utilities of VGAM2063 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGKB. The function of DGKB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM497.Myelin Oligoden-

drocyte Glycoprotein (MOG, Accession NM_002433) is another VGAM2063 host target gene. MOG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MOG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MOG BINDING SITE, designated SEQ ID:8278, to the nucleotide sequence of VGAM2063 RNA, herein designated VGAM RNA, also designated SEQ ID:4774.

[72184] Another function of VGAM2063 is therefore inhibition of Myelin Oligodendrocyte Glycoprotein (MOG, Accession NM_002433). Accordingly, utilities of VGAM2063 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOG. SAC1 Suppressor of Actin Mutations 1-like (yeast) (SACM1L, Accession NM_014016) is another VGAM2063 host target gene. SACM1L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SACM1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SACM1L BINDING SITE, designated SEQ

ID:15236, to the nucleotide sequence of VGAM2063 RNA, herein designated VGAM RNA, also designated SEQ ID:4774.

[72185] Another function of VGAM2063 is therefore inhibition of SAC1 Suppressor of Actin Mutations 1-like (yeast) (SACM1L, Accession NM_014016), a gene which suggests the presence of a tumor suppressor gene. Accordingly, utilities of VGAM2063 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SACM1L. The function of SACM1L has been established by previous studies. 2. Chen, Y.; Cann, M. J.; Litvin, T. N.; Iourgenko, V.; Sinclair, M. L.; Levin, L. R.; Buck, J. : Soluble adenylyl cyclase as an evolutionarily conserved bicarbonate sensor. Science 289: 625-628, 2000. PubMed ID : 10915626 3. Reed, B. Y.; Gitomer, W. L.; Heller, H. J.; Hsu, M. C.; Lemke, M.; Padalino, P.; Pak, C. Y. C. : Identification and characterization of a gene with base substitutions associated with the absorptive hypercalciuria phenotype and low spinal bone density. J. Clin. Endocr. Metab. 87: 1476-1485, 2002. PubMed ID : 11932268

[72186] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[72187] Kiss, H.; Kedra, D.; Kiss, C.; Kost-Alimova, M.; Yang, Y.; Klein, G.; Imreh, S.; Dumanski, J. P. : The LZTFL1 gene is a part of a transcriptional map covering 250 kb within the common eliminated region 1 (C3CER1) in 3p21.3. Genomics 73: 10-19, 2001. ; and

[72188] Nagase, T.; Kikuno, R.; Hattori, A.; Kondo, Y.; Okumura, K.; Ohara, O. : Prediction of the coding sequences of unidentified human genes. XIX. The complete sequences of 100 new cDNA clon.

[72189] Further studies establishing the function and utilities of SACM1L are found in John Hopkins OMIM database record ID 606569, and in sited publications numbered 555 and 6104 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Vascular Cell Adhesion Molecule 1 (VCAM1, Accession NM_080682) is another VGAM2063 host target gene. VCAM1 BINDING SITE1 and VCAM1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by VCAM1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VCAM1 BINDING SITE1 and VCAM1 BINDING SITE2, designated SEQ ID:27985 and SEQ ID:6739 respec-

tively, to the nucleotide sequence of VGAM2063 RNA, herein designated VGAM RNA, also designated SEQ ID:4774.

[72190] Another function of VGAM2063 is therefore inhibition of Vascular Cell Adhesion Molecule 1 (VCAM1, Accession NM_080682). Accordingly, utilities of VGAM2063 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VCAM1. FLJ00060 (Accession XM_028154) is another VGAM2063 host target gene. FLJ00060 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00060, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00060 BINDING SITE, designated SEQ ID:30626, to the nucleotide sequence of VGAM2063 RNA, herein designated VGAM RNA, also designated SEQ ID:4774.

[72191] Another function of VGAM2063 is therefore inhibition of FLJ00060 (Accession XM_028154). Accordingly, utilities of VGAM2063 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00060. KIAA0419 (Accession NM_014711) is another

VGAM2063 host target gene. KIAA0419 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0419, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0419 BINDING SITE, designated SEQ ID:16259, to the nucleotide sequence of VGAM2063 RNA, herein designated VGAM RNA, also designated SEQ ID:4774.

[72192] Another function of VGAM2063 is therefore inhibition of KIAA0419 (Accession NM_014711). Accordingly, utilities of VGAM2063 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0419. Lipoma HMGIC Fusion Partner-like 2 (LHFPL2, Accession XM_046054) is another VGAM2063 host target gene. LHFPL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LHFPL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LHFPL2 BINDING SITE, designated SEQ ID:34659, to the nucleotide sequence of VGAM2063 RNA, herein designated VGAM RNA, also designated SEQ

ID:4774.

[72193] Another function of VGAM2063 is therefore inhibition of Lipoma HMGIC Fusion Partner-like 2 (LHFPL2, Accession XM_046054). Accordingly, utilities of VGAM2063 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHFPL2. LOC256683 (Accession XM_172321) is another VGAM2063 host target gene. LOC256683 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256683, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256683 BINDING SITE, designated SEQ ID:46069, to the nucleotide sequence of VGAM2063 RNA, herein designated VGAM RNA, also designated SEQ ID:4774.

[72194] Another function of VGAM2063 is therefore inhibition of LOC256683 (Accession XM_172321). Accordingly, utilities of VGAM2063 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256683. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2064 (VGAM2064) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72195] VGAM2064 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2064 was detected is described hereinabove with reference to Figs. 1-8.

[72196] VGAM2064 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Peanut Bud Necrosis Virus. VGAM2064 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72197] VGAM2064 gene encodes a VGAM2064 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2064 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2064 precursor RNA is designated SEQ ID:2050, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2050 is located at position 3726 relative to the genome of Peanut Bud Necrosis Virus.

[72198] VGAM2064 precursor RNA folds onto itself, forming VGAM2064 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72199] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2064 folded precursor RNA into VGAM2064 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2064 RNA is designated SEQ ID:4775, and is provided hereinbelow with reference to the sequence listing part.

[72200] VGAM2064 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2064 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2064 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72201] VGAM2064 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2064 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2064 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2064 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2064 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72202] The complementary binding of VGAM2064 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2064 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2064 host target RNA into VGAM2064 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72203] It is appreciated that VGAM2064 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2064 host target genes. The mRNA of each one of this plurality of VGAM2064 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2064 RNA, herein designated VGAM RNA, and which when bound by VGAM2064 RNA causes inhibition of translation of respective one or more VGAM2064 host target proteins.

[72204] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2064 gene, herein designated VGAM GENE, on one or more VGAM2064 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72205] It is yet further appreciated that a function of VGAM2064 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2064 include diagnosis, prevention and treatment of viral infection by Peanut Bud Necrosis Virus. Specific functions, and accordingly utilities, of VGAM2064 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2064 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72206] Nucleotide sequences of the VGAM2064 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2064 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2064 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2064 are further described hereinbelow with reference to Table 1.

[72207] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2064 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2064 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72208] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2064 gene, herein designated VGAM is inhibition of expression of VGAM2064 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2064 correlate with, and may be deduced from, the identity of the target genes which VGAM2064

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72209] CD44 Antigen (homing function and Indian blood group system) (CD44, Accession NM_000610) is a VGAM2064 host target gene. CD44 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CD44, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD44 BINDING SITE, designated SEQ ID:6212, to the nucleotide sequence of VGAM2064 RNA, herein designated VGAM RNA, also designated SEQ ID:4775.

[72210] A function of VGAM2064 is therefore inhibition of CD44 Antigen (homing function and Indian blood group system) (CD44, Accession NM_000610), a gene which is main cell surface receptor for hyaluronate, and involves in matrix adhesion, lymphocyte activation and lymph node homing. Accordingly, utilities of VGAM2064 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD44. The function of CD44 and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to VGAM1928.Mitochondrial Ribosomal Protein L49 (MRPL49, Accession XM_045499) is another VGAM2064 host target gene. MRPL49 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPL49, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPL49 BINDING SITE, designated SEQ ID:34476, to the nucleotide sequence of VGAM2064 RNA, herein designated VGAM RNA, also designated SEQ ID:4775.

[72211] Another function of VGAM2064 is therefore inhibition of Mitochondrial Ribosomal Protein L49 (MRPL49, Accession XM_045499). Accordingly, utilities of VGAM2064 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL49. Neuronal Pentraxin I (NPTX1, Accession NM_002522) is another VGAM2064 host target gene. NPTX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NPTX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPTX1 BINDING SITE,

designated SEQ ID:8354, to the nucleotide sequence of VGAM2064 RNA, herein designated VGAM RNA, also designated SEQ ID:4775.

[72212] Another function of VGAM2064 is therefore inhibition of Neuronal Pentraxin I (NPTX1, Accession NM_002522), a gene which may be involved in synaptic uptake of extracellular material and is very strongly similar to rat NP1. Accordingly, utilities of VGAM2064 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTX1. The function of NPTX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM111.Staufen, RNA Binding Protein (Drosophila) (STAU, Accession NM_004602) is another VGAM2064 host target gene. STAU BINDING SITE1 through STAU BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by STAU, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAU BINDING SITE1 through STAU BINDING SITE4, designated SEQ ID:10943, SEQ ID:18915, SEQ ID:18921 and SEQ ID:18927 respec-

tively, to the nucleotide sequence of VGAM2064 RNA, herein designated VGAM RNA, also designated SEQ ID:4775.

[72213] Another function of VGAM2064 is therefore inhibition of Staufen, RNA Binding Protein (Drosophila) (STAU, Accession NM_004602), a gene which may play a role in specific positioning of mrnas at given sites in the cell and in stimulating their translation at the site. Accordingly, utilities of VGAM2064 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAU. The function of STAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM916.Hairy/enhancer-of-split Related with YRPW Motif 1 (HEY1, Accession XM_166062) is another VGAM2064 host target gene. HEY1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HEY1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HEY1 BINDING SITE, designated SEQ ID:43847, to the nucleotide sequence of VGAM2064 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4775.

[72214] Another function of VGAM2064 is therefore inhibition of Hairy/enhancer-of-split Related with YRPW Motif 1 (HEY1, Accession XM_166062). Accordingly, utilities of VGAM2064 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEY1. KIAA0335 (Accession NM_014803) is another VGAM2064 host target gene. KIAA0335 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0335, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0335 BINDING SITE, designated SEQ ID:16731, to the nucleotide sequence of VGAM2064 RNA, herein designated VGAM RNA, also designated SEQ ID:4775.

[72215] Another function of VGAM2064 is therefore inhibition of KIAA0335 (Accession NM_014803). Accordingly, utilities of VGAM2064 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0335. KIAA0763 (Accession NM_014869) is another VGAM2064 host target gene. KIAA0763 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA0763, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0763 BINDING SITE, designated SEQ ID:16967, to the nucleotide sequence of VGAM2064 RNA, herein designated VGAM RNA, also designated SEQ ID:4775.

[72216] Another function of VGAM2064 is therefore inhibition of KIAA0763 (Accession NM_014869). Accordingly, utilities of VGAM2064 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0763. LOC221683 (Accession XM_168089) is another VGAM2064 host target gene. LOC221683 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221683, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221683 BINDING SITE, designated SEQ ID:45002, to the nucleotide sequence of VGAM2064 RNA, herein designated VGAM RNA, also designated SEQ ID:4775.

[72217] Another function of VGAM2064 is therefore inhibition of LOC221683 (Accession XM_168089). Accordingly, utilities

of VGAM2064 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221683. LOC91445 (Accession XM_018516) is another VGAM2064 host target gene. LOC91445 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91445 BINDING SITE, designated SEQ ID:30370, to the nucleotide sequence of VGAM2064 RNA, herein designated VGAM RNA, also designated SEQ ID:4775.

[72218] Another function of VGAM2064 is therefore inhibition of LOC91445 (Accession XM_018516). Accordingly, utilities of VGAM2064 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91445. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2065 (VGAM2065) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72219] VGAM2065 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2065 was detected is described hereinabove with reference to Figs. 1-8.

[72220] VGAM2065 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2065 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72221] VGAM2065 gene encodes a VGAM2065 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2065 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2065 precursor RNA is designated SEQ ID:2051, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2051 is located at position 18973 relative to the genome of Ectromelia Virus.

[72222] VGAM2065 precursor RNA folds onto itself, forming VGAM2065 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72223] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2065 folded precursor RNA into VGAM2065 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2065 RNA is designated SEQ ID:4776, and is provided hereinbelow with reference to the sequence listing part.

[72224] VGAM2065 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2065 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2065 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[72225] VGAM2065 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2065 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2065 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2065 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2065 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72226] The complementary binding of VGAM2065 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2065 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2065 host target RNA into VGAM2065 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72227] It is appreciated that VGAM2065 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2065 host target genes. The mRNA of each one of this plurality of VGAM2065 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2065 RNA, herein designated VGAM RNA, and which when bound by VGAM2065 RNA causes inhibition of translation of respective one or more VGAM2065 host target proteins.

[72228] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2065 gene, herein designated VGAM GENE, on one or more VGAM2065 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72229] It is yet further appreciated that a function of VGAM2065 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2065 correlate with, and may be deduced from, the identity of the host target genes which VGAM2065 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72230] Nucleotide sequences of the VGAM2065 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2065 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2065 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2065 are further described hereinbelow with reference to Table 1.

[72231] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2065 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2065 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72232] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2065 gene, herein designated VGAM is inhibition of expression of VGAM2065 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2065 correlate with, and may be deduced from, the identity of the target genes which VGAM2065 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72233] APM1 (Accession NM_004797) is a VGAM2065 host target gene. APM1 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by APM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APM1 BINDING SITE, designated SEQ ID:11208, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72234] A function of VGAM2065 is therefore inhibition of APM1 (Accession NM_004797). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APM1. Protein Kinase C, Beta 1 (PRKCB1, Accession XM_047187) is another VGAM2065 host target gene. PRKCB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKCB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKCB1 BINDING SITE, designated SEQ ID:34903, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72235] Another function of VGAM2065 is therefore inhibition of Protein Kinase C, Beta 1 (PRKCB1, Accession XM_047187),

a gene which is a calcium-activated, phospholipid-dependent, serine- and threonine-specific enzyme. Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKCB1. The function of PRKCB1 has been established by previous studies. Greenham et al. (1998) determined the genomic structure of the PRKCB gene. The PRKCB gene consists of 18 exons spanning 375 kb, with a particularly large intron of over 150 kb between exons 2 and 3. Exons range from 32 to 174 bp in length. Francke et al. (1989) stated that the most likely location of PKCB is 16p11.2. Animal model experiments lend further support to the function of PRKCB1. Leitges et al. (1996) found that mice homozygous for a targeted disruption of the Prkcb1 gene develop an immunodeficiency characterized by impaired humoral immune responses and reduced cellular responses of B cells similar to X-linked immunodeficiency (Xid) in mice (see OMIM Ref. No. 300300). Thus, they concluded that the 2 isoforms, PKC-beta-I (OMIM Ref. No. PRKCB1) and PKC-beta-II (OMIM Ref. No. PRKCB2), play an important role in B-cell activation and may be functionally linked to Bruton tyrosine kinase (OMIM Ref. No. 300300) in antigen receptor-mediated signal transduction. Su et al.

(2002) showed that mice lacking Prkcb are unable to activate Nfkb (OMIM Ref. No. 164011) and promote cell survival in B cells upon BCR signaling, or even in mast cells which, unlike B cells, also express Prkcq (OMIM Ref. No. 600448). The failure to activate Nfkb is associated with a lack of Ikba (OMIM Ref. No. 164008) degradation as well as an absence of Ikka (OMIM Ref. No. 600664) phosphorylation activity. Prkcb -/- mice, lacking the Prkcb enzyme in lipid rafts after BCR stimulation, are also unable to recruit Ikka and Ikkb (OMIM Ref. No. 603258) to the rafts in B cells and have a reduced capacity to recruit other members of the BCR signalosome. However, Prkcb-deficient mice, unlike Xid mice, do have mature B cells expressing IgM and IgD, suggesting that the cells are maintained by an alternative Nfkb-activating pathway, e.g., through CD40 (OMIM Ref. No. 109535). Su et al. (2002) observed that specific Prkcb small molecule inhibitors block the survival of non-Hodgkin diffuse large B cell lymphoma (DLBCL) cell lines, with the effective dose depending on the level of cellular Prkcb. DLBCL lines not expressing Prkcb were not susceptible to the inhibitors. Su et al. (2002) proposed that PRKCB inhibitors and inhibitors of other PRKC isoforms may be effective in treating disorders

characterized by dysregulated NFKB survival signaling.

[72236] It is appreciated that the abovementioned animal model for PRKCB1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[72237] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[72238] Leitges, M.; Schmedt, C.; Guinamard, R.; Davoust, J.; Schaal, S.; Stabel, S.; Tarakhovsky, A. : Immunodeficiency in protein kinase C-beta-deficient mice. Science 273: 788-791, 1996. ; and

[72239] Su, T. T.; Guo, B.; Kawakami, Y.; Sommer, K.; Chae, K.; Humphries, L. A.; Kato, R. M.; Kang, S.; Patrone, L.; Wall, R.; Teitell, M.; Leitges, M.; Kawakami, T.; Rawlings, D. J. : PKC-beta.

[72240] Further studies establishing the function and utilities of PRKCB1 are found in John Hopkins OMIM database record ID 176970, and in sited publications numbered 154 and 1544-1546 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Calcium/calmodulin-dependent Protein Kinase (CaM kinase) II Gamma (CAMK2G, Accession XM_044349) is an-

other VGAM2065 host target gene. CAMK2G BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CAMK2G, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAMK2G BINDING SITE, designated SEQ ID:34191, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72241] Another function of VGAM2065 is therefore inhibition of Calcium/calmodulin-dependent Protein Kinase (CaM kinase) II Gamma (CAMK2G, Accession XM_044349). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMK2G. FLJ13769 (Accession NM_025012) is another VGAM2065 host target gene. FLJ13769 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13769, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13769 BINDING SITE, designated SEQ ID:24591, to the nucleotide sequence of VGAM2065 RNA,

herein designated VGAM RNA, also designated SEQ ID:4776.

[72242] Another function of VGAM2065 is therefore inhibition of FLJ13769 (Accession NM_025012). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13769. FLJ13955 (Accession NM_024759) is another VGAM2065 host target gene. FLJ13955 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13955 BINDING SITE, designated SEQ ID:24109, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72243] Another function of VGAM2065 is therefore inhibition of FLJ13955 (Accession NM_024759). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13955. FLJ13964 (Accession NM_032186) is another VGAM2065 host target gene. FLJ13964 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ13964, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13964 BINDING SITE, designated SEQ ID:25902, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72244] Another function of VGAM2065 is therefore inhibition of FLJ13964 (Accession NM_032186). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13964. HEMK (Accession NM_016173) is another VGAM2065 host target gene. HEMK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HEMK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HEMK BINDING SITE, designated SEQ ID:18266, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72245] Another function of VGAM2065 is therefore inhibition of HEMK (Accession NM_016173). Accordingly, utilities of

VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEMK. Heat Shock 90kDa Protein 1, Alpha-like 3 (HSPCAL3, Accession XM_084514) is another VGAM2065 host target gene. HSPCAL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSPCAL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPCAL3 BINDING SITE, designated SEQ ID:37618, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72246] Another function of VGAM2065 is therefore inhibition of Heat Shock 90kDa Protein 1, Alpha-like 3 (HSPCAL3, Accession XM_084514). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPCAL3. KIAA0217 (Accession XM_040265) is another VGAM2065 host target gene. KIAA0217 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0217, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0217 BINDING SITE, designated SEQ ID:33279, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72247] Another function of VGAM2065 is therefore inhibition of KIAA0217 (Accession XM_040265). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0217. Rpo1-2 (Accession NM_019014) is another VGAM2065 host target gene. Rpo1-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Rpo1-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rpo1-2 BINDING SITE, designated SEQ ID:21097, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72248] Another function of VGAM2065 is therefore inhibition of Rpo1-2 (Accession NM_019014). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

Rpo1-2. Trans-golgi Network Protein 2 (TGOLN2, Accession XM_034215) is another VGAM2065 host target gene. TGOLN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TGOLN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TGOLN2 BINDING SITE, designated SEQ ID:32023, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72249] Another function of VGAM2065 is therefore inhibition of Trans-golgi Network Protein 2 (TGOLN2, Accession XM_034215). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGOLN2. LOC149844 (Accession XM_086675) is another VGAM2065 host target gene. LOC149844 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149844, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149844 BINDING SITE, desig-

nated SEQ ID:38821, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72250] Another function of VGAM2065 is therefore inhibition of LOC149844 (Accession XM_086675). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149844. LOC157567 (Accession XM_088328) is another VGAM2065 host target gene. LOC157567 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157567, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157567 BINDING SITE, designated SEQ ID:39612, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72251] Another function of VGAM2065 is therefore inhibition of LOC157567 (Accession XM_088328). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157567. LOC158219 (Accession XM_088514) is another VGAM2065 host target gene. LOC158219 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158219 BINDING SITE, designated SEQ ID:39762, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72252] Another function of VGAM2065 is therefore inhibition of LOC158219 (Accession XM_088514). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158219. LOC170132 (Accession XM_093119) is another VGAM2065 host target gene. LOC170132 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC170132, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC170132 BINDING SITE, designated SEQ ID:40177, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72253] Another function of VGAM2065 is therefore inhibition of

LOC170132 (Accession XM_093119). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170132. LOC203350 (Accession XM_117536) is another VGAM2065 host target gene. LOC203350 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203350, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203350 BINDING SITE, designated SEQ ID:43533, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72254] Another function of VGAM2065 is therefore inhibition of LOC203350 (Accession XM_117536). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203350. LOC51313 (Accession NM_016613) is another VGAM2065 host target gene. LOC51313 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51313, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of LOC51313 BINDING SITE, designated SEQ ID:18719, to the nucleotide sequence of VGAM2065 RNA, herein designated VGAM RNA, also designated SEQ ID:4776.

[72255] Another function of VGAM2065 is therefore inhibition of LOC51313 (Accession NM_016613). Accordingly, utilities of VGAM2065 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51313. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2066 (VGAM2066) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72256] VGAM2066 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2066 was detected is described hereinabove with reference to Figs. 1-8.

[72257] VGAM2066 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2066 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[72258] VGAM2066 gene encodes a VGAM2066 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2066 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2066 precursor RNA is designated SEQ ID:2052, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2052 is located at position 9912 relative to the genome of Ectromelia Virus.

[72259] VGAM2066 precursor RNA folds onto itself, forming VGAM2066 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72260] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2066 folded precursor RNA into VGAM2066 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2066 RNA is designated SEQ ID:4777, and is provided hereinbelow with reference to the sequence listing part.

[72261] VGAM2066 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2066 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2066 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72262] VGAM2066 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2066 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2066 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2066 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2066 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72263] The complementary binding of VGAM2066 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2066 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2066 host target RNA into VGAM2066 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72264] It is appreciated that VGAM2066 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2066 host target genes. The mRNA of each one of this plurality of VGAM2066 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2066 RNA, herein designated VGAM RNA, and which when bound by VGAM2066 RNA causes inhibition of translation of respective one or more VGAM2066 host target proteins.

[72265] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2066 gene, herein designated VGAM GENE, on one or more VGAM2066 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72266] It is yet further appreciated that a function of VGAM2066 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2066 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2066 correlate with, and may be deduced from, the identity of the host target genes which VGAM2066 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72267] Nucleotide sequences of the VGAM2066 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2066 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2066 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2066 are further described hereinbelow with reference to Table 1.

[72268] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2066 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2066 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72269] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2066 gene, herein designated VGAM is inhibition of expression of VGAM2066 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2066 correlate with, and may be deduced from, the identity of the target genes which VGAM2066 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72270] Brain and Acute Leukemia, Cytoplasmic (BAALC, Accession NM_024812) is a VGAM2066 host target gene. BAALC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAALC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAALC BINDING SITE, designated SEQ ID:24198, to the nucleotide sequence of VGAM2066 RNA, herein designated VGAM RNA, also designated SEQ ID:4777.

[72271] A function of VGAM2066 is therefore inhibition of Brain and Acute Leukemia, Cytoplasmic (BAALC, Accession NM_024812). Accordingly, utilities of VGAM2066 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAALC. Ceramide Kinase (cerk, Accession NM_022766) is another VGAM2066 host target gene. cerk BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by cerk, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of cerk BINDING SITE, designated SEQ ID:23014, to the nucleotide sequence of VGAM2066 RNA, herein designated VGAM RNA, also designated SEQ ID:4777.

[72272] Another function of VGAM2066 is therefore inhibition of Ceramide Kinase (cerk, Accession NM_022766). Accordingly, utilities of VGAM2066 include diagnosis, prevention and treatment of diseases and clinical conditions associated with cerk. Dynein, Cytoplasmic, Light Intermediate Polypeptide 1 (DNCLI1, Accession XM_003119) is another VGAM2066 host target gene. DNCLI1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by DNCLI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNCLI1 BINDING SITE, designated SEQ ID:29929, to the nucleotide sequence of VGAM2066 RNA, herein designated VGAM RNA, also designated SEQ ID:4777.

[72273] Another function of VGAM2066 is therefore inhibition of Dynein, Cytoplasmic, Light Intermediate Polypeptide 1 (DNCLI1, Accession XM_003119). Accordingly, utilities of VGAM2066 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNCLI1. Histamine Receptor H4 (HRH4, Accession NM_021624) is another VGAM2066 host target gene. HRH4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HRH4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRH4 BINDING SITE, designated SEQ ID:22265, to the nucleotide sequence of VGAM2066 RNA, herein designated VGAM RNA, also designated SEQ ID:4777.

[72274] Another function of VGAM2066 is therefore inhibition of

Histamine Receptor H4 (HRH4, Accession NM_021624). Accordingly, utilities of VGAM2066 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRH4. KIAA0368 (Accession XM_036708) is another VGAM2066 host target gene. KIAA0368 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0368, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0368 BINDING SITE, designated SEQ ID:32491, to the nucleotide sequence of VGAM2066 RNA, herein designated VGAM RNA, also designated SEQ ID:4777.

[72275] Another function of VGAM2066 is therefore inhibition of KIAA0368 (Accession XM_036708). Accordingly, utilities of VGAM2066 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0368. Sema Domain, Immunoglobulin Domain (Ig), Short Basic Domain, Secreted, (semaphorin) 3E (SEMA3E, Accession NM_012431) is another VGAM2066 host target gene. SEMA3E BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

SEMA3E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEMA3E BINDING SITE, designated SEQ ID:14811, to the nucleotide sequence of VGAM2066 RNA, herein designated VGAM RNA, also designated SEQ ID:4777.

[72276] Another function of VGAM2066 is therefore inhibition of Sema Domain, Immunoglobulin Domain (Ig), Short Basic Domain, Secreted, (semaphorin) 3E (SEMA3E, Accession NM_012431). Accordingly, utilities of VGAM2066 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA3E. LOC153139 (Accession XM_098318) is another VGAM2066 host target gene. LOC153139 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153139 BINDING SITE, designated SEQ ID:41575, to the nucleotide sequence of VGAM2066 RNA, herein designated VGAM RNA, also designated SEQ ID:4777.

[72277] Another function of VGAM2066 is therefore inhibition of LOC153139 (Accession XM_098318). Accordingly, utilities of VGAM2066 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153139. LOC154184 (Accession XM_098488) is another VGAM2066 host target gene. LOC154184 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154184, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154184 BINDING SITE, designated SEQ ID:41687, to the nucleotide sequence of VGAM2066 RNA, herein designated VGAM RNA, also designated SEQ ID:4777.

[72278] Another function of VGAM2066 is therefore inhibition of LOC154184 (Accession XM_098488). Accordingly, utilities of VGAM2066 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154184. LOC221601 (Accession XM_168071) is another VGAM2066 host target gene. LOC221601 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221601, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221601 BINDING SITE, designated SEQ ID:44984, to the nucleotide sequence of VGAM2066 RNA, herein designated VGAM RNA, also designated SEQ ID:4777.

[72279] Another function of VGAM2066 is therefore inhibition of LOC221601 (Accession XM_168071). Accordingly, utilities of VGAM2066 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221601. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2067 (VGAM2067) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72280] VGAM2067 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2067 was detected is described hereinabove with reference to Figs. 1-8.

[72281] VGAM2067 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2067 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[72282] VGAM2067 gene encodes a VGAM2067 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2067 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2067 precursor RNA is designated SEQ ID:2053, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2053 is located at position 7556 relative to the genome of Ectromelia Virus.

[72283] VGAM2067 precursor RNA folds onto itself, forming VGAM2067 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72284] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2067 folded precursor RNA into VGAM2067

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2067 RNA is designated SEQ ID:4778, and is provided hereinbelow with reference to the sequence listing part.

[72285] VGAM2067 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2067 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2067 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72286] VGAM2067 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2067 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2067 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2067 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2067 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72287] The complementary binding of VGAM2067 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2067 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2067 host target RNA into VGAM2067 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[72288] It is appreciated that VGAM2067 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2067 host target genes. The mRNA of each one of this plurality of VGAM2067 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2067 RNA, herein designated VGAM RNA, and which when bound by VGAM2067 RNA causes inhibition of translation of respective one or more VGAM2067 host target proteins.

[72289] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2067 gene, herein designated VGAM GENE, on one or more VGAM2067 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72290] It is yet further appreciated that a function of VGAM2067 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2067 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2067 correlate with, and may be deduced from, the identity of the host target genes which VGAM2067 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72291] Nucleotide sequences of the VGAM2067 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2067 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2067 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2067 are further described hereinbelow with reference to Table 1.

[72292] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2067 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2067 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72293] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2067 gene, herein designated VGAM is inhibition of expression of VGAM2067 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2067 correlate with, and may be deduced from, the identity of the target genes which VGAM2067 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72294] KIAA1323 (Accession XM_032146) is a VGAM2067 host target gene. KIAA1323 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1323 BINDING SITE, designated SEQ ID:31571, to the nucleotide sequence of VGAM2067 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4778.

[72295] A function of VGAM2067 is therefore inhibition of KIAA1323 (Accession XM_032146). Accordingly, utilities of VGAM2067 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1323. MAP (Accession NM_022818) is another VGAM2067 host target gene. MAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP BINDING SITE, designated SEQ ID:23098, to the nucleotide sequence of VGAM2067 RNA, herein designated VGAM RNA, also designated SEQ ID:4778.

[72296] Another function of VGAM2067 is therefore inhibition of MAP (Accession NM_022818). Accordingly, utilities of VGAM2067 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP. PP1044 (Accession NM_021730) is another VGAM2067 host target gene. PP1044 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PP1044, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP1044 BINDING SITE, designated SEQ ID:22327, to the nucleotide sequence of VGAM2067 RNA, herein designated VGAM RNA, also designated SEQ ID:4778.

[72297] Another function of VGAM2067 is therefore inhibition of PP1044 (Accession NM_021730). Accordingly, utilities of VGAM2067 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1044. Signal-regulatory Protein Beta 1 (SIRPB1, Accession NM_006065) is another VGAM2067 host target gene. SIRPB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIRPB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIRPB1 BINDING SITE, designated SEQ ID:12712, to the nucleotide sequence of VGAM2067 RNA, herein designated VGAM RNA, also designated SEQ ID:4778.

[72298] Another function of VGAM2067 is therefore inhibition of Signal-regulatory Protein Beta 1 (SIRPB1, Accession

NM_006065). Accordingly, utilities of VGAM2067 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIRPB1. LOC93496 (Accession XM_051698) is another VGAM2067 host target gene. LOC93496 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93496, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93496 BINDING SITE, designated SEQ ID:35867, to the nucleotide sequence of VGAM2067 RNA, herein designated VGAM RNA, also designated SEQ ID:4778.

[72299] Another function of VGAM2067 is therefore inhibition of LOC93496 (Accession XM_051698). Accordingly, utilities of VGAM2067 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93496. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2068 (VGAM2068) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[72300] VGAM2068 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2068 was detected is described hereinabove with reference to Figs. 1-8.

[72301] VGAM2068 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2068 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72302] VGAM2068 gene encodes a VGAM2068 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2068 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2068 precursor RNA is designated SEQ ID:2054, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2054 is located at position 18952 relative to the genome of Monkeypox Virus.

[72303] VGAM2068 precursor RNA folds onto itself, forming VGAM2068 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72304] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2068 folded precursor RNA into VGAM2068 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2068 RNA is designated SEQ ID:4779, and is provided hereinbelow with reference to the sequence listing part.

[72305] VGAM2068 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2068 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2068 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72306] VGAM2068 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2068 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2068 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2068 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2068 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[72307] The complementary binding of VGAM2068 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2068 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2068 host target RNA into VGAM2068 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72308] It is appreciated that VGAM2068 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2068 host target genes. The mRNA of each one of this plurality of VGAM2068 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2068 RNA, herein designated VGAM RNA, and which when bound by VGAM2068 RNA causes inhibition of translation of respective one or more VGAM2068 host target proteins.

[72309] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2068 gene, herein designated VGAM GENE, on one

or more VGAM2068 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72310] It is yet further appreciated that a function of VGAM2068 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2068 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2068 correlate with, and may be deduced from, the identity of the host target genes which VGAM2068 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72311] Nucleotide sequences of the VGAM2068 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2068 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2068 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2068 are further described hereinbelow with reference to Table 1.

[72312] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2068 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2068 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72313] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2068 gene, herein designated VGAM is inhibition of expression of VGAM2068 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2068 correlate with, and may be deduced from, the identity of the target genes which VGAM2068 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72314] ATP-binding Cassette, Sub-family B (MDR/TAP), Member

10 (ABCB10, Accession NM_012089) is a VGAM2068 host target gene. ABCB10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCB10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCB10 BINDING SITE, designated SEQ ID:14373, to the nucleotide sequence of VGAM2068 RNA, herein designated VGAM RNA, also designated SEQ ID:4779.

[72315] A function of VGAM2068 is therefore inhibition of ATP-binding Cassette, Sub-family B (MDR/TAP), Member 10 (ABCB10, Accession NM_012089), a gene which a member of the superfamily of ATP-binding cassette (ABC) transporters. Accordingly, utilities of VGAM2068 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCB10. The function of ABCB10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1523.Protocadherin Alpha 9 (PCDHA9, Accession NM_014005) is another VGAM2068 host target gene. PCDHA9 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by PCDHA9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA9 BINDING SITE, designated SEQ ID:15207, to the nucleotide sequence of VGAM2068 RNA, herein designated VGAM RNA, also designated SEQ ID:4779.

[72316] Another function of VGAM2068 is therefore inhibition of Protocadherin Alpha 9 (PCDHA9, Accession NM_014005), a gene which is a calcium-dependent cell-adhesion protein. Accordingly, utilities of VGAM2068 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA9. The function of PCDHA9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM71.Prostaglandin-endoperoxide Synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1, Accession NM_080591) is another VGAM2068 host target gene. PTGS1 BINDING SITE1 and PTGS1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTGS1, corresponding to HOST TAR-

GET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTGS1 BINDING SITE1 and PTGS1 BINDING SITE2, designated SEQ ID:27898 and SEQ ID:6677 respectively, to the nucleotide sequence of VGAM2068 RNA, herein designated VGAM RNA, also designated SEQ ID:4779.

[72317] Another function of VGAM2068 is therefore inhibition of Prostaglandin-endoperoxide Synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1, Accession NM_080591), a gene which may play an important role in regulating or promoting cell proliferation in some normal and neoplastically transformed cells. Accordingly, utilities of VGAM2068 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGS1. The function of PTGS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1224.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2069 (VGAM2069) viral gene, which modulates expression of respective host tar-

get genes thereof, the function and utility of which host target genes is known in the art.

[72318] VGAM2069 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2069 was detected is described hereinabove with reference to Figs. 1-8.

[72319] VGAM2069 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2069 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72320] VGAM2069 gene encodes a VGAM2069 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2069 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2069 precursor RNA is designated SEQ ID:2055, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2055 is located at position 20862 relative to the genome of Monkeypox Virus.

[72321] VGAM2069 precursor RNA folds onto itself, forming VGAM2069 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72322] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2069 folded precursor RNA into VGAM2069 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2069 RNA is designated SEQ ID:4780, and is provided hereinbelow with reference to the sequence listing part.

[72323] VGAM2069 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2069 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2069 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72324] VGAM2069 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2069 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2069 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2069 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2069 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72325] The complementary binding of VGAM2069 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2069 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2069 host target RNA into VGAM2069 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72326] It is appreciated that VGAM2069 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2069 host target genes. The mRNA of each one of this plurality of VGAM2069 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2069 RNA, herein designated VGAM RNA, and which when bound by VGAM2069 RNA causes inhibition of translation of respective one or more VGAM2069 host target proteins.

[72327] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2069 gene, herein designated VGAM GENE, on one or more VGAM2069 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72328] It is yet further appreciated that a function of VGAM2069 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2069 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2069 correlate with, and may be deduced from, the identity of the host target genes which VGAM2069 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[72329] Nucleotide sequences of the VGAM2069 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2069 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2069 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2069 are further described hereinbelow with reference to Table 1.

[72330] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2069 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2069 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72331] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2069 gene, herein designated VGAM is inhibition of expression of VGAM2069 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2069 correlate with, and may be deduced from, the identity of the target genes which VGAM2069 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72332] ATP-binding Cassette, Sub-family B (MDR/TAP), Member 10 (ABCB10, Accession NM_012089) is a VGAM2069 host target gene. ABCB10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCB10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCB10 BINDING SITE, designated SEQ ID:14375, to the nucleotide sequence of VGAM2069 RNA, herein designated VGAM RNA, also designated SEQ ID:4780.

[72333] A function of VGAM2069 is therefore inhibition of ATP-binding Cassette, Sub-family B (MDR/TAP), Member 10 (ABCB10, Accession NM_012089), a gene which a member of the superfamily of ATP-binding cassette (ABC) transporters. Accordingly, utilities of VGAM2069 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCB10. The function of ABCB10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1523.Component of Oligomeric Golgi Complex 3 (COG3, Accession NM_031431) is another VGAM2069 host

target gene. COG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COG3 BINDING SITE, designated SEQ ID:25425, to the nucleotide sequence of VGAM2069 RNA, herein designated VGAM RNA, also designated SEQ ID:4780.

[72334] Another function of VGAM2069 is therefore inhibition of Component of Oligomeric Golgi Complex 3 (COG3, Accession NM_031431), a gene which is critical for the structure and function of the Golgi apparatus. Accordingly, utilities of VGAM2069 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COG3. The function of COG3 has been established by previous studies. Multiprotein complexes are key determinants of Golgi apparatus structure and its capacity for intracellular transport and glycoprotein modification. Several complexes have been identified, including the Golgi transport complex (GTC), the LDLC complex, which is involved in glycosylation reactions, and the SEC34 complex, which is involved in vesicular transport. These 3 com-

plexes are identical and have been termed the conserved oligomeric Golgi (COG) complex, which includes COG3 (Ungar et al., 2002). By SDS-PAGE analysis of bovine brain cytosol, Ungar et al. (2002) identified the 8 subunits of the COG complex. Immunofluorescence microscopy demonstrated that COG1 (LDLB; 606973) colocalizes with COG7 (OMIM Ref. No. 606978), as well as with COG3 and COG5 (OMIM Ref. No. 606821), with a Golgi marker in a perinuclear distribution. Immunoprecipitation analysis showed that all COG subunits interact with COG2 (LDLC; 606974). Ungar et al. (2002) concluded that the COG complex is critical for the structure and function of the Golgi apparatus and can influence intracellular membrane trafficking

[72335] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[72336] Suvorova, E. S.; Kurten, R. C.; Lupashin, V. V. : Identification of a human orthologue of Sec34p as a component of the cis-Golgi vesicle tethering machinery. J. Biol. Chem. 276: 22810-22818, 2001. ; and

[72337] Ungar, D.; Oka, T.; Brittle, E. E.; Vasile, E.; Lupashin, V. V.; Chatterton, J. E.; Heuser, J. E.; Krieger, M.; Waters, M. G. :

Characterization of a mammalian Golgi-localized protein c.

[72338] Further studies establishing the function and utilities of COG3 are found in John Hopkins OMIM database record ID 606975, and in sited publications numbered 515 and 6340 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Dmx-like 1 (DMXL1, Accession NM_005509) is another VGAM2069 host target gene. DMXL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DMXL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DMXL1 BINDING SITE, designated SEQ ID:12022, to the nucleotide sequence of VGAM2069 RNA, herein designated VGAM RNA, also designated SEQ ID:4780.

[72339] Another function of VGAM2069 is therefore inhibition of Dmx-like 1 (DMXL1, Accession NM_005509). Accordingly, utilities of VGAM2069 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMXL1. Growth Differentiation Factor 8 (GDF8, Accession NM_005259) is another VGAM2069 host target

gene. GDF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GDF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GDF8 BINDING SITE, designated SEQ ID:11763, to the nucleotide sequence of VGAM2069 RNA, herein designated VGAM RNA, also designated SEQ ID:4780.

[72340] Another function of VGAM2069 is therefore inhibition of Growth Differentiation Factor 8 (GDF8, Accession NM_005259), a gene which acts specifically as a negative regulator of skeletal muscle growth. Accordingly, utilities of VGAM2069 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GDF8. The function of GDF8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM386.Alpha 1,4-galactosyltransferase (A4GALT, Accession NM_017436) is another VGAM2069 host target gene. A4GALT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by A4GALT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of A4GALT BINDING SITE, designated SEQ ID:18893, to the nucleotide sequence of VGAM2069 RNA, herein designated VGAM RNA, also designated SEQ ID:4780.

[72341] Another function of VGAM2069 is therefore inhibition of Alpha 1,4-galactosyltransferase (A4GALT, Accession NM_017436). Accordingly, utilities of VGAM2069 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A4GALT. KIAA1317 (Accession XM_098368) is another VGAM2069 host target gene. KIAA1317 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1317, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1317 BINDING SITE, designated SEQ ID:41623, to the nucleotide sequence of VGAM2069 RNA, herein designated VGAM RNA, also designated SEQ ID:4780.

[72342] Another function of VGAM2069 is therefore inhibition of KIAA1317 (Accession XM_098368). Accordingly, utilities of VGAM2069 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1317. LOC114932 (Accession XM_052614) is another VGAM2069 host target gene. LOC114932 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC114932, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC114932 BINDING SITE, designated SEQ ID:36003, to the nucleotide sequence of VGAM2069 RNA, herein designated VGAM RNA, also designated SEQ ID:4780.

[72343] Another function of VGAM2069 is therefore inhibition of LOC114932 (Accession XM_052614). Accordingly, utilities of VGAM2069 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC114932. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2070 (VGAM2070) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72344] VGAM2070 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2070 was detected is described hereinabove with reference to Figs. 1-8.

[72345] VGAM2070 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2070 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72346] VGAM2070 gene encodes a VGAM2070 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2070 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2070 precursor RNA is designated SEQ ID:2056, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2056 is located at position 20302 relative to the genome of Monkeypox Virus.

[72347] VGAM2070 precursor RNA folds onto itself, forming VGAM2070 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72348] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2070 folded precursor RNA into VGAM2070 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2070 RNA is designated SEQ ID:4781, and is provided hereinbelow with reference to the sequence listing part.

[72349] VGAM2070 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2070 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2070 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72350] VGAM2070 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2070 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2070 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2070 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2070 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72351] The complementary binding of VGAM2070 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2070 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2070 host target RNA into VGAM2070 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72352] It is appreciated that VGAM2070 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2070 host target genes. The mRNA of each one of this plurality of VGAM2070 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2070 RNA, herein designated VGAM RNA, and which when bound by VGAM2070 RNA causes inhibition of translation of respective one or more VGAM2070 host target proteins.

[72353] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2070 gene, herein designated VGAM GENE, on one or more VGAM2070 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72354] It is yet further appreciated that a function of VGAM2070 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2070 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2070 correlate with, and may be deduced from, the identity of the host target genes which VGAM2070 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72355] Nucleotide sequences of the VGAM2070 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2070 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2070 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2070 are further described hereinbelow with reference to Table 1.

[72356] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2070 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2070 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72357] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2070 gene, herein designated VGAM is inhibition of expression of VGAM2070 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2070 correlate with, and may be deduced from, the identity of the target genes which VGAM2070 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72358] Lipoprotein Lipase (LPL, Accession NM_000237) is a VGAM2070 host target gene. LPL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by LPL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LPL BINDING SITE, designated SEQ ID:5751, to the nucleotide sequence of VGAM2070 RNA, herein designated VGAM RNA, also designated SEQ ID:4781.

[72359] A function of VGAM2070 is therefore inhibition of Lipoprotein Lipase (LPL, Accession NM_000237), a gene which is the hydrolysis of triglycerides of circulating chylomicrons and very low density lipoproteins (vldl). the enzyme functions in the presence of apolipoprotein c-2 on the luminal surface of vascular. Accordingly, utilities of VGAM2070 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPL. The function of LPL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.FLJ14624 (Accession XM_049060) is another VGAM2070 host target gene. FLJ14624 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14624, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14624 BINDING SITE, designated SEQ ID:35336, to the nucleotide sequence of VGAM2070 RNA, herein designated VGAM RNA, also designated SEQ ID:4781.

[72360] Another function of VGAM2070 is therefore inhibition of FLJ14624 (Accession XM_049060). Accordingly, utilities of VGAM2070 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14624. Glutamate Receptor, Ionotropic, Delta 1 (GRID1, Accession XM_043613) is another VGAM2070 host target gene. GRID1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRID1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRID1 BINDING SITE, designated SEQ ID:33981, to the nucleotide sequence of VGAM2070 RNA, herein designated VGAM RNA, also designated SEQ ID:4781.

[72361] Another function of VGAM2070 is therefore inhibition of Glutamate Receptor, Ionotropic, Delta 1 (GRID1, Accession XM_043613). Accordingly, utilities of VGAM2070 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with GRID1. KIAA1336 (Accession XM_051306) is another VGAM2070 host target gene. KIAA1336 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1336, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1336 BINDING SITE, designated SEQ ID:35803, to the nucleotide sequence of VGAM2070 RNA, herein designated VGAM RNA, also designated SEQ ID:4781.

[72362] Another function of VGAM2070 is therefore inhibition of KIAA1336 (Accession XM_051306). Accordingly, utilities of VGAM2070 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1336. STRIN (Accession NM_016271) is another VGAM2070 host target gene. STRIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STRIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STRIN BINDING SITE,

designated SEQ ID:18397, to the nucleotide sequence of VGAM2070 RNA, herein designated VGAM RNA, also designated SEQ ID:4781.

[72363] Another function of VGAM2070 is therefore inhibition of STRIN (Accession NM_016271). Accordingly, utilities of VGAM2070 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STRIN. LOC158314 (Accession XM_098920) is another VGAM2070 host target gene. LOC158314 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158314, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158314 BINDING SITE, designated SEQ ID:41953, to the nucleotide sequence of VGAM2070 RNA, herein designated VGAM RNA, also designated SEQ ID:4781.

[72364] Another function of VGAM2070 is therefore inhibition of LOC158314 (Accession XM_098920). Accordingly, utilities of VGAM2070 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158314. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2071 (VGAM2071) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72365] VGAM2071 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2071 was detected is described hereinabove with reference to Figs. 1-8.

[72366] VGAM2071 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2071 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72367] VGAM2071 gene encodes a VGAM2071 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2071 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2071 precursor RNA is designated SEQ ID:2057, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2057 is located at position 28091 relative to the genome of Monkeypox Virus.

[72368] VGAM2071 precursor RNA folds onto itself, forming VGAM2071 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72369] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2071 folded precursor RNA into VGAM2071 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM2071 RNA is designated SEQ ID:4782, and is provided hereinbelow with reference to the sequence listing part.

[72370] VGAM2071 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2071 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2071 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[72371] VGAM2071 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2071 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2071 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2071 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2071 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72372] The complementary binding of VGAM2071 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2071 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2071 host target RNA into VGAM2071 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72373] It is appreciated that VGAM2071 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2071 host target genes. The mRNA of each one of this plurality of VGAM2071 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2071 RNA, herein designated VGAM RNA, and which when bound by VGAM2071 RNA causes inhibition of translation of respective one or more VGAM2071 host target proteins.

[72374] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2071 gene, herein designated VGAM GENE, on one or more VGAM2071 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72375] It is yet further appreciated that a function of VGAM2071 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2071 correlate with, and may be deduced from, the identity of the host target genes which VGAM2071 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72376] Nucleotide sequences of the VGAM2071 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2071 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2071 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2071 are further described hereinbelow with reference to Table 1.

[72377] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2071 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2071 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72378] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2071 gene, herein designated VGAM is inhibition of expression of VGAM2071 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2071 correlate with, and may be deduced from, the identity of the target genes which VGAM2071 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72379] Adenosine Deaminase, RNA-specific (ADAR, Accession NM_001111) is a VGAM2071 host target gene. ADAR

BINDING SITE1 through ADAR BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ADAR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAR BINDING SITE1 through ADAR BINDING SITE3, designated SEQ ID:6771, SEQ ID:17957 and SEQ ID:17964 respectively, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72380] A function of VGAM2071 is therefore inhibition of Adenosine Deaminase, RNA-specific (ADAR, Accession NM_001111), a gene which converts adenosine to inosine in double-stranded RNA. Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAR. The function of ADAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM323.Endometrial Bleeding Associated Factor (left-right determination, factor A; transforming growth factor beta superfamily) (EBAF, Accession XM_037302) is another VGAM2071 host target gene. EBAF BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EBAF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EBAF BINDING SITE, designated SEQ ID:32606, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72381] Another function of VGAM2071 is therefore inhibition of Endometrial Bleeding Associated Factor (left-right determination, factor A; transforming growth factor beta superfamily) (EBAF, Accession XM_037302), a gene which LEFT-RIGHT AXIS MALFORMATIONS. Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EBAF. The function of EBAF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM93.Gap Junction Protein, Beta 1, 32kDa (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked) (GJB1, Accession XM_010141) is another VGAM2071 host target gene. GJB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by GJB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GJB1 BINDING SITE, designated SEQ ID:30129, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72382] Another function of VGAM2071 is therefore inhibition of Gap Junction Protein, Beta 1, 32kDa (connexin 32, Charcot-Marie-Tooth neuropathy, X-linked) (GJB1, Accession XM_010141). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GJB1. Hippocalcin-like 1 (HPCAL1, Accession NM_134421) is another VGAM2071 host target gene. HPCAL1 BINDING SITE1 and HPCAL1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HPCAL1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HPCAL1 BINDING SITE1 and HPCAL1 BINDING SITE2, designated SEQ ID:28637 and SEQ ID:7930 respectively, to the nucleotide sequence of VGAM2071 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4782.

[72383] Another function of VGAM2071 is therefore inhibition of Hippocalcin-like 1 (HPCAL1, Accession NM_134421). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HPCAL1. Interleukin 2 Receptor, Alpha (IL2RA, Accession NM_000417) is another VGAM2071 host target gene. IL2RA BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IL2RA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL2RA BINDING SITE, designated SEQ ID:5999, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72384] Another function of VGAM2071 is therefore inhibition of Interleukin 2 Receptor, Alpha (IL2RA, Accession NM_000417), a gene which plays a role in T cell mediated immune response. Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL2RA. The function of IL2RA and its association with various diseases and clini-

cal conditions, has been established by previous studies, as described hereinabove with reference to VGAM1168.Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog (mouse) (MEIS1, Accession NM_002398) is another VGAM2071 host target gene. MEIS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEIS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEIS1 BINDING SITE, designated SEQ ID:8217, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72385] Another function of VGAM2071 is therefore inhibition of Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog (mouse) (MEIS1, Accession NM_002398), a gene which may regulate gene expression and control cell differentiation. Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEIS1. The function of MEIS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM894.NPR2L

(Accession NM_006545) is another VGAM2071 host target gene. NPR2L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NPR2L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPR2L BINDING SITE, designated SEQ ID:13299, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72386] Another function of VGAM2071 is therefore inhibition of NPR2L (Accession NM_006545). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPR2L. Poliovirus Receptor (PVR, Accession NM_006505) is another VGAM2071 host target gene. PVR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PVR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PVR BINDING SITE, designated SEQ ID:13254, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA,

also designated SEQ ID:4782.

[72387] Another function of VGAM2071 is therefore inhibition of Poliovirus Receptor (PVR, Accession NM_006505), a gene which is a poliovirus receptor. Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PVR. The function of PVR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1411.Tight Junction Protein 1 (zona occludens 1) (TJP1, Accession NM_003257) is another VGAM2071 host target gene. TJP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TJP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TJP1 BINDING SITE, designated SEQ ID:9262, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72388] Another function of VGAM2071 is therefore inhibition of Tight Junction Protein 1 (zona occludens 1) (TJP1, Accession NM_003257), a gene which colocalizes and interacts with cadherins in cells lacking tight junctions. Accord-

ingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TJP1. The function of TJP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM95.Chromosome X Open Reading Frame 1 (CXorf1, Accession NM_004709) is another VGAM2071 host target gene. CXorf1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CXorf1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CXorf1 BINDING SITE, designated SEQ ID:11054, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72389] Another function of VGAM2071 is therefore inhibition of Chromosome X Open Reading Frame 1 (CXorf1, Accession NM_004709). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXorf1. DKFZP434K1772 (Accession XM_041936) is another VGAM2071 host target gene. DKFZP434K1772 BINDING SITE is HOST TARGET

binding site found in the 5` untranslated region of mRNA encoded by DKFZP434K1772, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434K1772 BINDING SITE, designated SEQ ID:33629, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72390] Another function of VGAM2071 is therefore inhibition of DKFZP434K1772 (Accession XM_041936). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434K1772. DKFZp547D155 (Accession XM_046977) is another VGAM2071 host target gene. DKFZp547D155 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp547D155, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547D155 BINDING SITE, designated SEQ ID:34867, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72391] Another function of VGAM2071 is therefore inhibition of DKFZp547D155 (Accession XM_046977). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547D155. FLJ12242 (Accession NM_024681) is another VGAM2071 host target gene. FLJ12242 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12242, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12242 BINDING SITE, designated SEQ ID:23994, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72392] Another function of VGAM2071 is therefore inhibition of FLJ12242 (Accession NM_024681). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12242. FLJ12387 (Accession NM_022822) is another VGAM2071 host target gene. FLJ12387 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12387, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12387 BINDING SITE, designated SEQ ID:23100, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72393] Another function of VGAM2071 is therefore inhibition of FLJ12387 (Accession NM_022822). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12387. FLJ12975 (Accession XM_045522) is another VGAM2071 host target gene. FLJ12975 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12975, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12975 BINDING SITE, designated SEQ ID:34479, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72394] Another function of VGAM2071 is therefore inhibition of FLJ12975 (Accession XM_045522). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ12975. KIAA0155 (Accession NM_014633) is another VGAM2071 host target gene. KIAA0155 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0155, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0155 BINDING SITE, designated SEQ ID:16002, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72395] Another function of VGAM2071 is therefore inhibition of KIAA0155 (Accession NM_014633). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0155. KIAA1649 (Accession NM_032311) is another VGAM2071 host target gene. KIAA1649 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1649, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1649 BINDING SITE, designated SEQ ID:26104, to the nucleotide sequence of VGAM2071 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4782.

[72396] Another function of VGAM2071 is therefore inhibition of KIAA1649 (Accession NM_032311). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1649. PRO0899 (Accession NM_018565) is another VGAM2071 host target gene. PRO0899 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0899, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0899 BINDING SITE, designated SEQ ID:20648, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72397] Another function of VGAM2071 is therefore inhibition of PRO0899 (Accession NM_018565). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0899. Translocation Protein 1 (TLOC1, Accession NM_003262) is another VGAM2071 host target gene. TLOC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

TLOC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TLOC1 BINDING SITE, designated SEQ ID:9272, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72398] Another function of VGAM2071 is therefore inhibition of Translocation Protein 1 (TLOC1, Accession NM_003262). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLOC1. LOC151877 (Accession XM_098132) is another VGAM2071 host target gene. LOC151877 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151877, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151877 BINDING SITE, designated SEQ ID:41394, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72399] Another function of VGAM2071 is therefore inhibition of

LOC151877 (Accession XM_098132). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151877. LOC152179 (Accession XM_098170) is another VGAM2071 host target gene. LOC152179 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152179, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152179 BINDING SITE, designated SEQ ID:41432, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72400] Another function of VGAM2071 is therefore inhibition of LOC152179 (Accession XM_098170). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152179. LOC164714 (Accession XM_104657) is another VGAM2071 host target gene. LOC164714 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC164714, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC164714 BINDING SITE, designated SEQ ID:42176, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72401] Another function of VGAM2071 is therefore inhibition of LOC164714 (Accession XM_104657). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164714. LOC253783 (Accession XM_170873) is another VGAM2071 host target gene. LOC253783 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253783, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253783 BINDING SITE, designated SEQ ID:45641, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72402] Another function of VGAM2071 is therefore inhibition of LOC253783 (Accession XM_170873). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253783. LOC93166 (Accession XM_049619) is an-

other VGAM2071 host target gene. LOC93166 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93166, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93166 BINDING SITE, designated SEQ ID:35460, to the nucleotide sequence of VGAM2071 RNA, herein designated VGAM RNA, also designated SEQ ID:4782.

[72403] Another function of VGAM2071 is therefore inhibition of LOC93166 (Accession XM_049619). Accordingly, utilities of VGAM2071 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93166. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2072 (VGAM2072) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72404] VGAM2072 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2072 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[72405] VGAM2072 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2072 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72406] VGAM2072 gene encodes a VGAM2072 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2072 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2072 precursor RNA is designated SEQ ID:2058, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2058 is located at position 23821 relative to the genome of Ectromelia Virus.

[72407] VGAM2072 precursor RNA folds onto itself, forming VGAM2072 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72408] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2072 folded precursor RNA into VGAM2072 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM2072 RNA is designated SEQ ID:4783, and is provided hereinbelow with reference to the sequence listing part.

[72409] VGAM2072 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2072 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2072 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72410] VGAM2072 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2072 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2072 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2072 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2072 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72411] The complementary binding of VGAM2072 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2072 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2072 host target RNA into VGAM2072 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72412] It is appreciated that VGAM2072 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2072 host target genes. The mRNA of each one of this plurality of VGAM2072 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2072 RNA, herein designated VGAM RNA, and which when bound by VGAM2072 RNA causes inhibition of translation of respective one or more VGAM2072 host target proteins.

[72413] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2072 gene, herein designated VGAM GENE, on one or more VGAM2072 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72414] It is yet further appreciated that a function of VGAM2072 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2072 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2072 correlate with, and may be deduced from, the identity of the host target genes which VGAM2072 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72415] Nucleotide sequences of the VGAM2072 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2072 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2072 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2072 are further described hereinbelow with reference to Table 1.

[72416] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2072 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2072 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72417] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2072 gene, herein designated VGAM is inhibition of expression of VGAM2072 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2072 correlate with, and may be deduced from, the identity of the target genes which VGAM2072 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72418] Collagen, Type XVII, Alpha 1 (COL17A1, Accession NM_000494) is a VGAM2072 host target gene. COL17A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL17A1, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL17A1 BINDING SITE, designated SEQ ID:6106, to the nucleotide sequence of VGAM2072 RNA, herein designated VGAM RNA, also designated SEQ ID:4783.

[72419] A function of VGAM2072 is therefore inhibition of Collagen, Type XVII, Alpha 1 (COL17A1, Accession NM_000494). Accordingly, utilities of VGAM2072 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL17A1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2073 (VGAM2073) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72420] VGAM2073 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2073 was detected is described hereinabove with reference to Figs. 1-8.

[72421] VGAM2073 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus.

VGAM2073 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72422] VGAM2073 gene encodes a VGAM2073 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2073 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2073 precursor RNA is designated SEQ ID:2059, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2059 is located at position 16020 relative to the genome of Monkeypox Virus.

[72423] VGAM2073 precursor RNA folds onto itself, forming VGAM2073 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72424] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2073 folded precursor RNA into VGAM2073 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2073 RNA is designated SEQ ID:4784, and is provided hereinbelow with reference to the sequence listing part.

[72425] VGAM2073 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2073 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2073 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72426] VGAM2073 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2073 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2073 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2073 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2073 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72427] The complementary binding of VGAM2073 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2073 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2073 host target RNA into VGAM2073 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72428] It is appreciated that VGAM2073 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2073 host target genes. The mRNA of each one of this plurality of VGAM2073 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2073 RNA, herein designated VGAM RNA, and which when bound by VGAM2073 RNA causes inhibition of translation of respective one or more VGAM2073 host target proteins.

[72429] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2073 gene, herein designated VGAM GENE, on one or more VGAM2073 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72430] It is yet further appreciated that a function of VGAM2073 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2073 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2073 correlate with, and may be deduced from, the identity of the host target genes which VGAM2073 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72431] Nucleotide sequences of the VGAM2073 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2073 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2073 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2073 are further described hereinbelow with reference to Table 1.

[72432] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2073 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2073 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72433] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2073 gene, herein designated VGAM is inhibition of expression of VGAM2073 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2073 correlate with, and may be deduced from, the identity of the target genes which VGAM2073 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72434] Chromosome 20 Open Reading Frame 98 (C20orf98, Accession XM_049398) is a VGAM2073 host target gene. C20orf98 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf98, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf98 BINDING SITE, designated SEQ

ID:35415, to the nucleotide sequence of VGAM2073 RNA, herein designated VGAM RNA, also designated SEQ ID:4784.

[72435] A function of VGAM2073 is therefore inhibition of Chromosome 20 Open Reading Frame 98 (C20orf98, Accession XM_049398). Accordingly, utilities of VGAM2073 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf98. Potassium Channel, Subfamily V, Member 1 (KCNV1, Accession NM_014379) is another VGAM2073 host target gene. KCNV1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNV1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNV1 BINDING SITE, designated SEQ ID:15710, to the nucleotide sequence of VGAM2073 RNA, herein designated VGAM RNA, also designated SEQ ID:4784.

[72436] Another function of VGAM2073 is therefore inhibition of Potassium Channel, Subfamily V, Member 1 (KCNV1, Accession NM_014379). Accordingly, utilities of VGAM2073 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with KCNV1. KIAA0087 (Accession NM_014769) is another VGAM2073 host target gene. KIAA0087 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0087, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0087 BINDING SITE, designated SEQ ID:16562, to the nucleotide sequence of VGAM2073 RNA, herein designated VGAM RNA, also designated SEQ ID:4784.

[72437] Another function of VGAM2073 is therefore inhibition of KIAA0087 (Accession NM_014769). Accordingly, utilities of VGAM2073 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0087. KIAA1877 (Accession XM_038616) is another VGAM2073 host target gene. KIAA1877 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1877, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1877 BINDING SITE, designated SEQ ID:32879, to the

nucleotide sequence of VGAM2073 RNA, herein designated VGAM RNA, also designated SEQ ID:4784.

[72438] Another function of VGAM2073 is therefore inhibition of KIAA1877 (Accession XM_038616). Accordingly, utilities of VGAM2073 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1877. MGC4643 (Accession NM_032715) is another VGAM2073 host target gene. MGC4643 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4643, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4643 BINDING SITE, designated SEQ ID:26441, to the nucleotide sequence of VGAM2073 RNA, herein designated VGAM RNA, also designated SEQ ID:4784.

[72439] Another function of VGAM2073 is therefore inhibition of MGC4643 (Accession NM_032715). Accordingly, utilities of VGAM2073 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4643. LOC219818 (Accession XM_165589) is another VGAM2073 host target gene. LOC219818 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC219818, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219818 BINDING SITE, designated SEQ ID:43698, to the nucleotide sequence of VGAM2073 RNA, herein designated VGAM RNA, also designated SEQ ID:4784.

[72440] Another function of VGAM2073 is therefore inhibition of LOC219818 (Accession XM_165589). Accordingly, utilities of VGAM2073 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219818. LOC254219 (Accession XM_172913) is another VGAM2073 host target gene. LOC254219 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254219 BINDING SITE, designated SEQ ID:46173, to the nucleotide sequence of VGAM2073 RNA, herein designated VGAM RNA, also designated SEQ ID:4784.

[72441] Another function of VGAM2073 is therefore inhibition of LOC254219 (Accession XM_172913). Accordingly, utilities

of VGAM2073 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254219. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2074 (VGAM2074) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72442] VGAM2074 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2074 was detected is described hereinabove with reference to Figs. 1-8.

[72443] VGAM2074 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2074 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72444] VGAM2074 gene encodes a VGAM2074 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2074 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2074 precursor RNA is designated SEQ ID:2060, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2060 is located at position 25479 relative to the genome of Monkeypox Virus.

[72445] VGAM2074 precursor RNA folds onto itself, forming VGAM2074 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72446] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2074 folded precursor RNA into VGAM2074 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2074 RNA is designated SEQ ID:4785, and

is provided hereinbelow with reference to the sequence listing part.

[72447] VGAM2074 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2074 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2074 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72448] VGAM2074 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2074 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2074 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2074 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2074 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72449] The complementary binding of VGAM2074 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2074 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2074 host target RNA into VGAM2074 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72450] It is appreciated that VGAM2074 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2074 host target genes. The mRNA of each one of this plurality of VGAM2074 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2074 RNA, herein designated VGAM RNA, and which when bound by VGAM2074 RNA causes inhibition of translation of respective one or more VGAM2074 host target proteins.

[72451] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2074 gene, herein designated VGAM GENE, on one or more VGAM2074 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72452] It is yet further appreciated that a function of VGAM2074 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2074 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2074 correlate with, and may be deduced from, the identity of the host target genes which VGAM2074 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72453] Nucleotide sequences of the VGAM2074 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2074 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2074 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2074 are further described hereinbelow with reference to Table 1.

[72454] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2074 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2074 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72455] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2074 gene, herein designated VGAM is inhibition of expression of VGAM2074 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2074 correlate with, and may be deduced from, the identity of the target genes which VGAM2074 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72456] FLJ22405 (Accession NM_022485) is a VGAM2074 host target gene. FLJ22405 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22405, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22405 BINDING SITE, designated SEQ ID:22864, to the nucleotide sequence of VGAM2074 RNA, herein designated VGAM RNA, also designated SEQ ID:4785.

[72457] A function of VGAM2074 is therefore inhibition of FLJ22405 (Accession NM_022485). Accordingly, utilities of VGAM2074 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22405. KIAA1143 (Accession XM_044014) is another VGAM2074 host target gene. KIAA1143 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1143, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1143 BINDING SITE, designated SEQ ID:34078, to the nucleotide sequence of VGAM2074 RNA, herein designated VGAM RNA, also designated SEQ ID:4785.

[72458] Another function of VGAM2074 is therefore inhibition of KIAA1143 (Accession XM_044014). Accordingly, utilities of VGAM2074 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1143. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2075 (VGAM2075) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72459] VGAM2075 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2075 was detected is described hereinabove with reference to Figs. 1-8.

[72460] VGAM2075 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola Virus. VGAM2075 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72461] VGAM2075 gene encodes a VGAM2075 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2075 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2075 precursor RNA is designated SEQ ID:2061, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2061 is located at position 177494 relative to the genome of Variola Virus.

[72462] VGAM2075 precursor RNA folds onto itself, forming VGAM2075 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[72463] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2075 folded precursor RNA into VGAM2075 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2075 RNA is designated SEQ ID:4786, and is provided hereinbelow with reference to the sequence listing part.

[72464] VGAM2075 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2075 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2075 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72465] VGAM2075 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2075 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2075 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2075 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2075 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72466] The complementary binding of VGAM2075 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2075 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2075 host target RNA into VGAM2075 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72467] It is appreciated that VGAM2075 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2075 host target genes. The mRNA of each one of this plurality of VGAM2075 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2075 RNA, herein designated VGAM RNA, and which when bound by VGAM2075 RNA causes inhibition of translation of respective one or more VGAM2075 host target proteins.

[72468] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2075 gene, herein designated VGAM GENE, on one or more VGAM2075 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72469] It is yet further appreciated that a function of VGAM2075 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGAM2075 correlate with, and may be deduced from, the identity of the host target genes which VGAM2075 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72470] Nucleotide sequences of the VGAM2075 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2075 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2075 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2075 are further described hereinbelow with reference to Table 1.

[72471] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2075 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2075 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72472] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2075 gene, herein designated VGAM is inhibition of expression of VGAM2075 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2075 correlate with, and may be deduced from, the identity of the target genes which VGAM2075 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72473] Estrogen-related Receptor Gamma (ESRRG, Accession XM_039053) is a VGAM2075 host target gene. ESRRG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ESRRG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of ESRRG BINDING SITE, designated SEQ ID:32999, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72474] A function of VGAM2075 is therefore inhibition of Estrogen-related Receptor Gamma (ESRRG, Accession XM_039053), a gene which Estrogen-related receptor gamma. Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESRRG. The function of ESRRG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM359.Integrin, Alpha L (antigen CD11A (p180), Lymphocyte Function-associated Antigen 1; Alpha Polypeptide) (ITGAL, Accession NM_002209) is another VGAM2075 host target gene. ITGAL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGAL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGAL BINDING SITE, designated SEQ ID:7972, to the nucleotide sequence of VGAM2075 RNA, herein

designated VGAM RNA, also designated SEQ ID:4786.

[72475] Another function of VGAM2075 is therefore inhibition of Integrin, Alpha L (antigen CD11A (p180), Lymphocyte Function-associated Antigen 1; Alpha Polypeptide) (ITGAL, Accession NM_002209), a gene which s a receptor for icam1, icam2, icam3 and icam4. it is involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, cytotoxic t-cell mediated killing, and antibody dependent killing by granulocytes and monocytes. Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAL. The function of ITGAL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Nuclear Fragile X Mental Retardation Protein Interacting Protein 1 (NUFIP1, Accession NM_012345) is another VGAM2075 host target gene. NUFIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUFIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUFIP1 BINDING SITE, designated SEQ

ID:14737, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72476] Another function of VGAM2075 is therefore inhibition of Nuclear Fragile X Mental Retardation Protein Interacting Protein 1 (NUFIP1, Accession NM_012345), a gene which binds and colocalizes with nuclear fragile X mental retardation protein. Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUFIP1. The function of NUFIP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM733.POU Domain, Class 2, Associating Factor 1 (POU2AF1, Accession NM_006235) is another VGAM2075 host target gene. POU2AF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POU2AF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POU2AF1 BINDING SITE, designated SEQ ID:12892, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ

ID:4786.

[72477] Another function of VGAM2075 is therefore inhibition of POU Domain, Class 2, Associating Factor 1 (POU2AF1, Accession NM_006235), a gene which is a transcriptional coactivator that specifically associates with either oct1 or oct2. Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU2AF1. The function of POU2AF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM171.Recombination Activating Gene 2 (RAG2, Accession XM_089839) is another VGAM2075 host target gene. RAG2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAG2 BINDING SITE, designated SEQ ID:39985, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72478] Another function of VGAM2075 is therefore inhibition of Recombination Activating Gene 2 (RAG2, Accession

XM_089839). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAG2. Tensin (TNS, Accession NM_022648) is another VGAM2075 host target gene. TNS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNS BINDING SITE, designated SEQ ID:22903, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72479] Another function of VGAM2075 is therefore inhibition of Tensin (TNS, Accession NM_022648). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNS. DKFZP434I092 (Accession XM_042042) is another VGAM2075 host target gene. DKFZP434I092 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434I092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DK-

FZP434I092 BINDING SITE, designated SEQ ID:33673, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72480] Another function of VGAM2075 is therefore inhibition of DKFZP434I092 (Accession XM_042042). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434I092. FLJ10656 (Accession NM_018170) is another VGAM2075 host target gene. FLJ10656 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10656, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10656 BINDING SITE, designated SEQ ID:19988, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72481] Another function of VGAM2075 is therefore inhibition of FLJ10656 (Accession NM_018170). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10656. GABA(A) Receptor-associated Protein Like 1 (GABARAPL1, Accession NM_031412) is another

VGAM2075 host target gene. GABARAPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABARAPL1 BINDING SITE, designated SEQ ID:25392, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72482] Another function of VGAM2075 is therefore inhibition of GABA(A) Receptor-associated Protein Like 1 (GABARAPL1, Accession NM_031412). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL1. GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568) is another VGAM2075 host target gene. GABARAPL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABARAPL3 BINDING SITE, designated SEQ ID:26300, to

the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72483] Another function of VGAM2075 is therefore inhibition of GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL3. HT002 (Accession NM_014066) is another VGAM2075 host target gene. HT002 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HT002, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HT002 BINDING SITE, designated SEQ ID:15281, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72484] Another function of VGAM2075 is therefore inhibition of HT002 (Accession NM_014066). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HT002. KIAA0475 (Accession NM_014864) is another VGAM2075 host target gene. KIAA0475 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:16949, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72485] Another function of VGAM2075 is therefore inhibition of KIAA0475 (Accession NM_014864). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0475. KIAA0712 (Accession NM_014715) is another VGAM2075 host target gene. KIAA0712 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0712, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0712 BINDING SITE, designated SEQ ID:16262, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72486] Another function of VGAM2075 is therefore inhibition of

KIAA0712 (Accession NM_014715). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0712. KIAA1301 (Accession XM_038999) is another VGAM2075 host target gene. KIAA1301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1301 BINDING SITE, designated SEQ ID:32978, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72487] Another function of VGAM2075 is therefore inhibition of KIAA1301 (Accession XM_038999). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1301. Seizure Related 6 Homolog (mouse) (SEZ6, Accession XM_058869) is another VGAM2075 host target gene. SEZ6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEZ6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Ta-

ble 2 illustrates the complementarity of the nucleotide sequences of SEZ6 BINDING SITE, designated SEQ ID:36774, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72488] Another function of VGAM2075 is therefore inhibition of Seizure Related 6 Homolog (mouse) (SEZ6, Accession XM_058869). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEZ6. VMP1 (Accession NM_030938) is another VGAM2075 host target gene. VMP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VMP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VMP1 BINDING SITE, designated SEQ ID:25204, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72489] Another function of VGAM2075 is therefore inhibition of VMP1 (Accession NM_030938). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VMP1. LOC115110 (Accession XM_049825) is another

VGAM2075 host target gene. LOC115110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115110 BINDING SITE, designated SEQ ID:35503, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72490] Another function of VGAM2075 is therefore inhibition of LOC115110 (Accession XM_049825). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115110. LOC132235 (Accession XM_072302) is another VGAM2075 host target gene. LOC132235 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC132235, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132235 BINDING SITE, designated SEQ ID:37483, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72491] Another function of VGAM2075 is therefore inhibition of LOC132235 (Accession XM_072302). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132235. LOC142941 (Accession XM_096363) is another VGAM2075 host target gene. LOC142941 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC142941, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC142941 BINDING SITE, designated SEQ ID:40322, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72492] Another function of VGAM2075 is therefore inhibition of LOC142941 (Accession XM_096363). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142941. LOC158549 (Accession XM_098963) is another VGAM2075 host target gene. LOC158549 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158549, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158549 BINDING SITE, designated SEQ ID:42007, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72493] Another function of VGAM2075 is therefore inhibition of LOC158549 (Accession XM_098963). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158549. LOC221882 (Accession XM_166507) is another VGAM2075 host target gene. LOC221882 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221882, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221882 BINDING SITE, designated SEQ ID:44434, to the nucleotide sequence of VGAM2075 RNA, herein designated VGAM RNA, also designated SEQ ID:4786.

[72494] Another function of VGAM2075 is therefore inhibition of LOC221882 (Accession XM_166507). Accordingly, utilities of VGAM2075 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC221882. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2076 (VGAM2076) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72495] VGAM2076 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2076 was detected is described hereinabove with reference to Figs. 1-8.

[72496] VGAM2076 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola Virus. VGAM2076 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72497] VGAM2076 gene encodes a VGAM2076 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2076 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2076 precursor RNA is designated SEQ ID:2062, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2062 is located at position 175023 relative to the genome of Variola Virus.

[72498] VGAM2076 precursor RNA folds onto itself, forming VGAM2076 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72499] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2076 folded precursor RNA into VGAM2076 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2076 RNA is designated SEQ ID:4787, and is provided hereinbelow with reference to the sequence listing part.

[72500] VGAM2076 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2076 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2076 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72501] VGAM2076 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2076 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2076 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2076 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2076 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72502] The complementary binding of VGAM2076 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2076 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2076 host target RNA into VGAM2076 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72503] It is appreciated that VGAM2076 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2076 host target genes. The mRNA of each one of this plurality of VGAM2076 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2076 RNA, herein designated VGAM RNA, and which when bound by VGAM2076 RNA causes

inhibition of translation of respective one or more VGAM2076 host target proteins.

[72504] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2076 gene, herein designated VGAM GENE, on one or more VGAM2076 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72505] It is yet further appreciated that a function of VGAM2076 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2076 include diagnosis, prevention and

treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGAM2076 correlate with, and may be deduced from, the identity of the host target genes which VGAM2076 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72506] Nucleotide sequences of the VGAM2076 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2076 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2076 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2076 are further described hereinbelow with reference to Table 1.

[72507] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2076 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2076 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72508] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2076 gene, herein designated VGAM is inhibition of expression of VGAM2076 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2076 correlate with, and may be deduced from, the identity of the target genes which VGAM2076 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72509] DKFZP434F2021 (Accession XM_039951) is a VGAM2076 host target gene. DKFZP434F2021 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434F2021, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434F2021 BINDING SITE, designated SEQ ID:33235, to the nucleotide sequence of VGAM2076 RNA, herein designated VGAM RNA, also designated SEQ ID:4787.

[72510] A function of VGAM2076 is therefore inhibition of DKFZP434F2021 (Accession XM_039951). Accordingly, utilities of VGAM2076 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F2021. PRO2435 (Accession NM_018527) is another VGAM2076 host target gene. PRO2435 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2435, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2435 BINDING SITE, designated SEQ ID:20601, to the nucleotide sequence of VGAM2076 RNA, herein designated VGAM RNA, also designated SEQ ID:4787.

[72511] Another function of VGAM2076 is therefore inhibition of PRO2435 (Accession NM_018527). Accordingly, utilities of VGAM2076 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2435. LOC220980 (Accession XM_167629) is another VGAM2076 host target gene. LOC220980 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220980, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220980 BINDING SITE, designated SEQ ID:44740, to the nucleotide sequence of VGAM2076 RNA, herein designated VGAM RNA, also designated SEQ ID:4787.

[72512] Another function of VGAM2076 is therefore inhibition of LOC220980 (Accession XM_167629). Accordingly, utilities of VGAM2076 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC220980. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2077 (VGAM2077) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72513] VGAM2077 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2077 was detected is described hereinabove with reference to Figs. 1-8.

[72514] VGAM2077 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola Virus. VGAM2077 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72515] VGAM2077 gene encodes a VGAM2077 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2077 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2077 precursor RNA is desig-

nated SEQ ID:2063, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2063 is located at position 178760 relative to the genome of Variola Virus.

[72516] VGAM2077 precursor RNA folds onto itself, forming VGAM2077 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72517] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2077 folded precursor RNA into VGAM2077 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2077 RNA is designated SEQ ID:4788, and is provided hereinbelow with reference to the sequence

listing part.

[72518] VGAM2077 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2077 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2077 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72519] VGAM2077 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2077 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2077 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2077 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2077 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72520] The complementary binding of VGAM2077 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2077 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2077 host target RNA into VGAM2077 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72521] It is appreciated that VGAM2077 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2077 host target genes. The mRNA of each one of this plurality of VGAM2077 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2077 RNA, herein designated VGAM

RNA, and which when bound by VGAM2077 RNA causes inhibition of translation of respective one or more VGAM2077 host target proteins.

[72522] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2077 gene, herein designated VGAM GENE, on one or more VGAM2077 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72523] It is yet further appreciated that a function of VGAM2077 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2077 include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGAM2077 correlate with, and may be deduced from, the identity of the host target genes which VGAM2077 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72524] Nucleotide sequences of the VGAM2077 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2077 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2077 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2077 are further described hereinbelow with reference to Table 1.

[72525] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2077 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2077 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72526] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2077 gene, herein designated VGAM is

inhibition of expression of VGAM2077 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2077 correlate with, and may be deduced from, the identity of the target genes which VGAM2077 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72527] KIAA1582 (Accession XM_037262) is a VGAM2077 host target gene. KIAA1582 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1582, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1582 BINDING SITE, designated SEQ ID:32583, to the nucleotide sequence of VGAM2077 RNA, herein designated VGAM RNA, also designated SEQ ID:4788.

[72528] A function of VGAM2077 is therefore inhibition of KIAA1582 (Accession XM_037262). Accordingly, utilities of VGAM2077 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1582. LOC148709 (Accession XM_086281) is another VGAM2077 host target gene. LOC148709 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC148709, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148709 BINDING SITE, designated SEQ ID:38584, to the nucleotide sequence of VGAM2077 RNA, herein designated VGAM RNA, also designated SEQ ID:4788.

[72529] Another function of VGAM2077 is therefore inhibition of LOC148709 (Accession XM_086281). Accordingly, utilities of VGAM2077 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148709. LOC57795 (Accession XM_045110) is another VGAM2077 host target gene. LOC57795 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57795, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57795 BINDING SITE, designated SEQ ID:34359, to the nucleotide sequence of VGAM2077 RNA, herein designated VGAM RNA, also designated SEQ ID:4788.

[72530] Another function of VGAM2077 is therefore inhibition of LOC57795 (Accession XM_045110). Accordingly, utilities

of VGAM2077 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57795. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2078 (VGAM2078) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72531] VGAM2078 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2078 was detected is described hereinabove with reference to Figs. 1-8.

[72532] VGAM2078 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola Virus. VGAM2078 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72533] VGAM2078 gene encodes a VGAM2078 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2078 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2078 precursor RNA is designated SEQ ID:2064, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2064 is located at position 168720 relative to the genome of Variola Virus.

[72534] VGAM2078 precursor RNA folds onto itself, forming VGAM2078 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72535] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2078 folded precursor RNA into VGAM2078 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2078 RNA is designated SEQ ID:4789, and

is provided hereinbelow with reference to the sequence listing part.

[72536] VGAM2078 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2078 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2078 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72537] VGAM2078 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2078 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2078 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2078 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2078 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72538] The complementary binding of VGAM2078 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2078 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2078 host target RNA into VGAM2078 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72539] It is appreciated that VGAM2078 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2078 host target genes. The mRNA of each one of this plurality of VGAM2078 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2078 RNA, herein designated VGAM RNA, and which when bound by VGAM2078 RNA causes inhibition of translation of respective one or more VGAM2078 host target proteins.

[72540] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2078 gene, herein designated VGAM GENE, on one or more VGAM2078 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72541] It is yet further appreciated that a function of VGAM2078 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2078 include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGAM2078 correlate with, and may be deduced from, the identity of the host target genes which VGAM2078 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72542] Nucleotide sequences of the VGAM2078 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2078 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2078 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2078 are further described hereinbelow with reference to Table 1.

[72543] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2078 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2078 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72544] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2078 gene, herein designated VGAM is inhibition of expression of VGAM2078 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2078 correlate with, and may be deduced from, the identity of the target genes which VGAM2078 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72545] Capping Protein (actin filament) Muscle Z-line, Alpha 1 (CAPZA1, Accession XM_052116) is a VGAM2078 host target gene. CAPZA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAPZA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAPZA1 BINDING SITE, designated SEQ ID:35947, to the nucleotide sequence of VGAM2078 RNA, herein designated VGAM RNA, also designated SEQ ID:4789.

[72546] A function of VGAM2078 is therefore inhibition of Capping Protein (actin filament) Muscle Z-line, Alpha 1 (CAPZA1, Accession XM_052116), a gene which is alpha 1 subunit of actin filament capping protein; binds actin, has roles in cell motility and actin assembly. Accordingly, util-

ities of VGAM2078 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPZA1. The function of CAPZA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM547.DKFZP586M1120 (Accession NM_031294) is another VGAM2078 host target gene. DKFZP586M1120 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP586M1120, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586M1120 BINDING SITE, designated SEQ ID:25325, to the nucleotide sequence of VGAM2078 RNA, herein designated VGAM RNA, also designated SEQ ID:4789.

[72547] Another function of VGAM2078 is therefore inhibition of DKFZP586M1120 (Accession NM_031294). Accordingly, utilities of VGAM2078 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586M1120. KIAA0555 (Accession XM_011347) is another VGAM2078 host target gene. KIAA0555 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by KIAA0555, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0555 BINDING SITE, designated SEQ ID:30188, to the nucleotide sequence of VGAM2078 RNA, herein designated VGAM RNA, also designated SEQ ID:4789.

[72548] Another function of VGAM2078 is therefore inhibition of KIAA0555 (Accession XM_011347). Accordingly, utilities of VGAM2078 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0555. Pellino Homolog 1 (Drosophila) (PELI1, Accession NM_020651) is another VGAM2078 host target gene. PELI1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PELI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PELI1 BINDING SITE, designated SEQ ID:21819, to the nucleotide sequence of VGAM2078 RNA, herein designated VGAM RNA, also designated SEQ ID:4789.

[72549] Another function of VGAM2078 is therefore inhibition of Pellino Homolog 1 (Drosophila) (PELI1, Accession

NM_020651). Accordingly, utilities of VGAM2078 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PELI1. Ras and Rab Interactor 3 (RIN3, Accession NM_024832) is another VGAM2078 host target gene. RIN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RIN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RIN3 BINDING SITE, designated SEQ ID:24234, to the nucleotide sequence of VGAM2078 RNA, herein designated VGAM RNA, also designated SEQ ID:4789.

[72550] Another function of VGAM2078 is therefore inhibition of Ras and Rab Interactor 3 (RIN3, Accession NM_024832). Accordingly, utilities of VGAM2078 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RIN3. LOC133686 (Accession XM_059667) is another VGAM2078 host target gene. LOC133686 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC133686, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133686 BINDING SITE, designated SEQ ID:37055, to the nucleotide sequence of VGAM2078 RNA, herein designated VGAM RNA, also designated SEQ ID:4789.

[72551] Another function of VGAM2078 is therefore inhibition of LOC133686 (Accession XM_059667). Accordingly, utilities of VGAM2078 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133686. LOC153205 (Accession XM_098322) is another VGAM2078 host target gene. LOC153205 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153205, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153205 BINDING SITE, designated SEQ ID:41582, to the nucleotide sequence of VGAM2078 RNA, herein designated VGAM RNA, also designated SEQ ID:4789.

[72552] Another function of VGAM2078 is therefore inhibition of LOC153205 (Accession XM_098322). Accordingly, utilities of VGAM2078 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC153205. LOC221810 (Accession XM_168222) is another VGAM2078 host target gene. LOC221810 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221810, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221810 BINDING SITE, designated SEQ ID:45084, to the nucleotide sequence of VGAM2078 RNA, herein designated VGAM RNA, also designated SEQ ID:4789.

[72553] Another function of VGAM2078 is therefore inhibition of LOC221810 (Accession XM_168222). Accordingly, utilities of VGAM2078 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221810. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2079 (VGAM2079) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72554] VGAM2079 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2079 was detected is described hereinabove with reference to Figs. 1-8.

[72555] VGAM2079 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola Virus. VGAM2079 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72556] VGAM2079 gene encodes a VGAM2079 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2079 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2079 precursor RNA is designated SEQ ID:2065, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2065 is located at position 171525 relative to the genome of Variola Virus.

[72557] VGAM2079 precursor RNA folds onto itself, forming VGAM2079 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72558] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2079 folded precursor RNA into VGAM2079 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2079 RNA is designated SEQ ID:4790, and is provided hereinbelow with reference to the sequence listing part.

[72559] VGAM2079 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2079 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2079 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72560] VGAM2079 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2079 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2079 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2079 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2079 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72561] The complementary binding of VGAM2079 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2079 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2079 host target RNA into VGAM2079 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72562] It is appreciated that VGAM2079 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2079 host target genes. The mRNA of each one of this plurality of VGAM2079 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2079 RNA, herein designated VGAM RNA, and which when bound by VGAM2079 RNA causes inhibition of translation of respective one or more VGAM2079 host target proteins.

[72563] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2079 gene, herein designated VGAM GENE, on one or more VGAM2079 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72564] It is yet further appreciated that a function of VGAM2079 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2079 include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGAM2079 correlate with, and may be deduced from, the identity of the host target genes which VGAM2079 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72565] Nucleotide sequences of the VGAM2079 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2079 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2079 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2079 are further described hereinbelow with reference to Table 1.

[72566] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2079 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2079 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72567] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2079 gene, herein designated VGAM is inhibition of expression of VGAM2079 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2079 correlate with, and may be deduced from, the identity of the target genes which VGAM2079 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72568] DXF68S1E (Accession XM_010289) is a VGAM2079 host target gene. DXF68S1E BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DXF68S1E, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DXF68S1E BINDING SITE, designated SEQ ID:30151, to the nucleotide sequence of VGAM2079 RNA, herein designated VGAM RNA, also designated SEQ ID:4790.

[72569] A function of VGAM2079 is therefore inhibition of DXF68S1E (Accession XM_010289). Accordingly, utilities of VGAM2079 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DXF68S1E. Pleiomorphic Adenoma Gene 1 (PLAG1, Accession NM_002655) is another VGAM2079 host target gene. PLAG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLAG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLAG1 BINDING SITE, designated SEQ ID:8517, to the nucleotide sequence of VGAM2079 RNA, herein designated VGAM RNA, also designated SEQ ID:4790.

[72570] Another function of VGAM2079 is therefore inhibition of Pleiomorphic Adenoma Gene 1 (PLAG1, Accession NM_002655), a gene which contains a zinc finger domain.

Accordingly, utilities of VGAM2079 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAG1. The function of PLAG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM29.ELL2 (Accession NM_012081) is another VGAM2079 host target gene. ELL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELL2 BINDING SITE, designated SEQ ID:14366, to the nucleotide sequence of VGAM2079 RNA, herein designated VGAM RNA, also designated SEQ ID:4790.

[72571] Another function of VGAM2079 is therefore inhibition of ELL2 (Accession NM_012081). Accordingly, utilities of VGAM2079 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELL2. KIAA0090 (Accession XM_114045) is another VGAM2079 host target gene. KIAA0090 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0090, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0090 BINDING SITE, designated SEQ ID:42652, to the nucleotide sequence of VGAM2079 RNA, herein designated VGAM RNA, also designated SEQ ID:4790.

[72572] Another function of VGAM2079 is therefore inhibition of KIAA0090 (Accession XM_114045). Accordingly, utilities of VGAM2079 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0090. KIAA1622 (Accession NM_058237) is another VGAM2079 host target gene. KIAA1622 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1622, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1622 BINDING SITE, designated SEQ ID:27764, to the nucleotide sequence of VGAM2079 RNA, herein designated VGAM RNA, also designated SEQ ID:4790.

[72573] Another function of VGAM2079 is therefore inhibition of KIAA1622 (Accession NM_058237). Accordingly, utilities of VGAM2079 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1622. RAS-like, Estrogen-regulated, Growth-inhibitor (RERG, Accession NM_032918) is another VGAM2079 host target gene. RERG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RERG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RERG BINDING SITE, designated SEQ ID:26738, to the nucleotide sequence of VGAM2079 RNA, herein designated VGAM RNA, also designated SEQ ID:4790.

[72574] Another function of VGAM2079 is therefore inhibition of RAS-like, Estrogen-regulated, Growth-inhibitor (RERG, Accession NM_032918). Accordingly, utilities of VGAM2079 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RERG. LOC221288 (Accession XM_168058) is another VGAM2079 host target gene. LOC221288 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC221288 BINDING SITE, designated SEQ ID:44970, to the nucleotide sequence of VGAM2079 RNA, herein designated VGAM RNA, also designated SEQ ID:4790.

[72575] Another function of VGAM2079 is therefore inhibition of LOC221288 (Accession XM_168058). Accordingly, utilities of VGAM2079 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221288. LOC90488 (Accession XM_032129) is another VGAM2079 host target gene. LOC90488 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90488, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90488 BINDING SITE, designated SEQ ID:31557, to the nucleotide sequence of VGAM2079 RNA, herein designated VGAM RNA, also designated SEQ ID:4790.

[72576] Another function of VGAM2079 is therefore inhibition of LOC90488 (Accession XM_032129). Accordingly, utilities of VGAM2079 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90488. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2080 (VGAM2080) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72577] VGAM2080 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2080 was detected is described hereinabove with reference to Figs. 1-8.

[72578] VGAM2080 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola Virus. VGAM2080 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72579] VGAM2080 gene encodes a VGAM2080 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2080 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2080 precursor RNA is designated SEQ ID:2066, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2066 is located at position 176691 relative to the genome of Variola Virus.

[72580] VGAM2080 precursor RNA folds onto itself, forming VGAM2080 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72581] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2080 folded precursor RNA into VGAM2080 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2080 RNA is designated SEQ ID:4791, and is provided hereinbelow with reference to the sequence listing part.

[72582] VGAM2080 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2080 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2080 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72583] VGAM2080 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2080 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2080 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2080 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2080 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72584] The complementary binding of VGAM2080 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2080 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2080 host target RNA into VGAM2080 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72585] It is appreciated that VGAM2080 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2080 host target genes. The mRNA of each one of this plurality of VGAM2080 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2080 RNA, herein designated VGAM RNA, and which when bound by VGAM2080 RNA causes inhibition of translation of respective one or more

VGAM2080 host target proteins.

[72586] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2080 gene, herein designated VGAM GENE, on one or more VGAM2080 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72587] It is yet further appreciated that a function of VGAM2080 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2080 include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific func-

tions, and accordingly utilities, of VGAM2080 correlate with, and may be deduced from, the identity of the host target genes which VGAM2080 binds and inhibits, and the function of these host target genes, as elaborated herein-below.

[72588] Nucleotide sequences of the VGAM2080 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2080 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2080 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2080 are further described hereinbelow with reference to Table 1.

[72589] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2080 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2080 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72590] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2080 gene, herein designated VGAM is inhibition of expression of VGAM2080 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2080 correlate with, and may be deduced from, the identity of the target genes which VGAM2080 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72591] Chemokine (C-X3-C motif) Receptor 1 (CX3CR1, Accession XM_047502) is a VGAM2080 host target gene. CX3CR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CX3CR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CX3CR1 BINDING SITE, designated SEQ ID:34983, to the nucleotide sequence of VGAM2080 RNA, herein designated VGAM RNA, also designated SEQ ID:4791.

[72592] A function of VGAM2080 is therefore inhibition of Chemokine (C-X3-C motif) Receptor 1 (CX3CR1, Accession XM_047502), a gene which mediates both the adhesive and migratory functions of fractalkine. Accordingly, utilities of VGAM2080 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CX3CR1. The function of CX3CR1 and its association with various diseases and clinical conditions, has been es-

tablished by previous studies, as described hereinabove with reference to VGAM25.KIAA0720 (Accession XM_030970) is another VGAM2080 host target gene. KIAA0720 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0720, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0720 BINDING SITE, designated SEQ ID:31231, to the nucleotide sequence of VGAM2080 RNA, herein designated VGAM RNA, also designated SEQ ID:4791.

[72593] Another function of VGAM2080 is therefore inhibition of KIAA0720 (Accession XM_030970). Accordingly, utilities of VGAM2080 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0720. KIAA1102 (Accession XM_044461) is another VGAM2080 host target gene. KIAA1102 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1102, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1102 BINDING SITE, designated SEQ ID:34213, to the nucleotide sequence of VGAM2080 RNA, herein designated VGAM RNA, also designated SEQ ID:4791.

[72594] Another function of VGAM2080 is therefore inhibition of KIAA1102 (Accession XM_044461). Accordingly, utilities of VGAM2080 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1102. KIAA1257 (Accession XM_031577) is another VGAM2080 host target gene. KIAA1257 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1257, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1257 BINDING SITE, designated SEQ ID:31430, to the nucleotide sequence of VGAM2080 RNA, herein designated VGAM RNA, also designated SEQ ID:4791.

[72595] Another function of VGAM2080 is therefore inhibition of KIAA1257 (Accession XM_031577). Accordingly, utilities of VGAM2080 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1257. PFTAIRE Protein Kinase 1 (PFTK1, Accession NM_012395) is another VGAM2080 host target gene.

PFTK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PFTK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PFTK1 BINDING SITE, designated SEQ ID:14751, to the nucleotide sequence of VGAM2080 RNA, herein designated VGAM RNA, also designated SEQ ID:4791.

[72596] Another function of VGAM2080 is therefore inhibition of PFTAIRE Protein Kinase 1 (PFTK1, Accession NM_012395). Accordingly, utilities of VGAM2080 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PFTK1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2081 (VGAM2081) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72597] VGAM2081 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2081 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[72598] VGAM2081 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola Virus. VGAM2081 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72599] VGAM2081 gene encodes a VGAM2081 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2081 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2081 precursor RNA is designated SEQ ID:2067, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2067 is located at position 180298 relative to the genome of Variola Virus.

[72600] VGAM2081 precursor RNA folds onto itself, forming VGAM2081 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72601] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2081 folded precursor RNA into VGAM2081 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2081 RNA is designated SEQ ID:4792, and is provided hereinbelow with reference to the sequence listing part.

[72602] VGAM2081 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2081 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2081 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72603] VGAM2081 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2081 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2081 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2081 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2081 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72604] The complementary binding of VGAM2081 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2081 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2081 host target RNA into VGAM2081 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72605] It is appreciated that VGAM2081 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2081 host target genes. The mRNA of each one of this plurality of VGAM2081 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2081 RNA, herein designated VGAM RNA, and which when bound by VGAM2081 RNA causes inhibition of translation of respective one or more VGAM2081 host target proteins.

[72606] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2081 gene, herein designated VGAM GENE, on one or more VGAM2081 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72607] It is yet further appreciated that a function of VGAM2081 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGAM2081 correlate with, and may be deduced from, the identity of the host target genes which VGAM2081 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72608] Nucleotide sequences of the VGAM2081 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2081 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2081 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2081 are further described hereinbelow with reference to Table 1.

[72609] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2081 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2081 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72610] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2081 gene, herein designated VGAM is inhibition of expression of VGAM2081 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2081 correlate with, and may be deduced from, the identity of the target genes which VGAM2081 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72611] Ceroid-lipofuscinosis, Neuronal 5 (CLN5, Accession NM_006493) is a VGAM2081 host target gene. CLN5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CLN5, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLN5 BINDING SITE, designated SEQ ID:13226, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72612] A function of VGAM2081 is therefore inhibition of Ceroid-lipofuscinosis, Neuronal 5 (CLN5, Accession NM_006493). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLN5. ADP-ribosylation Factor GTPase Activating Protein 3 (ARFGAP3, Accession NM_014570) is another VGAM2081 host target gene. ARFGAP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARFGAP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARFGAP3 BINDING SITE, designated SEQ ID:15925, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72613] Another function of VGAM2081 is therefore inhibition of ADP-ribosylation Factor GTPase Activating Protein 3

(ARFGAP3, Accession NM_014570). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARFGAP3. FLJ30532 (Accession NM_144724) is another VGAM2081 host target gene. FLJ30532 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ30532, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ30532 BINDING SITE, designated SEQ ID:29546, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72614] Another function of VGAM2081 is therefore inhibition of FLJ30532 (Accession NM_144724). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30532. KIAA0319 (Accession NM_014809) is another VGAM2081 host target gene. KIAA0319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0319, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0319 BINDING SITE, designated SEQ ID:16764, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72615] Another function of VGAM2081 is therefore inhibition of KIAA0319 (Accession NM_014809). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0319. KIAA0416 (Accession NM_015564) is another VGAM2081 host target gene. KIAA0416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0416 BINDING SITE, designated SEQ ID:17834, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72616] Another function of VGAM2081 is therefore inhibition of KIAA0416 (Accession NM_015564). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0416. KIAA0555 (Accession XM_011347) is another

VGAM2081 host target gene. KIAA0555 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0555, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0555 BINDING SITE, designated SEQ ID:30186, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72617] Another function of VGAM2081 is therefore inhibition of KIAA0555 (Accession XM_011347). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0555. MGC30052 (Accession NM_144721) is another VGAM2081 host target gene. MGC30052 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC30052, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC30052 BINDING SITE, designated SEQ ID:29542, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72618] Another function of VGAM2081 is therefore inhibition of MGC30052 (Accession NM_144721). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC30052. MGC5139 (Accession XM_058587) is another VGAM2081 host target gene. MGC5139 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC5139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5139 BINDING SITE, designated SEQ ID:36677, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72619] Another function of VGAM2081 is therefore inhibition of MGC5139 (Accession XM_058587). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5139. NSG-X (Accession NM_014411) is another VGAM2081 host target gene. NSG-X BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NSG-X, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NSG-X BINDING SITE, designated SEQ ID:15754, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72620] Another function of VGAM2081 is therefore inhibition of NSG-X (Accession NM_014411). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NSG-X. Solute Carrier Family 12, (potassium-chloride transporter) Member 5 (SLC12A5, Accession NM_020708) is another VGAM2081 host target gene. SLC12A5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC12A5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC12A5 BINDING SITE, designated SEQ ID:21856, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72621] Another function of VGAM2081 is therefore inhibition of Solute Carrier Family 12, (potassium-chloride transporter) Member 5 (SLC12A5, Accession NM_020708). Accordingly,

utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC12A5. TRIP-Br2 (Accession NM_014755) is another VGAM2081 host target gene. TRIP-Br2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIP-Br2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIP-Br2 BINDING SITE, designated SEQ ID:16489, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72622] Another function of VGAM2081 is therefore inhibition of TRIP-Br2 (Accession NM_014755). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIP-Br2. LOC128954 (Accession XM_066252) is another VGAM2081 host target gene. LOC128954 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC128954, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC128954 BINDING SITE, designated SEQ ID:37320, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72623] Another function of VGAM2081 is therefore inhibition of LOC128954 (Accession XM_066252). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128954. LOC91948 (Accession XM_041723) is another VGAM2081 host target gene. LOC91948 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91948, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91948 BINDING SITE, designated SEQ ID:33574, to the nucleotide sequence of VGAM2081 RNA, herein designated VGAM RNA, also designated SEQ ID:4792.

[72624] Another function of VGAM2081 is therefore inhibition of LOC91948 (Accession XM_041723). Accordingly, utilities of VGAM2081 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91948. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2082 (VGAM2082) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72625] VGAM2082 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2082 was detected is described hereinabove with reference to Figs. 1-8.

[72626] VGAM2082 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola Virus. VGAM2082 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72627] VGAM2082 gene encodes a VGAM2082 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2082 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2082 precursor RNA is designated SEQ ID:2068, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2068 is located at position 174739 relative to the

genome of Variola Virus.

[72628] VGAM2082 precursor RNA folds onto itself, forming VGAM2082 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72629] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2082 folded precursor RNA into VGAM2082 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2082 RNA is designated SEQ ID:4793, and is provided hereinbelow with reference to the sequence listing part.

[72630] VGAM2082 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2082 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2082 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72631] VGAM2082 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2082 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2082 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2082 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2082 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72632] The complementary binding of VGAM2082 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2082 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2082 host target RNA into VGAM2082 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72633] It is appreciated that VGAM2082 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2082 host target genes. The mRNA of each one of this plurality of VGAM2082 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2082 RNA, herein designated VGAM RNA, and which when bound by VGAM2082 RNA causes inhibition of translation of respective one or more VGAM2082 host target proteins.

[72634] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2082 gene, herein designated VGAM GENE, on one or more VGAM2082 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72635] It is yet further appreciated that a function of VGAM2082 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGAM2082 correlate

with, and may be deduced from, the identity of the host target genes which VGAM2082 binds and inhibits, and the function of these host target genes, as elaborated herein-below.

[72636] Nucleotide sequences of the VGAM2082 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2082 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2082 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2082 are further described hereinbelow with reference to Table 1.

[72637] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2082 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2082 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72638] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2082 gene, herein designated VGAM is inhibition of expression of VGAM2082 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2082 correlate with, and may be deduced

from, the identity of the target genes which VGAM2082 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72639] Capping Protein (actin filament) Muscle Z-line, Alpha 1 (CAPZA1, Accession XM_052116) is a VGAM2082 host target gene. CAPZA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAPZA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAPZA1 BINDING SITE, designated SEQ ID:35952, to the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72640] A function of VGAM2082 is therefore inhibition of Capping Protein (actin filament) Muscle Z-line, Alpha 1 (CAPZA1, Accession XM_052116), a gene which is alpha 1 subunit of actin filament capping protein; binds actin, has roles in cell motility and actin assembly. Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPZA1. The function of CAPZA1 and its association with various diseases and clinical conditions, has been es-

tablished by previous studies, as described hereinabove with reference to VGAM547.Frizzled Homolog 4 (Drosophila) (FZD4, Accession NM_012193) is another VGAM2082 host target gene. FZD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FZD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FZD4 BINDING SITE, designated SEQ ID:14485, to the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72641] Another function of VGAM2082 is therefore inhibition of Frizzled Homolog 4 (Drosophila) (FZD4, Accession NM_012193), a gene which may function in cell polarity, cell fate specification and cancer; similar to frizzled receptor family, has seven transmembrane domains. Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FZD4. The function of FZD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM309.Solute Carrier Family

17 (sodium phosphate), Member 4 (SLC17A4, Accession NM_005495) is another VGAM2082 host target gene. SLC17A4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC17A4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC17A4 BINDING SITE, designated SEQ ID:11997, to the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72642] Another function of VGAM2082 is therefore inhibition of Solute Carrier Family 17 (sodium phosphate), Member 4 (SLC17A4, Accession NM_005495). Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC17A4. C6orf5 (Accession NM_015524) is another VGAM2082 host target gene. C6orf5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C6orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C6orf5 BIND-

ING SITE, designated SEQ ID:17781, to the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72643] Another function of VGAM2082 is therefore inhibition of C6orf5 (Accession NM_015524). Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf5. DKFZp434G179 (Accession XM_087065) is another VGAM2082 host target gene. DKFZp434G179 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434G179, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434G179 BINDING SITE, designated SEQ ID:39041, to the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72644] Another function of VGAM2082 is therefore inhibition of DKFZp434G179 (Accession XM_087065). Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434G179. FLJ20712 (Accession NM_017937) is

another VGAM2082 host target gene. FLJ20712 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20712, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20712 BINDING SITE, designated SEQ ID:19629, to the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72645] Another function of VGAM2082 is therefore inhibition of FLJ20712 (Accession NM_017937). Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20712. KIAA1301 (Accession XM_038999) is another VGAM2082 host target gene. KIAA1301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1301 BINDING SITE, designated SEQ ID:32977, to the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72646] Another function of VGAM2082 is therefore inhibition of KIAA1301 (Accession XM_038999). Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1301. Retinoic Acid Induced 17 (RAI17, Accession XM_166091) is another VGAM2082 host target gene. RAI17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAI17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAI17 BINDING SITE, designated SEQ ID:43857, to the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72647] Another function of VGAM2082 is therefore inhibition of Retinoic Acid Induced 17 (RAI17, Accession XM_166091). Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI17. LOC150630 (Accession XM_097931) is another VGAM2082 host target gene. LOC150630 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150630, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150630 BINDING SITE, designated SEQ ID:41236, to the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72648] Another function of VGAM2082 is therefore inhibition of LOC150630 (Accession XM_097931). Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150630. LOC153259 (Accession XM_098342) is another VGAM2082 host target gene. LOC153259 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153259 BINDING SITE, designated SEQ ID:41601, to the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72649] Another function of VGAM2082 is therefore inhibition of LOC153259 (Accession XM_098342). Accordingly, utilities of VGAM2082 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC153259. LOC201799 (Accession XM_114380) is another VGAM2082 host target gene. LOC201799 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201799, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201799 BINDING SITE, designated SEQ ID:42911, to the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72650] Another function of VGAM2082 is therefore inhibition of LOC201799 (Accession XM_114380). Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201799. LOC219578 (Accession XM_170012) is another VGAM2082 host target gene. LOC219578 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219578, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219578 BINDING SITE, designated SEQ ID:45308, to

the nucleotide sequence of VGAM2082 RNA, herein designated VGAM RNA, also designated SEQ ID:4793.

[72651] Another function of VGAM2082 is therefore inhibition of LOC219578 (Accession XM_170012). Accordingly, utilities of VGAM2082 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219578. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2083 (VGAM2083) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72652] VGAM2083 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2083 was detected is described hereinabove with reference to Figs. 1-8.

[72653] VGAM2083 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2083 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72654] VGAM2083 gene encodes a VGAM2083 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2083 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2083 precursor RNA is designated SEQ ID:2069, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2069 is located at position 190806 relative to the genome of Camelpox Virus.

[72655] VGAM2083 precursor RNA folds onto itself, forming VGAM2083 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72656] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2083 folded precursor RNA into VGAM2083 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2083 RNA is designated SEQ ID:4794, and is provided hereinbelow with reference to the sequence listing part.

[72657] VGAM2083 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2083 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2083 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72658] VGAM2083 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2083 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2083 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2083 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2083 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72659] The complementary binding of VGAM2083 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2083 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2083 host target RNA into VGAM2083 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72660] It is appreciated that VGAM2083 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2083 host target genes. The mRNA of each one of this plurality of VGAM2083 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2083 RNA, herein designated VGAM RNA, and which when bound by VGAM2083 RNA causes inhibition of translation of respective one or more VGAM2083 host target proteins.

[72661] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2083 gene, herein designated VGAM GENE, on one or more VGAM2083 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72662] It is yet further appreciated that a function of VGAM2083 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2083 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2083 correlate with, and may be deduced from, the identity of the host target genes which VGAM2083 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72663] Nucleotide sequences of the VGAM2083 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2083 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2083 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2083 are further described hereinbelow with reference to Table 1.

[72664] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2083 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2083 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72665] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2083 gene, herein designated VGAM is inhibition of expression of VGAM2083 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2083 correlate with, and may be deduced from, the identity of the target genes which VGAM2083 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72666] CDK2-associated Protein 1 (CDK2AP1, Accession NM_004642) is a VGAM2083 host target gene. CDK2AP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDK2AP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDK2AP1 BINDING SITE, designated SEQ ID:11017, to the nucleotide sequence of VGAM2083 RNA, herein designated VGAM RNA, also designated SEQ ID:4794.

[72667] A function of VGAM2083 is therefore inhibition of

CDK2-associated Protein 1 (CDK2AP1, Accession NM_004642), a gene which negatively regulates CDK2 activity. Accordingly, utilities of VGAM2083 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDK2AP1. The function of CDK2AP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1923.UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7, Accession NM_017423) is another VGAM2083 host target gene. GALNT7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GALNT7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALNT7 BINDING SITE, designated SEQ ID:18876, to the nucleotide sequence of VGAM2083 RNA, herein designated VGAM RNA, also designated SEQ ID:4794.

[72668] Another function of VGAM2083 is therefore inhibition of UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7,

Accession NM_017423). Accordingly, utilities of VGAM2083 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNT7. RAP1 (Accession NM_018975) is another VGAM2083 host target gene. RAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAP1 BINDING SITE, designated SEQ ID:21046, to the nucleotide sequence of VGAM2083 RNA, herein designated VGAM RNA, also designated SEQ ID:4794.

[72669] Another function of VGAM2083 is therefore inhibition of RAP1 (Accession NM_018975), a gene which is an ortholog of the yeast telomeric protein Rap1 and may be a general characteristic of sequence-specific transcriptional factors. Accordingly, utilities of VGAM2083 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP1. The function of RAP1 has been established by previous studies. By performing a yeast 2-hybrid screen on a HeLa cell cDNA library using telomeric repeat-binding factor-2, or TRF2 (TERF2;

602027), as bait, followed by screening a breast cancer cDNA library, Li et al. (2000) isolated a full-length cDNA encoding RAP1, an ortholog of the yeast telomeric protein Rap1. The RAP1 cDNA is identical to the KAIA804 cDNA (GenBank AK000669) reported by the NEDO Japanese sequencing project. The predicted 47-kD RAP1 protein contains 399 amino acids. A motif search revealed that RAP1 has an N-terminal BRCT domain and a central Myb-type helix-turn-helix motif. RAP1 also has an acidic C terminus (amino acids 214 to 382; pI around 3.8) featuring a predicted 33-amino acid coiled-coil region and a bipartite nuclear localization signal. Sequence alignments showed an additional region of sequence similarity in the C termini of yeast and human RAP1 that coincides with the main protein-protein interaction domain of S. cerevisiae Rap1. Thus, human RAP1 has 3 conserved sequence motifs in common with yeast Rap1. Northern blot analysis detected ubiquitous expression of a 2.5-kb RAP1 transcript. The authors found that RAP1 is located at telomeres and affects telomere length. However, while yeast Rap1 binds telomeric DNA directly, human RAP1 is recruited to telomeres by TRF2. Extending the comparison of telomeric proteins to fission yeast, Li et al. (2000) iden-

tified the S. pombe Taz1 protein as a TRF ortholog, indicating that TRFs are conserved at eukaryotic telomeres. The data suggested that ancestral telomeres, like those of vertebrates, contained a TRF-like protein as well as RAP1. The authors proposed that budding yeast preserved Rap1 at telomeres but lost the TRF component, possibly concomitant with a change in the telomeric repeat sequence. Lieb et al. (2001) determined the distribution of RAP1 in vivo on the entire yeast genome, at a resolution of 2 kb. RAP1 is central to the cellular economy during rapid growth, targeting 294 loci, about 5% of yeast genes, and participating in the activation of 37% of all RNA polymerase II (see OMIM Ref. No. 180660) initiation events in exponentially growing cells. Although the DNA sequence recognized by RAP1 is found in both coding and intergenic sequences, the binding of RAP1 to the genome was highly specific to intergenic regions with the potential to act as promoters. Lieb et al. (2001) concluded that this global phenomenon, which may be a general characteristic of sequence-specific transcriptional factors, indicates the existence of a genomewide molecular mechanism for marking promoter regions.

[72670] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[72671] Li, B.; Oestreich, S.; de Lange, T. : Identification of human Rap1: implications for telomere evolution. Cell 101: 471-483, 2000. ; and

[72672] Lieb, J. D.; Liu, X.; Botstein, D.; Brown, P. O. : Promoter-specific binding of Rap1 revealed by genome-wide maps of protein-DNA association. Nature Genet. 28: 327-334, 2001.

[72673] Further studies establishing the function and utilities of RAP1 are found in John Hopkins OMIM database record ID 605061, and in sited publications numbered 6797-6798 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.KIAA1096 (Accession XM_043678) is another VGAM2083 host target gene. KIAA1096 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1096, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1096 BINDING SITE, designated SEQ ID:33998, to the nucleotide sequence of VGAM2083 RNA, herein designated VGAM RNA, also designated SEQ

ID:4794.

[72674] Another function of VGAM2083 is therefore inhibition of KIAA1096 (Accession XM_043678). Accordingly, utilities of VGAM2083 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1096. PRO0097 (Accession NM_014114) is another VGAM2083 host target gene. PRO0097 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0097, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0097 BINDING SITE, designated SEQ ID:15367, to the nucleotide sequence of VGAM2083 RNA, herein designated VGAM RNA, also designated SEQ ID:4794.

[72675] Another function of VGAM2083 is therefore inhibition of PRO0097 (Accession NM_014114). Accordingly, utilities of VGAM2083 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0097. LOC255196 (Accession XM_173157) is another VGAM2083 host target gene. LOC255196 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255196, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255196 BINDING SITE, designated SEQ ID:46416, to the nucleotide sequence of VGAM2083 RNA, herein designated VGAM RNA, also designated SEQ ID:4794.

[72676] Another function of VGAM2083 is therefore inhibition of LOC255196 (Accession XM_173157). Accordingly, utilities of VGAM2083 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255196. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2084 (VGAM2084) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72677] VGAM2084 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2084 was detected is described hereinabove with reference to Figs. 1-8.

[72678] VGAM2084 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Variola Virus.

VGAM2084 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72679] VGAM2084 gene encodes a VGAM2084 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2084 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2084 precursor RNA is designated SEQ ID:2070, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2070 is located at position 170712 relative to the genome of Variola Virus.

[72680] VGAM2084 precursor RNA folds onto itself, forming VGAM2084 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72681] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2084 folded precursor RNA into VGAM2084 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2084 RNA is designated SEQ ID:4795, and is provided hereinbelow with reference to the sequence listing part.

[72682] VGAM2084 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2084 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2084 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72683] VGAM2084 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2084 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2084 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2084 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2084 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72684] The complementary binding of VGAM2084 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2084 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2084 host target RNA into VGAM2084 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72685] It is appreciated that VGAM2084 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2084 host target genes. The mRNA of each one of this plurality of VGAM2084 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2084 RNA, herein designated VGAM RNA, and which when bound by VGAM2084 RNA causes inhibition of translation of respective one or more VGAM2084 host target proteins.

[72686] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2084 gene, herein designated VGAM GENE, on one or more VGAM2084 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72687] It is yet further appreciated that a function of VGAM2084 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2084 include diagnosis, prevention and treatment of viral infection by Variola Virus. Specific functions, and accordingly utilities, of VGAM2084 correlate with, and may be deduced from, the identity of the host target genes which VGAM2084 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72688] Nucleotide sequences of the VGAM2084 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2084 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2084 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2084 are further described hereinbelow with reference to Table 1.

[72689] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2084 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2084 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72690] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2084 gene, herein designated VGAM is inhibition of expression of VGAM2084 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2084 correlate with, and may be deduced from, the identity of the target genes which VGAM2084 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72691] Cytochrome P450, Subfamily I (dioxin-inducible), Polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1, Accession NM_000104) is a VGAM2084 host target gene. CYP1B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP1B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of CYP1B1 BINDING SITE, designated SEQ ID:5566, to the nucleotide sequence of VGAM2084 RNA, herein designated VGAM RNA, also designated SEQ ID:4795.

[72692] A function of VGAM2084 is therefore inhibition of Cytochrome P450, Subfamily I (dioxin-inducible), Polypeptide 1 (glaucoma 3, primary infantile) (CYP1B1, Accession NM_000104), a gene which participates in the metabolism of a molecule that is a participant in eye development. Accordingly, utilities of VGAM2084 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP1B1. The function of CYP1B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM894.FLJ14803 (Accession NM_032842) is another VGAM2084 host target gene. FLJ14803 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14803, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14803 BINDING SITE, designated SEQ ID:26628, to the nucleotide sequence of VGAM2084

RNA, herein designated VGAM RNA, also designated SEQ ID:4795.

[72693] Another function of VGAM2084 is therefore inhibition of FLJ14803 (Accession NM_032842). Accordingly, utilities of VGAM2084 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14803. Protein Tyrosine Kinase 9 (PTK9, Accession NM_002822) is another VGAM2084 host target gene. PTK9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTK9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTK9 BINDING SITE, designated SEQ ID:8690, to the nucleotide sequence of VGAM2084 RNA, herein designated VGAM RNA, also designated SEQ ID:4795.

[72694] Another function of VGAM2084 is therefore inhibition of Protein Tyrosine Kinase 9 (PTK9, Accession NM_002822). Accordingly, utilities of VGAM2084 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTK9. LOC122773 (Accession XM_058665) is another VGAM2084 host target gene. LOC122773 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by LOC122773, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122773 BINDING SITE, designated SEQ ID:36711, to the nucleotide sequence of VGAM2084 RNA, herein designated VGAM RNA, also designated SEQ ID:4795.

[72695] Another function of VGAM2084 is therefore inhibition of LOC122773 (Accession XM_058665). Accordingly, utilities of VGAM2084 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122773. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2085 (VGAM2085) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72696] VGAM2085 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2085 was detected is described hereinabove with reference to Figs. 1-8.

[72697] VGAM2085 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox Virus. VGAM2085 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72698] VGAM2085 gene encodes a VGAM2085 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2085 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2085 precursor RNA is designated SEQ ID:2071, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2071 is located at position 96465 relative to the genome of Fowlpox Virus.

[72699] VGAM2085 precursor RNA folds onto itself, forming VGAM2085 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[72700] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2085 folded precursor RNA into VGAM2085 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2085 RNA is designated SEQ ID:4796, and is provided hereinbelow with reference to the sequence listing part.

[72701] VGAM2085 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2085 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2085 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72702] VGAM2085 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2085 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2085 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2085 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2085 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72703] The complementary binding of VGAM2085 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2085 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2085 host target RNA into VGAM2085 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72704] It is appreciated that VGAM2085 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2085 host target genes. The mRNA of each one of this plurality of VGAM2085 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2085 RNA, herein designated VGAM RNA, and which when bound by VGAM2085 RNA causes inhibition of translation of respective one or more VGAM2085 host target proteins.

[72705] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2085 gene, herein designated VGAM GENE, on one or more VGAM2085 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72706] It is yet further appreciated that a function of VGAM2085 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2085 include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGAM2085 correlate with, and may be deduced from, the identity of the host target genes which VGAM2085 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72707] Nucleotide sequences of the VGAM2085 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2085 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2085 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2085 are further described hereinbelow with reference to Table 1.

[72708] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2085 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2085 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72709] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2085 gene, herein designated VGAM is inhibition of expression of VGAM2085 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2085 correlate with, and may be deduced from, the identity of the target genes which VGAM2085 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72710] Testis Specific Protein, Y-linked (TSPY, Accession XM_088755) is a VGAM2085 host target gene. TSPY BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TSPY, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates

the complementarity of the nucleotide sequences of TSPY BINDING SITE, designated SEQ ID:39944, to the nucleotide sequence of VGAM2085 RNA, herein designated VGAM RNA, also designated SEQ ID:4796.

[72711] A function of VGAM2085 is therefore inhibition of Testis Specific Protein, Y-linked (TSPY, Accession XM_088755), a gene which may be involved in sperm differentiation. Accordingly, utilities of VGAM2085 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSPY. The function of TSPY has been established by previous studies. Schnieders et al. (1996) reported that TSPY gives rise to a pool of heterogeneously composed transcripts, at least 1 of which yields a protein that is a member of a superfamily including the protooncogene SET (OMIM Ref. No. 600960) and NAP1 (OMIM Ref. No. 164060), a nucleosome assembly factor. Immunohistological studies reported by Schnieders et al. (1996) revealed that TSPY is concentrated in the cytoplasm of spermatogonia in normal as well as in pathological tissue. They further reported that TSPY was found in the early forms of seminomatous testicular tumors. The authors suggested that TSPY function is related to spermatogonial proliferation in a phosphorylation-dependent

manner Lau (1999) discussed the possible role of the TSPY gene in gonadoblastoma (GBY; 424500) and in testicular and prostate cancers. His Figure 1 presented an updated map of genes assigned to the Y chromosome.

[72712] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[72713] Schnieders, F.; Dork, T.; Arnemann, J.; Vogel, T.; Werner, M.; Schmidtke, J. : Testis-specific protein, Y-encoded (TSPY) expression in testicular tissues. Hum. Molec. Genet. 5: 1801-1807, 1996. ; and

[72714] Lau, Y.-F. C. : Sex chromosome genetics '99: gonadoblastoma, testicular and prostate cancers, and the TSPY gene. Am. J. Hum. Genet. 64: 921-927, 1999.

[72715] Further studies establishing the function and utilities of TSPY are found in John Hopkins OMIM database record ID 480100, and in sited publications numbered 8307-8316 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Death-associated Protein Kinase 2 (DAPK2, Accession NM_014326) is another VGAM2085 host target gene. DAPK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DAPK2, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAPK2 BINDING SITE, designated SEQ ID:15631, to the nucleotide sequence of VGAM2085 RNA, herein designated VGAM RNA, also designated SEQ ID:4796.

[72716] Another function of VGAM2085 is therefore inhibition of Death-associated Protein Kinase 2 (DAPK2, Accession NM_014326). Accordingly, utilities of VGAM2085 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAPK2. LOC120856 (Accession XM_058509) is another VGAM2085 host target gene. LOC120856 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120856, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120856 BINDING SITE, designated SEQ ID:36630, to the nucleotide sequence of VGAM2085 RNA, herein designated VGAM RNA, also designated SEQ ID:4796.

[72717] Another function of VGAM2085 is therefore inhibition of LOC120856 (Accession XM_058509). Accordingly, utilities

of VGAM2085 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120856. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2086 (VGAM2086) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72718] VGAM2086 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2086 was detected is described hereinabove with reference to Figs. 1-8.

[72719] VGAM2086 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox Virus. VGAM2086 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72720] VGAM2086 gene encodes a VGAM2086 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2086 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2086 precursor RNA is designated SEQ ID:2072, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2072 is located at position 106213 relative to the genome of Fowlpox Virus.

[72721] VGAM2086 precursor RNA folds onto itself, forming VGAM2086 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72722] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2086 folded precursor RNA into VGAM2086 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2086 RNA is designated SEQ ID:4797, and

is provided hereinbelow with reference to the sequence listing part.

[72723] VGAM2086 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2086 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2086 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72724] VGAM2086 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2086 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2086 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2086 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2086 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72725] The complementary binding of VGAM2086 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2086 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2086 host target RNA into VGAM2086 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72726] It is appreciated that VGAM2086 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2086 host target genes. The mRNA of each one of this plurality of VGAM2086 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2086 RNA, herein designated VGAM RNA, and which when bound by VGAM2086 RNA causes inhibition of translation of respective one or more VGAM2086 host target proteins.

[72727] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2086 gene, herein designated VGAM GENE, on one or more VGAM2086 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72728] It is yet further appreciated that a function of VGAM2086 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2086 include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGAM2086 correlate with, and may be deduced from, the identity of the host target genes which VGAM2086 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72729] Nucleotide sequences of the VGAM2086 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2086 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2086 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2086 are further described hereinbelow with reference to Table 1.

[72730] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2086 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2086 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72731] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2086 gene, herein designated VGAM is inhibition of expression of VGAM2086 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2086 correlate with, and may be deduced from, the identity of the target genes which VGAM2086 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72732] Brain and Acute Leukemia, Cytoplasmic (BAALC, Accession NM_024812) is a VGAM2086 host target gene. BAALC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAALC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAALC BINDING SITE, designated SEQ ID:24194, to the nucleotide sequence of VGAM2086 RNA, herein designated VGAM RNA, also designated SEQ ID:4797.

[72733] A function of VGAM2086 is therefore inhibition of Brain and Acute Leukemia, Cytoplasmic (BAALC, Accession NM_024812). Accordingly, utilities of VGAM2086 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAALC. Neuronal Pentraxin I (NPTX1, Accession NM_002522) is another VGAM2086

host target gene. NPTX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NPTX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPTX1 BINDING SITE, designated SEQ ID:8358, to the nucleotide sequence of VGAM2086 RNA, herein designated VGAM RNA, also designated SEQ ID:4797.

[72734] Another function of VGAM2086 is therefore inhibition of Neuronal Pentraxin I (NPTX1, Accession NM_002522), a gene which may be involved in synaptic uptake of extracellular material and is very strongly similar to rat NP1. Accordingly, utilities of VGAM2086 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTX1. The function of NPTX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM111.BART1 (Accession NM_012106) is another VGAM2086 host target gene. BART1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BART1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BART1 BINDING SITE, designated SEQ ID:14425, to the nucleotide sequence of VGAM2086 RNA, herein designated VGAM RNA, also designated SEQ ID:4797.

[72735] Another function of VGAM2086 is therefore inhibition of BART1 (Accession NM_012106). Accordingly, utilities of VGAM2086 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BART1. KIAA0871 (Accession NM_014961) is another VGAM2086 host target gene. KIAA0871 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0871 BINDING SITE, designated SEQ ID:17334, to the nucleotide sequence of VGAM2086 RNA, herein designated VGAM RNA, also designated SEQ ID:4797.

[72736] Another function of VGAM2086 is therefore inhibition of KIAA0871 (Accession NM_014961). Accordingly, utilities of VGAM2086 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0871. KIAA0984 (Accession XM_037557) is another VGAM2086 host target gene. KIAA0984 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0984, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0984 BINDING SITE, designated SEQ ID:32645, to the nucleotide sequence of VGAM2086 RNA, herein designated VGAM RNA, also designated SEQ ID:4797.

[72737] Another function of VGAM2086 is therefore inhibition of KIAA0984 (Accession XM_037557). Accordingly, utilities of VGAM2086 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0984. MGC11242 (Accession NM_024320) is another VGAM2086 host target gene. MGC11242 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC11242, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11242 BINDING SITE, designated SEQ ID:23609, to

the nucleotide sequence of VGAM2086 RNA, herein designated VGAM RNA, also designated SEQ ID:4797.

[72738] Another function of VGAM2086 is therefore inhibition of MGC11242 (Accession NM_024320). Accordingly, utilities of VGAM2086 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11242. Synovial Sarcoma Translocation Gene On Chromosome 18-like 1 (SS18L1, Accession XM_037202) is another VGAM2086 host target gene. SS18L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SS18L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SS18L1 BINDING SITE, designated SEQ ID:32564, to the nucleotide sequence of VGAM2086 RNA, herein designated VGAM RNA, also designated SEQ ID:4797.

[72739] Another function of VGAM2086 is therefore inhibition of Synovial Sarcoma Translocation Gene On Chromosome 18-like 1 (SS18L1, Accession XM_037202). Accordingly, utilities of VGAM2086 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SS18L1. LOC134553 (Accession XM_059723) is an-

other VGAM2086 host target gene. LOC134553 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC134553, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC134553 BINDING SITE, designated SEQ ID:37076, to the nucleotide sequence of VGAM2086 RNA, herein designated VGAM RNA, also designated SEQ ID:4797.

[72740] Another function of VGAM2086 is therefore inhibition of LOC134553 (Accession XM_059723). Accordingly, utilities of VGAM2086 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC134553. LOC165552 (Accession XM_092666) is another VGAM2086 host target gene. LOC165552 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC165552, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC165552 BINDING SITE, designated SEQ ID:40133, to the nucleotide sequence of VGAM2086 RNA, herein designated VGAM RNA, also designated SEQ ID:4797.

[72741] Another function of VGAM2086 is therefore inhibition of LOC165552 (Accession XM_092666). Accordingly, utilities of VGAM2086 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC165552. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2087 (VGAM2087) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72742] VGAM2087 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2087 was detected is described hereinabove with reference to Figs. 1-8.

[72743] VGAM2087 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox Virus. VGAM2087 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72744] VGAM2087 gene encodes a VGAM2087 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2087 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2087 precursor RNA is designated SEQ ID:2073, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2073 is located at position 115039 relative to the genome of Fowlpox Virus.

[72745] VGAM2087 precursor RNA folds onto itself, forming VGAM2087 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72746] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2087 folded precursor RNA into VGAM2087 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2087 RNA is designated SEQ ID:4798, and is provided hereinbelow with reference to the sequence listing part.

[72747] VGAM2087 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2087 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2087 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72748] VGAM2087 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2087 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2087 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2087 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2087 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72749] The complementary binding of VGAM2087 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2087 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2087 host target RNA into VGAM2087 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72750] It is appreciated that VGAM2087 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2087 host target genes. The mRNA of each one of this plurality of VGAM2087 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2087 RNA, herein designated VGAM RNA, and which when bound by VGAM2087 RNA causes inhibition of translation of respective one or more VGAM2087 host target proteins.

[72751] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2087 gene, herein designated VGAM GENE, on one or more VGAM2087 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72752] It is yet further appreciated that a function of VGAM2087 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGAM2087 correlate with, and may be deduced from, the identity of the host target genes which VGAM2087 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72753] Nucleotide sequences of the VGAM2087 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2087 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2087 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2087 are further described hereinbelow with reference to Table 1.

[72754] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2087 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2087 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[72755] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2087 gene, herein designated VGAM is inhibition of expression of VGAM2087 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2087 correlate with, and may be deduced from, the identity of the target genes which VGAM2087 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72756] AF3P21 (Accession NM_016453) is a VGAM2087 host target gene. AF3P21 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AF3P21, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AF3P21 BINDING SITE, designated SEQ ID:18567, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72757] A function of VGAM2087 is therefore inhibition of AF3P21 (Accession NM_016453), a gene which has an important role in stress fiber formation induced by active diaphanous protein homolog 1 (drf1). Accordingly, utilities

of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AF3P21. The function of AF3P21 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1280.Glucagon-like Peptide 1 Receptor (GLP1R, Accession NM_002062) is another VGAM2087 host target gene. GLP1R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GLP1R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GLP1R BINDING SITE, designated SEQ ID:7827, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72758] Another function of VGAM2087 is therefore inhibition of Glucagon-like Peptide 1 Receptor (GLP1R, Accession NM_002062), a gene which is mediated by g proteins which activate adenylyl cyclase. Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLP1R. The function of GLP1R and its association with various

diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1652.G Protein-coupled Receptor 4 (GPR4, Accession XM_009140) is another VGAM2087 host target gene. GPR4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GPR4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR4 BINDING SITE, designated SEQ ID:30100, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72759] Another function of VGAM2087 is therefore inhibition of G Protein-coupled Receptor 4 (GPR4, Accession XM_009140), a gene which stimulates to produce increased calcium by both SPC and LPC . Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR4. The function of GPR4 has been established by previous studies. Many cell membrane receptors are members of the G protein-coupled receptor (GPR) family. GPRs are characterized by the presence of 7 transmembrane domains and numerous conserved amino acids. Us-

ing degenerate PCR, Heiber et al. (1995) identified additional members of this family. Among these was GPR4, which encodes a putative 355-amino acid protein and was selected from a genomic DNA library using the PCR-derived product as a probe. GPR4 shares the greatest sequence similarity with the human platelet-activating factor receptor (Ye et al., 1991). GPR4 is more than 50% identical to OGR1 (GPR68; 601404), a high-affinity receptor for the sphingosylphosphorylcholine (SPC) signaling molecule. Zhu et al. (2001) showed that cells expressing GPR4 are stimulated to produce increased calcium by both SPC and LPC (lysophosphatidylcholine), a ligand for G2A (OMIM Ref. No. 606167). RNA dot blot analysis revealed highest expression of GPR4 in ovary, liver, lung, kidney, lymph node, and subthalamic nucleus; in contrast, OGR1 is most highly expressed in lung, placenta, spleen, testis, small intestine, and peripheral blood leukocytes. Binding analysis determined that GPR4 interacts with SPC with high affinity and with LPC with lower affinity. Both ligands enhanced proliferation and ERK mitogen-activated protein kinase (see OMIM Ref. No. MAP3K4; 602425) activation in a GPR4-dependent and pertussis toxin (PTX)-sensitive manner, whereas ERK activation is PTX-insensitive in

OGR1-mediated signaling. Cell migration analysis suggested that both LPC and SPC enhance chemotaxis, but not chemokinesis, through GPR4.

[72760] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[72761] Heiber, M.; Docherty, J. M.; Shah, G.; Nguyen, T.; Cheng, R.; Heng, H. H. Q.; Marchese, A.; Tsui, L.-C.; Shi, X.; George, S. R.; O'Dowd, B. F. : Isolation of three novel human genes encoding G protein-coupled receptors. DNA Cell Biol. 14: 25-35, 1995. ; and

[72762] Zhu, K.; Baudhuin, L. M.; Hong, G.; Williams, F. S.; Cristina, K. L.; Kabarowski, J. H. S.; Witte, O. N.; Xu, Y. : Sphingosylphosphorylcholine and lysophosphatidylcholine are ligands f.

[72763] Further studies establishing the function and utilities of GPR4 are found in John Hopkins OMIM database record ID 600551, and in sited publications numbered 7874-787 and 7883 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Homeo Box D4 (HOXD4, Accession NM_014621) is another VGAM2087 host target gene. HOXD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by HOXD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOXD4 BINDING SITE, designated SEQ ID:15979, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72764] Another function of VGAM2087 is therefore inhibition of Homeo Box D4 (HOXD4, Accession NM_014621), a gene which is part of a developmental regulatory system. Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXD4. The function of HOXD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM330.Baculoviral IAP Repeat-containing 3 (BIRC3, Accession XM_040715) is another VGAM2087 host target gene. BIRC3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BIRC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIRC3 BIND-

ING SITE, designated SEQ ID:33369, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72765] Another function of VGAM2087 is therefore inhibition of Baculoviral IAP Repeat-containing 3 (BIRC3, Accession XM_040715). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIRC3. Doublecortin and CaM Kinase-like 1 (DCAMKL1, Accession NM_004734) is another VGAM2087 host target gene. DCAMKL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCAMKL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCAMKL1 BINDING SITE, designated SEQ ID:11111, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72766] Another function of VGAM2087 is therefore inhibition of Doublecortin and CaM Kinase-like 1 (DCAMKL1, Accession NM_004734). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCAMKL1. DKFZP434C212

(Accession XM_044196) is another VGAM2087 host target gene. DKFZP434C212 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434C212, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434C212 BINDING SITE, designated SEQ ID:34171, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72767] Another function of VGAM2087 is therefore inhibition of DKFZP434C212 (Accession XM_044196). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434C212. FLJ14641 (Accession NM_032817) is another VGAM2087 host target gene. FLJ14641 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ14641, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14641 BINDING SITE, designated SEQ ID:26592, to the nucleotide sequence of VGAM2087 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4798.

[72768] Another function of VGAM2087 is therefore inhibition of FLJ14641 (Accession NM_032817). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14641. GDNF Family Receptor Alpha 4 (GFRA4, Accession NM_022139) is another VGAM2087 host target gene. GFRA4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GFRA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GFRA4 BINDING SITE, designated SEQ ID:22702, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72769] Another function of VGAM2087 is therefore inhibition of GDNF Family Receptor Alpha 4 (GFRA4, Accession NM_022139). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GFRA4. KIAA0939 (Accession XM_030524) is another VGAM2087 host target gene. KIAA0939 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by KIAA0939, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0939 BINDING SITE, designated SEQ ID:31057, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72770] Another function of VGAM2087 is therefore inhibition of KIAA0939 (Accession XM_030524). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0939. KIAA0961 (Accession NM_014898) is another VGAM2087 host target gene. KIAA0961 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0961, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0961 BINDING SITE, designated SEQ ID:17076, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72771] Another function of VGAM2087 is therefore inhibition of

KIAA0961 (Accession NM_014898). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0961. KIAA1054 (Accession XM_043493) is another VGAM2087 host target gene. KIAA1054 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1054 BINDING SITE, designated SEQ ID:33956, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72772] Another function of VGAM2087 is therefore inhibition of KIAA1054 (Accession XM_043493). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1054. KIAA1297 (Accession XM_051005) is another VGAM2087 host target gene. KIAA1297 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1297, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1297 BINDING SITE, designated SEQ ID:35706, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72773] Another function of VGAM2087 is therefore inhibition of KIAA1297 (Accession XM_051005). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1297. KIAA1854 (Accession XM_049884) is another VGAM2087 host target gene. KIAA1854 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1854, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1854 BINDING SITE, designated SEQ ID:35522, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72774] Another function of VGAM2087 is therefore inhibition of KIAA1854 (Accession XM_049884). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1854. MGC10715 (Accession NM_024325) is another

VGAM2087 host target gene. MGC10715 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC10715, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10715 BINDING SITE, designated SEQ ID:23612, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72775] Another function of VGAM2087 is therefore inhibition of MGC10715 (Accession NM_024325). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10715. My015 (Accession XM_039512) is another VGAM2087 host target gene. My015 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by My015, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of My015 BINDING SITE, designated SEQ ID:33104, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72776] Another function of VGAM2087 is therefore inhibition of My015 (Accession XM_039512). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with My015. PRO2893 (Accession NM_018634) is another VGAM2087 host target gene. PRO2893 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO2893, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2893 BINDING SITE, designated SEQ ID:20706, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72777] Another function of VGAM2087 is therefore inhibition of PRO2893 (Accession NM_018634). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2893. RNP24 (Accession NM_006815) is another VGAM2087 host target gene. RNP24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNP24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNP24 BINDING SITE, designated SEQ ID:13693, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72778] Another function of VGAM2087 is therefore inhibition of RNP24 (Accession NM_006815). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNP24. Trinucleotide Repeat Containing 9 (TNRC9, Accession XM_049037) is another VGAM2087 host target gene. TNRC9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNRC9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNRC9 BINDING SITE, designated SEQ ID:35319, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72779] Another function of VGAM2087 is therefore inhibition of Trinucleotide Repeat Containing 9 (TNRC9, Accession XM_049037). Accordingly, utilities of VGAM2087 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with TNRC9. LOC121838 (Accession XM_071772) is another VGAM2087 host target gene. LOC121838 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC121838, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC121838 BINDING SITE, designated SEQ ID:37419, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72780] Another function of VGAM2087 is therefore inhibition of LOC121838 (Accession XM_071772). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121838. LOC130814 (Accession XM_059471) is another VGAM2087 host target gene. LOC130814 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130814, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC130814 BINDING SITE, designated SEQ ID:37008, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72781] Another function of VGAM2087 is therefore inhibition of LOC130814 (Accession XM_059471). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130814. LOC144845 (Accession NM_138474) is another VGAM2087 host target gene. LOC144845 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144845, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144845 BINDING SITE, designated SEQ ID:28824, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72782] Another function of VGAM2087 is therefore inhibition of LOC144845 (Accession NM_138474). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144845. LOC93550 (Accession XM_051999) is another VGAM2087 host target gene. LOC93550 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93550, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93550 BINDING SITE, designated SEQ ID:35934, to the nucleotide sequence of VGAM2087 RNA, herein designated VGAM RNA, also designated SEQ ID:4798.

[72783] Another function of VGAM2087 is therefore inhibition of LOC93550 (Accession XM_051999). Accordingly, utilities of VGAM2087 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93550. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2088 (VGAM2088) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72784] VGAM2088 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2088 was detected is described hereinabove with reference to Figs. 1-8.

[72785] VGAM2088 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox Virus. VGAM2088 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72786] VGAM2088 gene encodes a VGAM2088 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2088 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2088 precursor RNA is designated SEQ ID:2074, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2074 is located at position 97767 relative to the genome of Fowlpox Virus.

[72787] VGAM2088 precursor RNA folds onto itself, forming VGAM2088 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[72788] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2088 folded precursor RNA into VGAM2088 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2088 RNA is designated SEQ ID:4799, and is provided hereinbelow with reference to the sequence listing part.

[72789] VGAM2088 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2088 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2088 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72790] VGAM2088 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2088 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2088 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2088 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2088 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72791] The complementary binding of VGAM2088 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2088 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2088 host target RNA into VGAM2088 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72792] It is appreciated that VGAM2088 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2088 host target genes. The mRNA of each one of this plurality of VGAM2088 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2088 RNA, herein designated VGAM RNA, and which when bound by VGAM2088 RNA causes inhibition of translation of respective one or more VGAM2088 host target proteins.

[72793] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2088 gene, herein designated VGAM GENE, on one or more VGAM2088 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72794] It is yet further appreciated that a function of VGAM2088 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGAM2088 correlate with, and may be deduced from, the identity of the host target genes which VGAM2088 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72795] Nucleotide sequences of the VGAM2088 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2088 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2088 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2088 are further described hereinbelow with reference to Table 1.

[72796] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2088 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2088 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72797] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2088 gene, herein designated VGAM is inhibition of expression of VGAM2088 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2088 correlate with, and may be deduced from, the identity of the target genes which VGAM2088 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72798] IQ Motif Containing GTPase Activating Protein 2 (IQGAP2, Accession NM_006633) is a VGAM2088 host target gene. IQGAP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IQGAP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Ta-

ble 2 illustrates the complementarity of the nucleotide sequences of IQGAP2 BINDING SITE, designated SEQ ID:13428, to the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA, also designated SEQ ID:4799.

[72799] A function of VGAM2088 is therefore inhibition of IQ Motif Containing GTPase Activating Protein 2 (IQGAP2, Accession NM_006633), a gene which Inhibits GTPase activity of Cdc42 and Rac1. Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IQGAP2. The function of IQGAP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM110.NCSTN (Accession XM_057331) is another VGAM2088 host target gene. NCSTN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NCSTN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCSTN BINDING SITE, designated SEQ ID:36509, to the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA,

also designated SEQ ID:4799.

[72800] Another function of VGAM2088 is therefore inhibition of NCSTN (Accession XM_057331), a gene which has a central role in presenilin-mediated processing of beta-amyloid precursor protein (beta-APP, MIM 104760) and some aspects of notch (MIM 190198)/glp-1 signaling in vivo. Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCSTN. The function of NCSTN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273) is another VGAM2088 host target gene. CHST3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHST3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHST3 BINDING SITE, designated SEQ ID:10487, to the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA, also designated SEQ ID:4799.

[72801] Another function of VGAM2088 is therefore inhibition of Carbohydrate (chondroitin 6) Sulfotransferase 3 (CHST3, Accession NM_004273). Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHST3. FLJ11577 (Accession NM_025159) is another VGAM2088 host target gene. FLJ11577 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11577 BINDING SITE, designated SEQ ID:24799, to the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA, also designated SEQ ID:4799.

[72802] Another function of VGAM2088 is therefore inhibition of FLJ11577 (Accession NM_025159). Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11577. Fused Toes Homolog (mouse) (FTS, Accession NM_022476) is another VGAM2088 host target gene. FTS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FTS, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FTS BINDING SITE, designated SEQ ID:22844, to the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA, also designated SEQ ID:4799.

[72803] Another function of VGAM2088 is therefore inhibition of Fused Toes Homolog (mouse) (FTS, Accession NM_022476). Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FTS. G Protein-coupled Receptor Kinase-interactor 2 (GIT2, Accession NM_014776) is another VGAM2088 host target gene. GIT2 BINDING SITE1 through GIT2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GIT2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GIT2 BINDING SITE1 through GIT2 BINDING SITE3, designated SEQ ID:16607, SEQ ID:27689 and SEQ ID:27702 respectively, to the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA, also designated SEQ ID:4799.

[72804] Another function of VGAM2088 is therefore inhibition of G Protein-coupled Receptor Kinase-interactor 2 (GIT2, Accession NM_014776). Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GIT2. KIAA0478 (Accession NM_014870) is another VGAM2088 host target gene. KIAA0478 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0478, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0478 BINDING SITE, designated SEQ ID:16985, to the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA, also designated SEQ ID:4799.

[72805] Another function of VGAM2088 is therefore inhibition of KIAA0478 (Accession NM_014870). Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0478. KIAA1681 (Accession XM_028059) is another VGAM2088 host target gene. KIAA1681 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1681, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1681 BINDING SITE, designated SEQ ID:30612, to the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA, also designated SEQ ID:4799.

[72806] Another function of VGAM2088 is therefore inhibition of KIAA1681 (Accession XM_028059). Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1681. LOC153688 (Accession XM_098416) is another VGAM2088 host target gene. LOC153688 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153688, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153688 BINDING SITE, designated SEQ ID:41664, to the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA, also designated SEQ ID:4799.

[72807] Another function of VGAM2088 is therefore inhibition of LOC153688 (Accession XM_098416). Accordingly, utilities of VGAM2088 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC153688. LOC200301 (Accession XM_114197) is another VGAM2088 host target gene. LOC200301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200301 BINDING SITE, designated SEQ ID:42780, to the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA, also designated SEQ ID:4799.

[72808] Another function of VGAM2088 is therefore inhibition of LOC200301 (Accession XM_114197). Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200301. LOC255458 (Accession XM_173150) is another VGAM2088 host target gene. LOC255458 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255458, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255458 BINDING SITE, designated SEQ ID:46408, to

the nucleotide sequence of VGAM2088 RNA, herein designated VGAM RNA, also designated SEQ ID:4799.

[72809] Another function of VGAM2088 is therefore inhibition of LOC255458 (Accession XM_173150). Accordingly, utilities of VGAM2088 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255458. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2089 (VGAM2089) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72810] VGAM2089 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2089 was detected is described hereinabove with reference to Figs. 1-8.

[72811] VGAM2089 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox Virus.
VGAM2089 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72812] VGAM2089 gene encodes a VGAM2089 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2089 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2089 precursor RNA is designated SEQ ID:2075, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2075 is located at position 103219 relative to the genome of Fowlpox Virus.

[72813] VGAM2089 precursor RNA folds onto itself, forming VGAM2089 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72814] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2089 folded precursor RNA into VGAM2089 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2089 RNA is designated SEQ ID:4800, and is provided hereinbelow with reference to the sequence listing part.

[72815] VGAM2089 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2089 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2089 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72816] VGAM2089 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2089 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2089 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2089 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2089 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72817] The complementary binding of VGAM2089 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2089 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2089 host target RNA into VGAM2089 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72818] It is appreciated that VGAM2089 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2089 host target genes. The mRNA of each one of this plurality of VGAM2089 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2089 RNA, herein designated VGAM RNA, and which when bound by VGAM2089 RNA causes inhibition of translation of respective one or more VGAM2089 host target proteins.

[72819] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2089 gene, herein designated VGAM GENE, on one or more VGAM2089 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72820] It is yet further appreciated that a function of VGAM2089 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2089 include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGAM2089 correlate with, and may be deduced from, the identity of the host target genes which VGAM2089 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72821] Nucleotide sequences of the VGAM2089 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2089 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2089 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2089 are further described hereinbelow with reference to Table 1.

[72822] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2089 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2089 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72823] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2089 gene, herein designated VGAM is inhibition of expression of VGAM2089 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2089 correlate with, and may be deduced from, the identity of the target genes which VGAM2089 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72824] Protein Kinase, CGMP-dependent, Type I (PRKG1, Accession NM_006258) is a VGAM2089 host target gene. PRKG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKG1 BINDING SITE, designated SEQ ID:12936, to the nucleotide sequence of VGAM2089 RNA, herein designated VGAM RNA, also designated SEQ ID:4800.

[72825] A function of VGAM2089 is therefore inhibition of Protein Kinase, CGMP-dependent, Type I (PRKG1, Accession

NM_006258), a gene which relaxes vascular smooth muscle and inhibits platelet aggregation. Accordingly, utilities of VGAM2089 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKG1. The function of PRKG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1571.Asporin (LRR class 1) (ASPN, Accession NM_017680) is another VGAM2089 host target gene. ASPN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ASPN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ASPN BINDING SITE, designated SEQ ID:19225, to the nucleotide sequence of VGAM2089 RNA, herein designated VGAM RNA, also designated SEQ ID:4800.

[72826] Another function of VGAM2089 is therefore inhibition of Asporin (LRR class 1) (ASPN, Accession NM_017680). Accordingly, utilities of VGAM2089 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASPN. DKFZp434A2417 (Accession XM_038526) is another VGAM2089 host target gene. DK-

FZp434A2417 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434A2417, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434A2417 BINDING SITE, designated SEQ ID:32863, to the nucleotide sequence of VGAM2089 RNA, herein designated VGAM RNA, also designated SEQ ID:4800.

[72827] Another function of VGAM2089 is therefore inhibition of DKFZp434A2417 (Accession XM_038526). Accordingly, utilities of VGAM2089 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434A2417. LOC257017 (Accession XM_173227) is another VGAM2089 host target gene. LOC257017 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257017, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257017 BINDING SITE, designated SEQ ID:46495, to the nucleotide sequence of VGAM2089 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4800.

[72828] Another function of VGAM2089 is therefore inhibition of LOC257017 (Accession XM_173227). Accordingly, utilities of VGAM2089 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257017. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2090 (VGAM2090) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72829] VGAM2090 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2090 was detected is described hereinabove with reference to Figs. 1-8.

[72830] VGAM2090 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox Virus. VGAM2090 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72831] VGAM2090 gene encodes a VGAM2090 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2090 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2090 precursor RNA is designated SEQ ID:2076, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2076 is located at position 110457 relative to the genome of Fowlpox Virus.

[72832] VGAM2090 precursor RNA folds onto itself, forming VGAM2090 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72833] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2090 folded precursor RNA into VGAM2090 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2090 RNA is designated SEQ ID:4801, and is provided hereinbelow with reference to the sequence listing part.

[72834] VGAM2090 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2090 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2090 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72835] VGAM2090 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2090 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2090 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2090 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2090 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72836] The complementary binding of VGAM2090 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2090 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2090 host target RNA into VGAM2090 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72837] It is appreciated that VGAM2090 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2090 host target genes. The mRNA of

each one of this plurality of VGAM2090 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2090 RNA, herein designated VGAM RNA, and which when bound by VGAM2090 RNA causes inhibition of translation of respective one or more VGAM2090 host target proteins.

[72838] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2090 gene, herein designated VGAM GENE, on one or more VGAM2090 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[72839] It is yet further appreciated that a function of VGAM2090 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGAM2090 correlate with, and may be deduced from, the identity of the host target genes which VGAM2090 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72840] Nucleotide sequences of the VGAM2090 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2090 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2090 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2090 are further described hereinbelow with reference to Table 1.

[72841] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2090 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2090 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72842] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2090 gene, herein designated VGAM is inhibition of expression of VGAM2090 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2090 correlate with, and may be deduced from, the identity of the target genes which VGAM2090 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72843] Membrane Component, Chromosome 11, Surface Marker 1 (M11S1, Accession NM_005898) is a VGAM2090 host target gene. M11S1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by M11S1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of M11S1 BINDING SITE, designated SEQ ID:12515, to the nucleotide sequence of VGAM2090 RNA, herein designated VGAM RNA, also designated SEQ ID:4801.

[72844] A function of VGAM2090 is therefore inhibition of Membrane Component, Chromosome 11, Surface Marker 1

(M11S1, Accession NM_005898), a gene which may play a role in transporting nutrients from the gut lumen across the gutlining epithelial cell layer. Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of diseases and clinical conditions associated with M11S1. The function of M11S1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM131.Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog 2 (mouse) (MEIS2, Accession NM_020149) is another VGAM2090 host target gene. MEIS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEIS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEIS2 BINDING SITE, designated SEQ ID:21346, to the nucleotide sequence of VGAM2090 RNA, herein designated VGAM RNA, also designated SEQ ID:4801.

[72845] Another function of VGAM2090 is therefore inhibition of Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog 2 (mouse) (MEIS2, Accession NM_020149), a gene which may regulate gene expression and control cell differentia-

tion. Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEIS2. The function of MEIS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1244.Ribonucleotide Reductase M2 Polypeptide (RRM2, Accession NM_001034) is another VGAM2090 host target gene. RRM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RRM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RRM2 BINDING SITE, designated SEQ ID:6697, to the nucleotide sequence of VGAM2090 RNA, herein designated VGAM RNA, also designated SEQ ID:4801.

[72846] Another function of VGAM2090 is therefore inhibition of Ribonucleotide Reductase M2 Polypeptide (RRM2, Accession NM_001034). Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RRM2. Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 4

(SLC4A4, Accession NM_003759) is another VGAM2090 host target gene. SLC4A4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC4A4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC4A4 BINDING SITE, designated SEQ ID:9836, to the nucleotide sequence of VGAM2090 RNA, herein designated VGAM RNA, also designated SEQ ID:4801.

[72847] Another function of VGAM2090 is therefore inhibition of Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 4 (SLC4A4, Accession NM_003759), a gene which is a sodium bicarbonate cotransporter. Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC4A4. The function of SLC4A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM222.Chromosome 1 Open Reading Frame 22 (C1orf22, Accession NM_025191) is another VGAM2090 host target gene. C1orf22 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by C1orf22, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf22 BINDING SITE, designated SEQ ID:24835, to the nucleotide sequence of VGAM2090 RNA, herein designated VGAM RNA, also designated SEQ ID:4801.

[72848] Another function of VGAM2090 is therefore inhibition of Chromosome 1 Open Reading Frame 22 (C1orf22, Accession NM_025191). Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf22. INSM2 (Accession NM_032594) is another VGAM2090 host target gene. INSM2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by INSM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of INSM2 BINDING SITE, designated SEQ ID:26325, to the nucleotide sequence of VGAM2090 RNA, herein designated VGAM RNA, also designated SEQ ID:4801.

[72849] Another function of VGAM2090 is therefore inhibition of

INSM2 (Accession NM_032594). Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INSM2. KIAA0352 (Accession NM_014830) is another VGAM2090 host target gene. KIAA0352 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0352, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0352 BINDING SITE, designated SEQ ID:16821, to the nucleotide sequence of VGAM2090 RNA, herein designated VGAM RNA, also designated SEQ ID:4801.

[72850] Another function of VGAM2090 is therefore inhibition of KIAA0352 (Accession NM_014830). Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0352. PRO2730 (Accession NM_025222) is another VGAM2090 host target gene. PRO2730 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2730, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PRO2730 BINDING SITE, designated SEQ ID:24897, to the nucleotide sequence of VGAM2090 RNA, herein designated VGAM RNA, also designated SEQ ID:4801.

[72851] Another function of VGAM2090 is therefore inhibition of PRO2730 (Accession NM_025222). Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2730. Spir-1 (Accession XM_035640) is another VGAM2090 host target gene. Spir-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Spir-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Spir-1 BINDING SITE, designated SEQ ID:32310, to the nucleotide sequence of VGAM2090 RNA, herein designated VGAM RNA, also designated SEQ ID:4801.

[72852] Another function of VGAM2090 is therefore inhibition of Spir-1 (Accession XM_035640). Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Spir-1. LOC253649 (Accession XM_171211) is another

VGAM2090 host target gene. LOC253649 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253649, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253649 BINDING SITE, designated SEQ ID:45998, to the nucleotide sequence of VGAM2090 RNA, herein designated VGAM RNA, also designated SEQ ID:4801.

[72853] Another function of VGAM2090 is therefore inhibition of LOC253649 (Accession XM_171211). Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253649. LOC253650 (Accession XM_171210) is another VGAM2090 host target gene. LOC253650 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253650, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253650 BINDING SITE, designated SEQ ID:45996, to the nucleotide sequence of VGAM2090 RNA, herein designated VGAM RNA, also designated SEQ ID:4801.

[72854] Another function of VGAM2090 is therefore inhibition of LOC253650 (Accession XM_171210). Accordingly, utilities of VGAM2090 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253650. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2091 (VGAM2091) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72855] VGAM2091 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2091 was detected is described hereinabove with reference to Figs. 1-8.

[72856] VGAM2091 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox Virus. VGAM2091 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72857] VGAM2091 gene encodes a VGAM2091 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2091 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2091 precursor RNA is designated SEQ ID:2077, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2077 is located at position 108768 relative to the genome of Fowlpox Virus.

[72858] VGAM2091 precursor RNA folds onto itself, forming VGAM2091 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72859] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2091 folded precursor RNA into VGAM2091 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2091 RNA is designated SEQ ID:4802, and is provided hereinbelow with reference to the sequence listing part.

[72860] VGAM2091 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2091 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2091 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72861] VGAM2091 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2091 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2091 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2091 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2091 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72862] The complementary binding of VGAM2091 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2091 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2091 host target RNA into VGAM2091 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72863] It is appreciated that VGAM2091 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2091 host target genes. The mRNA of each one of this plurality of VGAM2091 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2091 RNA, herein designated VGAM RNA, and which when bound by VGAM2091 RNA causes inhibition of translation of respective one or more VGAM2091 host target proteins.

[72864] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2091 gene, herein designated VGAM GENE, on one or more VGAM2091 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72865] It is yet further appreciated that a function of VGAM2091 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2091 include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGAM2091 correlate with, and may be deduced from, the identity of the host target genes which VGAM2091 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72866] Nucleotide sequences of the VGAM2091 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2091 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2091 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2091 are further described hereinbelow with reference to Table 1.

[72867] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2091 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2091 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[72868] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2091 gene, herein designated VGAM is inhibition of expression of VGAM2091 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2091 correlate with, and may be deduced from, the identity of the target genes which VGAM2091 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72869] Fibroblast Growth Factor 7 (keratinocyte growth factor) (FGF7, Accession NM_002009) is a VGAM2091 host target gene. FGF7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FGF7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF7 BINDING SITE, designated SEQ ID:7746, to the nucleotide sequence of VGAM2091 RNA, herein designated VGAM RNA, also designated SEQ ID:4802.

[72870] A function of VGAM2091 is therefore inhibition of Fibroblast Growth Factor 7 (keratinocyte growth factor) (FGF7, Accession NM_002009), a gene which growth factor active on keratinocytes. Accordingly, utilities of VGAM2091 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF7. The function of FGF7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM678.Glutamate Decarboxylase 1 (brain, 67kDa) (GAD1, Accession NM_000817) is another VGAM2091 host target gene. GAD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GAD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAD1 BINDING SITE, designated SEQ ID:6477, to the nucleotide sequence of VGAM2091 RNA, herein designated VGAM RNA, also designated SEQ ID:4802.

[72871] Another function of VGAM2091 is therefore inhibition of Glutamate Decarboxylase 1 (brain, 67kDa) (GAD1, Accession NM_000817), a gene which catalyzes the conversion of glutamic acid to gamma-aminobutyric acid. Accordingly, utilities of VGAM2091 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAD1. The function of GAD1 and its association

with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM691.Surfeit 4 (SURF4, Accession NM_033161) is another VGAM2091 host target gene. SURF4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SURF4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SURF4 BINDING SITE, designated SEQ ID:27013, to the nucleotide sequence of VGAM2091 RNA, herein designated VGAM RNA, also designated SEQ ID:4802.

[72872] Another function of VGAM2091 is therefore inhibition of Surfeit 4 (SURF4, Accession NM_033161), a gene which is a conserved integral membrane protein containing multiple putative transmembrane regions. Accordingly, utilities of VGAM2091 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SURF4. The function of SURF4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM496.KIAA1866 (Accession XM_027658)

is another VGAM2091 host target gene. KIAA1866 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1866, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1866 BINDING SITE, designated SEQ ID:30551, to the nucleotide sequence of VGAM2091 RNA, herein designated VGAM RNA, also designated SEQ ID:4802.

[72873] Another function of VGAM2091 is therefore inhibition of KIAA1866 (Accession XM_027658). Accordingly, utilities of VGAM2091 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1866. Regulator of G-protein Signalling 18 (RGS18, Accession NM_130782) is another VGAM2091 host target gene. RGS18 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RGS18, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RGS18 BINDING SITE, designated SEQ ID:28271, to the nucleotide sequence of VGAM2091 RNA, herein designated VGAM RNA, also designated SEQ

ID:4802.

[72874] Another function of VGAM2091 is therefore inhibition of Regulator of G-protein Signalling 18 (RGS18, Accession NM_130782). Accordingly, utilities of VGAM2091 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS18. Zinc Finger Protein 237 (ZNF237, Accession NM_014242) is another VGAM2091 host target gene. ZNF237 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF237, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF237 BINDING SITE, designated SEQ ID:15503, to the nucleotide sequence of VGAM2091 RNA, herein designated VGAM RNA, also designated SEQ ID:4802.

[72875] Another function of VGAM2091 is therefore inhibition of Zinc Finger Protein 237 (ZNF237, Accession NM_014242). Accordingly, utilities of VGAM2091 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF237. LOC144874 (Accession XM_096696) is another VGAM2091 host target gene. LOC144874 BINDING SITE is HOST TARGET binding site

found in the 5` untranslated region of mRNA encoded by LOC144874, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144874 BINDING SITE, designated SEQ ID:40467, to the nucleotide sequence of VGAM2091 RNA, herein designated VGAM RNA, also designated SEQ ID:4802.

[72876] Another function of VGAM2091 is therefore inhibition of LOC144874 (Accession XM_096696). Accordingly, utilities of VGAM2091 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144874. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2092 (VGAM2092) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72877] VGAM2092 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2092 was detected is described hereinabove with reference to Figs. 1-8.

[72878] VGAM2092 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Fowlpox Virus. VGAM2092 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72879] VGAM2092 gene encodes a VGAM2092 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2092 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2092 precursor RNA is designated SEQ ID:2078, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2078 is located at position 102276 relative to the genome of Fowlpox Virus.

[72880] VGAM2092 precursor RNA folds onto itself, forming VGAM2092 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[72881] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2092 folded precursor RNA into VGAM2092 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM2092 RNA is designated SEQ ID:4803, and is provided hereinbelow with reference to the sequence listing part.

[72882] VGAM2092 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2092 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2092 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72883] VGAM2092 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2092 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2092 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2092 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2092 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72884] The complementary binding of VGAM2092 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2092 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2092 host target RNA into VGAM2092 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72885] It is appreciated that VGAM2092 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2092 host target genes. The mRNA of each one of this plurality of VGAM2092 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2092 RNA, herein designated VGAM RNA, and which when bound by VGAM2092 RNA causes inhibition of translation of respective one or more VGAM2092 host target proteins.

[72886] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2092 gene, herein designated VGAM GENE, on one or more VGAM2092 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72887] It is yet further appreciated that a function of VGAM2092 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2092 include diagnosis, prevention and treatment of viral infection by Fowlpox Virus. Specific functions, and accordingly utilities, of VGAM2092 correlate with, and may be deduced from, the identity of the host target genes which VGAM2092 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72888] Nucleotide sequences of the VGAM2092 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2092 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2092 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2092 are further described hereinbelow with reference to Table 1.

[72889] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2092 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2092 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72890] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2092 gene, herein designated VGAM is inhibition of expression of VGAM2092 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2092 correlate with, and may be deduced from, the identity of the target genes which VGAM2092 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72891] TEM8 (Accession NM_032208) is a VGAM2092 host target gene. TEM8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEM8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of TEM8 BINDING SITE, designated SEQ ID:25920, to the nucleotide sequence of VGAM2092 RNA, herein designated VGAM RNA, also designated SEQ ID:4803.

[72892] A function of VGAM2092 is therefore inhibition of TEM8 (Accession NM_032208), a gene which is a tumor-specific endothelial marker. Accordingly, utilities of VGAM2092 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEM8. The function of TEM8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1489.FLJ10458 (Accession NM_018096) is another VGAM2092 host target gene. FLJ10458 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10458, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10458 BINDING SITE, designated SEQ ID:19867, to the nucleotide sequence of VGAM2092 RNA, herein designated VGAM RNA, also designated SEQ ID:4803.

[72893] Another function of VGAM2092 is therefore inhibition of FLJ10458 (Accession NM_018096). Accordingly, utilities of

VGAM2092 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10458. KIAA0478 (Accession NM_014870) is another VGAM2092 host target gene. KIAA0478 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0478, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0478 BINDING SITE, designated SEQ ID:16987, to the nucleotide sequence of VGAM2092 RNA, herein designated VGAM RNA, also designated SEQ ID:4803.

[72894] Another function of VGAM2092 is therefore inhibition of KIAA0478 (Accession NM_014870). Accordingly, utilities of VGAM2092 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0478. ZW10 Interactor (ZWINT, Accession NM_032997) is another VGAM2092 host target gene. ZWINT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZWINT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of ZWINT BINDING SITE, designated SEQ ID:26877, to the nucleotide sequence of VGAM2092 RNA, herein designated VGAM RNA, also designated SEQ ID:4803.

[72895] Another function of VGAM2092 is therefore inhibition of ZW10 Interactor (ZWINT, Accession NM_032997). Accordingly, utilities of VGAM2092 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZWINT. LOC144231 (Accession XM_096561) is another VGAM2092 host target gene. LOC144231 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144231 BINDING SITE, designated SEQ ID:40395, to the nucleotide sequence of VGAM2092 RNA, herein designated VGAM RNA, also designated SEQ ID:4803.

[72896] Another function of VGAM2092 is therefore inhibition of LOC144231 (Accession XM_096561). Accordingly, utilities of VGAM2092 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144231. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2093 (VGAM2093) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72897] VGAM2093 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2093 was detected is described hereinabove with reference to Figs. 1-8.

[72898] VGAM2093 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2093 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72899] VGAM2093 gene encodes a VGAM2093 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2093 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2093 precursor RNA is designated SEQ ID:2079, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2079 is located at position 164255 relative to the genome of Camelpox Virus.

[72900] VGAM2093 precursor RNA folds onto itself, forming VGAM2093 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72901] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2093 folded precursor RNA into VGAM2093 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2093 RNA is designated SEQ ID:4804, and is provided hereinbelow with reference to the sequence listing part.

[72902] VGAM2093 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2093 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2093 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72903] VGAM2093 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2093 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2093 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2093 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2093 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72904] The complementary binding of VGAM2093 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2093 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2093 host target RNA into VGAM2093 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72905] It is appreciated that VGAM2093 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2093 host target genes. The mRNA of each one of this plurality of VGAM2093 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2093 RNA, herein designated VGAM RNA, and which when bound by VGAM2093 RNA causes inhibition of translation of respective one or more

VGAM2093 host target proteins.

[72906] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2093 gene, herein designated VGAM GENE, on one or more VGAM2093 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72907] It is yet further appreciated that a function of VGAM2093 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2093 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific

functions, and accordingly utilities, of VGAM2093 correlate with, and may be deduced from, the identity of the host target genes which VGAM2093 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72908] Nucleotide sequences of the VGAM2093 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2093 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2093 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2093 are further described hereinbelow with reference to Table 1.

[72909] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2093 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2093 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72910] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2093 gene, herein designated VGAM is inhibition of expression of VGAM2093 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2093 correlate with, and may be deduced from, the identity of the target genes which VGAM2093 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72911] Adaptor-related Protein Complex 1, Sigma 2 Subunit (AP1S2, Accession NM_003916) is a VGAM2093 host target gene. AP1S2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP1S2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP1S2 BINDING SITE, designated SEQ ID:9999, to the nucleotide sequence of VGAM2093 RNA, herein designated VGAM RNA, also designated SEQ ID:4804.

[72912] A function of VGAM2093 is therefore inhibition of Adaptor-related Protein Complex 1, Sigma 2 Subunit (AP1S2, Accession NM_003916). Accordingly, utilities of VGAM2093 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP1S2. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger

2094 (VGAM2094) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72913] VGAM2094 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2094 was detected is described hereinabove with reference to Figs. 1-8.

[72914] VGAM2094 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2094 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72915] VGAM2094 gene encodes a VGAM2094 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2094 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2094 precursor RNA is designated SEQ ID:2080, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2080 is located at position 169679 relative to the genome of Camelpox Virus.

[72916] VGAM2094 precursor RNA folds onto itself, forming

VGAM2094 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72917] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2094 folded precursor RNA into VGAM2094 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2094 RNA is designated SEQ ID:4805, and is provided hereinbelow with reference to the sequence listing part.

[72918] VGAM2094 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2094 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2094 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72919] VGAM2094 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2094 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2094 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2094 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2094 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72920] The complementary binding of VGAM2094 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2094 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2094 host target RNA into VGAM2094 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72921] It is appreciated that VGAM2094 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2094 host target genes. The mRNA of each one of this plurality of VGAM2094 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2094 RNA, herein designated VGAM RNA, and which when bound by VGAM2094 RNA causes inhibition of translation of respective one or more VGAM2094 host target proteins.

[72922] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2094 gene, herein designated VGAM GENE, on one or more VGAM2094 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72923] It is yet further appreciated that a function of VGAM2094 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2094 correlate with, and may be deduced from, the identity of the host target genes which VGAM2094 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[72924] Nucleotide sequences of the VGAM2094 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2094 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2094 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2094 are further described hereinbelow with reference to Table 1.

[72925] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2094 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2094 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72926] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2094 gene, herein designated VGAM is inhibition of expression of VGAM2094 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2094 correlate with, and may be deduced from, the identity of the target genes which VGAM2094 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[72927] GM2 Ganglioside Activator Protein (GM2A, Accession XM_041978) is a VGAM2094 host target gene. GM2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GM2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GM2A BINDING SITE, designated SEQ ID:33658, to the nucleotide sequence of VGAM2094 RNA, herein designated VGAM RNA, also designated SEQ ID:4805.

[72928] A function of VGAM2094 is therefore inhibition of GM2 Ganglioside Activator Protein (GM2A, Accession XM_041978). Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GM2A. Lymphocyte Cytosolic Protein 1 (L-plastin) (LCP1, Accession NM_002298) is another VGAM2094 host target gene. LCP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LCP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LCP1 BINDING

SITE, designated SEQ ID:8081, to the nucleotide sequence of VGAM2094 RNA, herein designated VGAM RNA, also designated SEQ ID:4805.

[72929] Another function of VGAM2094 is therefore inhibition of Lymphocyte Cytosolic Protein 1 (L-plastin) (LCP1, Accession NM_002298), a gene which is involved in t cell antigen receptor mediated signaling. Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LCP1. The function of LCP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM418.Ribosomal Protein S6 Kinase, 90kDa, Polypeptide 5 (RPS6KA5, Accession NM_004755) is another VGAM2094 host target gene. RPS6KA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPS6KA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPS6KA5 BINDING SITE, designated SEQ ID:11142, to the nucleotide sequence of VGAM2094 RNA, herein designated VGAM RNA, also designated SEQ ID:4805.

[72930] Another function of VGAM2094 is therefore inhibition of Ribosomal Protein S6 Kinase, 90kDa, Polypeptide 5 (RPS6KA5, Accession NM_004755), a gene which plays an essential role in the proliferation of yeast cells. Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPS6KA5. The function of RPS6KA5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM191.Tumor Protein P63 (TP63, Accession NM_003722) is another VGAM2094 host target gene. TP63 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TP63, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TP63 BINDING SITE, designated SEQ ID:9814, to the nucleotide sequence of VGAM2094 RNA, herein designated VGAM RNA, also designated SEQ ID:4805.

[72931] Another function of VGAM2094 is therefore inhibition of Tumor Protein P63 (TP63, Accession NM_003722). Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with TP63. Vacuolar Protein Sorting 41 (yeast) (VPS41, Accession NM_014396) is another VGAM2094 host target gene. VPS41 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VPS41, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS41 BINDING SITE, designated SEQ ID:15737, to the nucleotide sequence of VGAM2094 RNA, herein designated VGAM RNA, also designated SEQ ID:4805.

[72932] Another function of VGAM2094 is therefore inhibition of Vacuolar Protein Sorting 41 (yeast) (VPS41, Accession NM_014396). Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS41. KIAA0766 (Accession NM_014805) is another VGAM2094 host target gene. KIAA0766 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0766, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0766 BINDING SITE, designated

SEQ ID:16740, to the nucleotide sequence of VGAM2094 RNA, herein designated VGAM RNA, also designated SEQ ID:4805.

[72933] Another function of VGAM2094 is therefore inhibition of KIAA0766 (Accession NM_014805). Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0766. Paternally Expressed 10 (PEG10, Accession NM_015068) is another VGAM2094 host target gene. PEG10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PEG10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEG10 BINDING SITE, designated SEQ ID:17422, to the nucleotide sequence of VGAM2094 RNA, herein designated VGAM RNA, also designated SEQ ID:4805.

[72934] Another function of VGAM2094 is therefore inhibition of Paternally Expressed 10 (PEG10, Accession NM_015068). Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEG10. LOC146506 (Accession

XM_085489) is another VGAM2094 host target gene. LOC146506 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146506, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146506 BINDING SITE, designated SEQ ID:38177, to the nucleotide sequence of VGAM2094 RNA, herein designated VGAM RNA, also designated SEQ ID:4805.

[72935] Another function of VGAM2094 is therefore inhibition of LOC146506 (Accession XM_085489). Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146506. LOC149301 (Accession XM_086480) is another VGAM2094 host target gene. LOC149301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149301 BINDING SITE, designated SEQ ID:38689, to the nucleotide sequence of VGAM2094 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4805.

[72936] Another function of VGAM2094 is therefore inhibition of LOC149301 (Accession XM_086480). Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149301. LOC153525 (Accession XM_098383) is another VGAM2094 host target gene. LOC153525 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153525, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153525 BINDING SITE, designated SEQ ID:41637, to the nucleotide sequence of VGAM2094 RNA, herein designated VGAM RNA, also designated SEQ ID:4805.

[72937] Another function of VGAM2094 is therefore inhibition of LOC153525 (Accession XM_098383). Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153525. LOC255520 (Accession XM_171073) is another VGAM2094 host target gene. LOC255520 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255520, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255520 BINDING SITE, designated SEQ ID:45878, to the nucleotide sequence of VGAM2094 RNA, herein designated VGAM RNA, also designated SEQ ID:4805.

[72938] Another function of VGAM2094 is therefore inhibition of LOC255520 (Accession XM_171073). Accordingly, utilities of VGAM2094 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255520. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2095 (VGAM2095) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72939] VGAM2095 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2095 was detected is described hereinabove with reference to Figs. 1-8.

[72940] VGAM2095 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus.

VGAM2095 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72941] VGAM2095 gene encodes a VGAM2095 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2095 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2095 precursor RNA is designated SEQ ID:2081, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2081 is located at position 174432 relative to the genome of Camelpox Virus.

[72942] VGAM2095 precursor RNA folds onto itself, forming VGAM2095 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72943] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2095 folded precursor RNA into VGAM2095 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2095 RNA is designated SEQ ID:4806, and is provided hereinbelow with reference to the sequence listing part.

[72944] VGAM2095 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2095 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2095 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72945] VGAM2095 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2095 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2095 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2095 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2095 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72946] The complementary binding of VGAM2095 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2095 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2095 host target RNA into VGAM2095 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72947] It is appreciated that VGAM2095 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2095 host target genes. The mRNA of each one of this plurality of VGAM2095 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2095 RNA, herein designated VGAM RNA, and which when bound by VGAM2095 RNA causes inhibition of translation of respective one or more VGAM2095 host target proteins.

[72948] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2095 gene, herein designated VGAM GENE, on one or more VGAM2095 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72949] It is yet further appreciated that a function of VGAM2095 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2095 correlate with, and may be deduced from, the identity of the host target genes which VGAM2095 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72950] Nucleotide sequences of the VGAM2095 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2095 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2095 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2095 are further described hereinbelow with reference to Table 1.

[72951] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2095 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2095 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72952] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2095 gene, herein designated VGAM is inhibition of expression of VGAM2095 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2095 correlate with, and may be deduced from, the identity of the target genes which VGAM2095 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72953] V-kit Hardy-Zuckerman 4 Feline Sarcoma Viral Oncogene Homolog (KIT, Accession NM_000222) is a VGAM2095 host target gene. KIT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIT BINDING SITE, designated SEQ

ID:5732, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72954] A function of VGAM2095 is therefore inhibition of V-kit Hardy-Zuckerman 4 Feline Sarcoma Viral Oncogene Homolog (KIT, Accession NM_000222), a gene which is the receptor for stem cell factor (mast cell growth factor) and has a tyrosine-protein kinase activity. Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIT. The function of KIT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM173.Pumilio Homolog 2 (Drosophila) (PUM2, Accession NM_015317) is another VGAM2095 host target gene. PUM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PUM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PUM2 BINDING SITE, designated SEQ ID:17634, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72955] Another function of VGAM2095 is therefore inhibition of Pumilio Homolog 2 (Drosophila) (PUM2, Accession NM_015317). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PUM2. Solute Carrier Family 25, Member 13 (citrin) (SLC25A13, Accession NM_014251) is another VGAM2095 host target gene. SLC25A13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC25A13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC25A13 BINDING SITE, designated SEQ ID:15523, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72956] Another function of VGAM2095 is therefore inhibition of Solute Carrier Family 25, Member 13 (citrin) (SLC25A13, Accession NM_014251). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC25A13. START Domain Containing 5 (STARD5, Accession NM_030574) is another VGAM2095 host target gene. STARD5 BINDING SITE is HOST TARGET binding site found

in the 5` untranslated region of mRNA encoded by STARD5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STARD5 BINDING SITE, designated SEQ ID:24947, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72957] Another function of VGAM2095 is therefore inhibition of START Domain Containing 5 (STARD5, Accession NM_030574). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STARD5. Transmembrane Protein 1 (TMEM1, Accession NM_003274) is another VGAM2095 host target gene. TMEM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TMEM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMEM1 BINDING SITE, designated SEQ ID:9287, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72958] Another function of VGAM2095 is therefore inhibition of Transmembrane Protein 1 (TMEM1, Accession NM_003274). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMEM1. BC022889 (Accession XM_096964) is another VGAM2095 host target gene. BC022889 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BC022889, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BC022889 BINDING SITE, designated SEQ ID:40682, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72959] Another function of VGAM2095 is therefore inhibition of BC022889 (Accession XM_096964). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BC022889. Chromosome 22 Open Reading Frame 19 (C22orf19, Accession NM_003678) is another VGAM2095 host target gene. C22orf19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by C22orf19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C22orf19 BINDING SITE, designated SEQ ID:9771, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72960] Another function of VGAM2095 is therefore inhibition of Chromosome 22 Open Reading Frame 19 (C22orf19, Accession NM_003678). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C22orf19. DKFZp761D221 (Accession NM_032291) is another VGAM2095 host target gene. DKFZp761D221 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761D221, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761D221 BINDING SITE, designated SEQ ID:26055, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72961] Another function of VGAM2095 is therefore inhibition of DKFZp761D221 (Accession NM_032291). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761D221. DKFZP761G1913 (Accession NM_031474) is another VGAM2095 host target gene. DKFZP761G1913 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP761G1913, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP761G1913 BINDING SITE, designated SEQ ID:25544, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72962] Another function of VGAM2095 is therefore inhibition of DKFZP761G1913 (Accession NM_031474). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761G1913. FLJ10706 (Accession NM_018186) is another VGAM2095 host target gene. FLJ10706 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10706, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10706 BINDING SITE, designated SEQ ID:20037, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72963] Another function of VGAM2095 is therefore inhibition of FLJ10706 (Accession NM_018186). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10706. Hydroxysteroid (17-beta) Dehydrogenase 12 (HSD17B12, Accession NM_016142) is another VGAM2095 host target gene. HSD17B12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSD17B12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSD17B12 BINDING SITE, designated SEQ ID:18226, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72964] Another function of VGAM2095 is therefore inhibition of Hydroxysteroid (17-beta) Dehydrogenase 12 (HSD17B12,

Accession NM_016142). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSD17B12. KIAA1078 (Accession XM_036589) is another VGAM2095 host target gene. KIAA1078 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1078, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1078 BINDING SITE, designated SEQ ID:32470, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72965] Another function of VGAM2095 is therefore inhibition of KIAA1078 (Accession XM_036589). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1078. SEC24 Related Gene Family, Member D (S. cerevisiae) (SEC24D, Accession NM_014822) is another VGAM2095 host target gene. SEC24D BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SEC24D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC24D BINDING SITE, designated SEQ ID:16800, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72966] Another function of VGAM2095 is therefore inhibition of SEC24 Related Gene Family, Member D (S. cerevisiae) (SEC24D, Accession NM_014822). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC24D. LOC158428 (Accession XM_047249) is another VGAM2095 host target gene. LOC158428 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158428, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158428 BINDING SITE, designated SEQ ID:34921, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72967] Another function of VGAM2095 is therefore inhibition of LOC158428 (Accession XM_047249). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC158428. LOC257428 (Accession XM_168584) is another VGAM2095 host target gene. LOC257428 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257428, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257428 BINDING SITE, designated SEQ ID:45262, to the nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72968] Another function of VGAM2095 is therefore inhibition of LOC257428 (Accession XM_168584). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257428. LOC91549 (Accession XM_039115) is another VGAM2095 host target gene. LOC91549 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91549, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91549 BINDING SITE, designated SEQ ID:33014, to the

nucleotide sequence of VGAM2095 RNA, herein designated VGAM RNA, also designated SEQ ID:4806.

[72969] Another function of VGAM2095 is therefore inhibition of LOC91549 (Accession XM_039115). Accordingly, utilities of VGAM2095 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91549. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2096 (VGAM2096) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72970] VGAM2096 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2096 was detected is described hereinabove with reference to Figs. 1-8.

[72971] VGAM2096 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2096 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72972] VGAM2096 gene encodes a VGAM2096 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2096 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2096 precursor RNA is designated SEQ ID:2082, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2082 is located at position 170764 relative to the genome of Camelpox Virus.

[72973] VGAM2096 precursor RNA folds onto itself, forming VGAM2096 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72974] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2096 folded precursor RNA into VGAM2096 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM2096 RNA is designated SEQ ID:4807, and is provided hereinbelow with reference to the sequence listing part.

[72975] VGAM2096 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2096 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2096 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72976] VGAM2096 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2096 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2096 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2096 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2096 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72977] The complementary binding of VGAM2096 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2096 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2096 host target RNA into VGAM2096 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72978] It is appreciated that VGAM2096 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2096 host target genes. The mRNA of each one of this plurality of VGAM2096 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2096 RNA, herein designated VGAM RNA, and which when bound by VGAM2096 RNA causes inhibition of translation of respective one or more VGAM2096 host target proteins.

[72979] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2096 gene, herein designated VGAM GENE, on one or more VGAM2096 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72980] It is yet further appreciated that a function of VGAM2096 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2096 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2096 correlate with, and may be deduced from, the identity of the host target genes which VGAM2096 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72981] Nucleotide sequences of the VGAM2096 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2096 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2096 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2096 are further described hereinbelow with reference to Table 1.

[72982] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2096 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2096 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72983] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2096 gene, herein designated VGAM is inhibition of expression of VGAM2096 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2096 correlate with, and may be deduced from, the identity of the target genes which VGAM2096 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[72984] LEC3 (Accession NM_015236) is a VGAM2096 host target gene. LEC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LEC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LEC3 BINDING SITE, designated SEQ ID:17574, to the nucleotide sequence of VGAM2096 RNA, herein designated VGAM RNA, also designated SEQ ID:4807.

[72985] A function of VGAM2096 is therefore inhibition of LEC3 (Accession NM_015236). Accordingly, utilities of VGAM2096 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with LEC3. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2097 (VGAM2097) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[72986] VGAM2097 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2097 was detected is described hereinabove with reference to Figs. 1-8.

[72987] VGAM2097 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2097 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[72988] VGAM2097 gene encodes a VGAM2097 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2097 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2097 precursor RNA is designated SEQ ID:2083, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2083 is located at position 176879 relative to the genome of Camelpox Virus.

[72989] VGAM2097 precursor RNA folds onto itself, forming VGAM2097 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[72990] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2097 folded precursor RNA into VGAM2097 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of VGAM2097 RNA is designated SEQ ID:4808, and is provided hereinbelow with reference to the sequence listing part.

[72991] VGAM2097 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2097 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2097 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[72992] VGAM2097 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2097 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2097 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2097 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2097 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[72993] The complementary binding of VGAM2097 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2097 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2097 host target RNA into VGAM2097 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[72994] It is appreciated that VGAM2097 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2097 host target genes. The mRNA of each one of this plurality of VGAM2097 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2097 RNA, herein designated VGAM RNA, and which when bound by VGAM2097 RNA causes

inhibition of translation of respective one or more VGAM2097 host target proteins.

[72995] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2097 gene, herein designated VGAM GENE, on one or more VGAM2097 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[72996] It is yet further appreciated that a function of VGAM2097 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2097 include diagnosis, prevention and

treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2097 correlate with, and may be deduced from, the identity of the host target genes which VGAM2097 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[72997] Nucleotide sequences of the VGAM2097 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2097 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2097 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2097 are further described hereinbelow with reference to Table 1.

[72998] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2097 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2097 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[72999] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2097 gene, herein designated VGAM is inhibition of expression of VGAM2097 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2097 correlate with, and may be deduced from, the identity of the target genes which VGAM2097 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73000] Phosphodiesterase 4D, CAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D, Accession XM_056815) is a VGAM2097 host target gene. PDE4D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE4D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE4D BINDING SITE, designated SEQ ID:36438, to the nucleotide sequence of VGAM2097 RNA, herein designated VGAM RNA, also designated SEQ ID:4808.

[73001] A function of VGAM2097 is therefore inhibition of Phosphodiesterase 4D, CAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D, Accession XM_056815), a gene which has similarity to Drosophila dnc, which is the affected protein in learning and memory mutant dunce. Accordingly, utilities of VGAM2097 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PDE4D. The function of PDE4D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM180.Trophinin (TRO, Accession NM_016157) is another VGAM2097 host target gene. TRO BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TRO, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRO BINDING SITE, designated SEQ ID:18247, to the nucleotide sequence of VGAM2097 RNA, herein designated VGAM RNA, also designated SEQ ID:4808.

[73002] Another function of VGAM2097 is therefore inhibition of Trophinin (TRO, Accession NM_016157), a gene which functions as an adhesion molecule. Accordingly, utilities of VGAM2097 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRO. The function of TRO has been established by previous studies. The initial attachment of the trophoblast to the endometrial epithelium during implantation occurs via the apical cell membranes of the embryonic and maternal

cells. Fukuda et al. (1995) found that cells from HT-H, a trophoblastic teratocarcinoma cell line, adhered efficiently to cells from SNG-M, an endometrial adenocarcinoma cell line. The adhesion was homophilic and cell type-specific, and occurred at the respective upper cell surfaces. To identify the adhesion molecules, the authors screened an HT-H expression library in COS-1 cells. They found that expression of 2 distinct cDNAs, encoding trophinin (cloned from trophoblastic cells) and tastin (OMIM Ref. No. 603872), was necessary for adhesion. The deduced 749-amino acid trophinin protein contains 69 tandem repeats of decapeptide sequences. In vitro translated trophinin has a molecular mass of 61 kD. Sequence and structural analyses revealed that trophinin is an intrinsic plasma membrane protein with 8 predicted transmembrane domains, an intracellular N-terminal region, and 3 hydrophilic regions exposed on the cell surface. COS-1 cells expressing trophinin and tastin aggregated in suspension, and soluble peptides of the cell surface domain of trophinin bound to the cell surface of trophinin-expressing cells. Northern blot analysis detected trophinin expression as 3.5-, 7.5-, and 10-kb mRNAs in both HT-H and SNG-M cells. However, neither trophinin nor tastin

was expressed in various other human cell types tested, with the exception of macrophages. Using immunofluorescence, Fukuda et al. (1995) detected strong expression of both genes in the trophectoderm surface of monkey blastocysts, as well as in human endometrial surface epithelium at a time consistent with that expected for the 'implantation window.' These authors suggested that trophinin and tastin might mediate the adhesion of the blastocyst to the endometrial epithelium at the time of implantation. Using immunohistochemistry, Suzuki et al. (1999) determined that trophinin and bystin (OMIM Ref. No. 603871), a trophinin- and tastin-binding protein, were found in the placenta from the sixth week of pregnancy. Trophinin and bystin were localized in the cytoplasm of the syncytiotrophoblast in the chorionic villi and in endometrial decidual cells at the uteroplacental interface. After week 10, the levels of trophinin, tastin, and bystin decreased and then disappeared from placental villi.

[73003] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[73004] Fukuda, M. N.; Sato, T.; Nakayama, J.; Klier, G.; Mikami,

M.; Aoki, D.; Nozawa, S. : Trophinin and tastin, a novel cell adhesion molecule complex with potential involvement in embryo implantation. Genes Dev. 9: 1199-1210, 1995. ; and

[73005] Suzuki, N.; Nakayama, J.; Shih, I. M.; Aoki, D.; Nozawa, S.; Fukuda, M. N. : Expression of trophinin, tastin, and bystin by trophoblast and endometrial cells in human placenta. Biol. Reprod.

[73006] Further studies establishing the function and utilities of TRO are found in John Hopkins OMIM database record ID 300132, and in sited publications numbered 10990-10992 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Splicing Factor, Arginine/serine-rich 12 (SFRS12, Accession NM_139168) is another VGAM2097 host target gene. SFRS12 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SFRS12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRS12 BINDING SITE, designated SEQ ID:29175, to the nucleotide sequence of VGAM2097 RNA, herein designated VGAM RNA, also designated SEQ

ID:4808.

[73007] Another function of VGAM2097 is therefore inhibition of Splicing Factor, Arginine/serine-rich 12 (SFRS12, Accession NM_139168). Accordingly, utilities of VGAM2097 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRS12. Transmembrane 4 Superfamily Member 11 (plasmolipin) (TM4SF11, Accession NM_015993) is another VGAM2097 host target gene. TM4SF11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TM4SF11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TM4SF11 BINDING SITE, designated SEQ ID:18083, to the nucleotide sequence of VGAM2097 RNA, herein designated VGAM RNA, also designated SEQ ID:4808.

[73008] Another function of VGAM2097 is therefore inhibition of Transmembrane 4 Superfamily Member 11 (plasmolipin) (TM4SF11, Accession NM_015993). Accordingly, utilities of VGAM2097 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TM4SF11. Zinc Finger Protein 11b (KOX 2) (ZNF11B, Ac-

cession XM_058399) is another VGAM2097 host target gene. ZNF11B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF11B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF11B BINDING SITE, designated SEQ ID:36614, to the nucleotide sequence of VGAM2097 RNA, herein designated VGAM RNA, also designated SEQ ID:4808.

[73009] Another function of VGAM2097 is therefore inhibition of Zinc Finger Protein 11b (KOX 2) (ZNF11B, Accession XM_058399). Accordingly, utilities of VGAM2097 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF11B. LOC158476 (Accession XM_098955) is another VGAM2097 host target gene. LOC158476 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158476, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158476 BINDING SITE, designated SEQ ID:41997, to the nucleotide sequence of

VGAM2097 RNA, herein designated VGAM RNA, also designated SEQ ID:4808.

[73010] Another function of VGAM2097 is therefore inhibition of LOC158476 (Accession XM_098955). Accordingly, utilities of VGAM2097 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158476. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2098 (VGAM2098) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73011] VGAM2098 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2098 was detected is described hereinabove with reference to Figs. 1-8.

[73012] VGAM2098 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2098 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73013] VGAM2098 gene encodes a VGAM2098 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2098 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2098 precursor RNA is designated SEQ ID:2084, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2084 is located at position 174573 relative to the genome of Camelpox Virus.

[73014] VGAM2098 precursor RNA folds onto itself, forming VGAM2098 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73015] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2098 folded precursor RNA into VGAM2098 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2098 RNA is designated SEQ ID:4809, and is provided hereinbelow with reference to the sequence listing part.

[73016] VGAM2098 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2098 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2098 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73017] VGAM2098 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2098 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2098 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2098 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2098 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73018] The complementary binding of VGAM2098 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2098 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2098 host target RNA into VGAM2098 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73019] It is appreciated that VGAM2098 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2098 host target genes. The mRNA of each one of this plurality of VGAM2098 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2098 RNA, herein designated VGAM RNA, and which when bound by VGAM2098 RNA causes inhibition of translation of respective one or more VGAM2098 host target proteins.

[73020] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2098 gene, herein designated VGAM GENE, on one or more VGAM2098 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73021] It is yet further appreciated that a function of VGAM2098 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2098 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2098 correlate with, and may be deduced from, the identity of the host target genes which VGAM2098 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73022] Nucleotide sequences of the VGAM2098 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2098 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2098 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2098 are further described hereinbelow with reference to Table 1.

[73023] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2098 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2098 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73024] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2098 gene, herein designated VGAM is inhibition of expression of VGAM2098 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2098 correlate with, and may be deduced from, the identity of the target genes which VGAM2098 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73025] ATP-binding Cassette, Sub-family B (MDR/TAP), Member 4 (ABCB4, Accession NM_000443) is a VGAM2098 host target gene. ABCB4 BINDING SITE1 and ABCB4 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ABCB4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCB4 BINDING SITE1 and ABCB4 BINDING SITE2, designated SEQ ID:6030 and SEQ ID:20835 respectively, to the nucleotide sequence of VGAM2098 RNA, herein designated VGAM RNA, also designated SEQ ID:4809.

[73026] A function of VGAM2098 is therefore inhibition of ATP-binding Cassette, Sub-family B (MDR/TAP), Member 4 (ABCB4, Accession NM_000443). Accordingly, utilities of VGAM2098 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCB4. FLJ20152 (Accession NM_019000) is another VGAM2098 host target gene. FLJ20152 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20152, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20152 BINDING SITE, designated SEQ ID:21071, to the nucleotide sequence of VGAM2098 RNA, herein designated VGAM RNA, also designated SEQ ID:4809.

[73027] Another function of VGAM2098 is therefore inhibition of FLJ20152 (Accession NM_019000). Accordingly, utilities of VGAM2098 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20152. KIAA0923 (Accession NM_014021) is another VGAM2098 host target gene. KIAA0923 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0923, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0923 BINDING SITE, designated SEQ ID:15244, to the nucleotide sequence of VGAM2098 RNA, herein designated VGAM RNA, also designated SEQ ID:4809.

[73028] Another function of VGAM2098 is therefore inhibition of KIAA0923 (Accession NM_014021). Accordingly, utilities of VGAM2098 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0923. LOC144920 (Accession XM_096688) is another VGAM2098 host target gene. LOC144920 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144920, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144920 BINDING SITE, designated SEQ ID:40465, to the nucleotide sequence of VGAM2098 RNA, herein designated VGAM RNA, also designated SEQ ID:4809.

[73029] Another function of VGAM2098 is therefore inhibition of LOC144920 (Accession XM_096688). Accordingly, utilities of VGAM2098 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC144920. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2099 (VGAM2099) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73030] VGAM2099 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2099 was detected is described hereinabove with reference to Figs. 1-8.

[73031] VGAM2099 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2099 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73032] VGAM2099 gene encodes a VGAM2099 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2099 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2099 precursor RNA is desig-

nated SEQ ID:2085, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2085 is located at position 174840 relative to the genome of Camelpox Virus.

[73033] VGAM2099 precursor RNA folds onto itself, forming VGAM2099 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73034] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2099 folded precursor RNA into VGAM2099 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2099 RNA is designated SEQ ID:4810, and is provided hereinbelow with reference to the sequence

listing part.

[73035] VGAM2099 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2099 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2099 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73036] VGAM2099 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2099 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2099 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2099 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2099 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73037] The complementary binding of VGAM2099 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2099 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2099 host target RNA into VGAM2099 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73038] It is appreciated that VGAM2099 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2099 host target genes. The mRNA of each one of this plurality of VGAM2099 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2099 RNA, herein designated VGAM

RNA, and which when bound by VGAM2099 RNA causes inhibition of translation of respective one or more VGAM2099 host target proteins.

[73039] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2099 gene, herein designated VGAM GENE, on one or more VGAM2099 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73040] It is yet further appreciated that a function of VGAM2099 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2099 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2099 correlate with, and may be deduced from, the identity of the host target genes which VGAM2099 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73041] Nucleotide sequences of the VGAM2099 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2099 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2099 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2099 are further described hereinbelow with reference to Table 1.

[73042] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2099 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2099 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73043] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2099 gene, herein designated VGAM is

inhibition of expression of VGAM2099 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2099 correlate with, and may be deduced from, the identity of the target genes which VGAM2099 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73044] NEBL (Accession NM_006393) is a VGAM2099 host target gene. NEBL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NEBL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NEBL BINDING SITE, designated SEQ ID:13095, to the nucleotide sequence of VGAM2099 RNA, herein designated VGAM RNA, also designated SEQ ID:4810.

[73045] A function of VGAM2099 is therefore inhibition of NEBL (Accession NM_006393). Accordingly, utilities of VGAM2099 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEBL. DKFZp761K1423 (Accession NM_018422) is another VGAM2099 host target gene. DKFZp761K1423 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761K1423,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761K1423 BINDING SITE, designated SEQ ID:20473, to the nucleotide sequence of VGAM2099 RNA, herein designated VGAM RNA, also designated SEQ ID:4810.

[73046] Another function of VGAM2099 is therefore inhibition of DKFZp761K1423 (Accession NM_018422). Accordingly, utilities of VGAM2099 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761K1423. NESHBP (Accession NM_015429) is another VGAM2099 host target gene. NESHBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NESHBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NESHBP BINDING SITE, designated SEQ ID:17726, to the nucleotide sequence of VGAM2099 RNA, herein designated VGAM RNA, also designated SEQ ID:4810.

[73047] Another function of VGAM2099 is therefore inhibition of NESHBP (Accession NM_015429). Accordingly, utilities of

VGAM2099 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NESHBP. LOC145786 (Accession XM_096860) is another VGAM2099 host target gene. LOC145786 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145786 BINDING SITE, designated SEQ ID:40589, to the nucleotide sequence of VGAM2099 RNA, herein designated VGAM RNA, also designated SEQ ID:4810.

[73048] Another function of VGAM2099 is therefore inhibition of LOC145786 (Accession XM_096860). Accordingly, utilities of VGAM2099 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145786. LOC157292 (Accession XM_098740) is another VGAM2099 host target gene. LOC157292 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157292, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC157292 BINDING SITE, designated SEQ ID:41773, to the nucleotide sequence of VGAM2099 RNA, herein designated VGAM RNA, also designated SEQ ID:4810.

[73049] Another function of VGAM2099 is therefore inhibition of LOC157292 (Accession XM_098740). Accordingly, utilities of VGAM2099 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157292. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2100 (VGAM2100) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73050] VGAM2100 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2100 was detected is described hereinabove with reference to Figs. 1-8.

[73051] VGAM2100 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2100 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73052] VGAM2100 gene encodes a VGAM2100 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2100 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2100 precursor RNA is designated SEQ ID:2086, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2086 is located at position 176689 relative to the genome of Camelpox Virus.

[73053] VGAM2100 precursor RNA folds onto itself, forming VGAM2100 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73054] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2100 folded precursor RNA into VGAM2100 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2100 RNA is designated SEQ ID:4811, and is provided hereinbelow with reference to the sequence listing part.

[73055] VGAM2100 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2100 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2100 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73056] VGAM2100 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2100 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2100 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2100 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2100 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73057] The complementary binding of VGAM2100 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2100 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2100 host target RNA into VGAM2100 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73058] It is appreciated that VGAM2100 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2100 host target genes. The mRNA of each one of this plurality of VGAM2100 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2100 RNA, herein designated VGAM RNA, and which when bound by VGAM2100 RNA causes inhibition of translation of respective one or more VGAM2100 host target proteins.

[73059] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2100 gene, herein designated VGAM GENE, on one or more VGAM2100 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73060] It is yet further appreciated that a function of VGAM2100 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2100 correlate with, and may be deduced from, the identity of the host target genes which VGAM2100 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73061] Nucleotide sequences of the VGAM2100 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2100 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2100 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2100 are further described hereinbelow with reference to Table 1.

[73062] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2100 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2100 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73063] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2100 gene, herein designated VGAM is inhibition of expression of VGAM2100 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2100 correlate with, and may be deduced from, the identity of the target genes which VGAM2100 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73064] Rho Guanine Nucleotide Exchange Factor (GEF) 12 (ARHGEF12, Accession NM_015313) is a VGAM2100 host target gene. ARHGEF12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHGEF12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGEF12 BINDING SITE, designated SEQ ID:17630, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73065] A function of VGAM2100 is therefore inhibition of Rho Guanine Nucleotide Exchange Factor (GEF) 12 (ARHGEF12, Accession NM_015313). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF12. Prostaglandin-endoperoxide Synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1, Accession NM_080591) is another VGAM2100 host target gene. PTGS1 BINDING SITE1 and PTGS1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTGS1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTGS1 BINDING SITE1 and PTGS1 BINDING SITE2, designated SEQ ID:27893 and SEQ ID:6672 respectively, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73066] Another function of VGAM2100 is therefore inhibition of Prostaglandin-endoperoxide Synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1, Accession NM_080591), a gene which may play an important role in regulating or promoting cell proliferation in some normal

and neoplastically transformed cells. Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGS1. The function of PTGS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1224.BCMP1 (Accession NM_031442) is another VGAM2100 host target gene. BCMP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCMP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCMP1 BINDING SITE, designated SEQ ID:25455, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73067] Another function of VGAM2100 is therefore inhibition of BCMP1 (Accession NM_031442). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCMP1. Chromosome 20 Open Reading Frame 45 (C20orf45, Accession NM_016045) is another VGAM2100 host target gene. C20orf45 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by C20orf45, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf45 BINDING SITE, designated SEQ ID:18121, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73068] Another function of VGAM2100 is therefore inhibition of Chromosome 20 Open Reading Frame 45 (C20orf45, Accession NM_016045). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf45. FLJ10726 (Accession NM_018195) is another VGAM2100 host target gene. FLJ10726 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10726, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10726 BINDING SITE, designated SEQ ID:20059, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73069] Another function of VGAM2100 is therefore inhibition of FLJ10726 (Accession NM_018195). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10726. FLJ20079 (Accession NM_017656) is another VGAM2100 host target gene. FLJ20079 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20079, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20079 BINDING SITE, designated SEQ ID:19171, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73070] Another function of VGAM2100 is therefore inhibition of FLJ20079 (Accession NM_017656). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20079. FLJ20508 (Accession NM_017850) is another VGAM2100 host target gene. FLJ20508 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20508, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20508 BINDING SITE, designated SEQ ID:19516, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73071] Another function of VGAM2100 is therefore inhibition of FLJ20508 (Accession NM_017850). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20508. FLJ22794 (Accession XM_166220) is another VGAM2100 host target gene. FLJ22794 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22794 BINDING SITE, designated SEQ ID:44039, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73072] Another function of VGAM2100 is therefore inhibition of FLJ22794 (Accession XM_166220). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ22794. Histamine Receptor H4 (HRH4, Accession NM_021624) is another VGAM2100 host target gene. HRH4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HRH4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRH4 BINDING SITE, designated SEQ ID:22263, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73073] Another function of VGAM2100 is therefore inhibition of Histamine Receptor H4 (HRH4, Accession NM_021624). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRH4. KIAA0565 (Accession XM_039912) is another VGAM2100 host target gene. KIAA0565 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0565, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0565 BINDING SITE, designated SEQ ID:33218, to the nucleotide sequence of VGAM2100 RNA,

herein designated VGAM RNA, also designated SEQ ID:4811.

[73074] Another function of VGAM2100 is therefore inhibition of KIAA0565 (Accession XM_039912). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0565. Phosphodiesterase 3A, CGMP-inhibited (PDE3A, Accession NM_000921) is another VGAM2100 host target gene. PDE3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE3A BINDING SITE, designated SEQ ID:6631, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73075] Another function of VGAM2100 is therefore inhibition of Phosphodiesterase 3A, CGMP-inhibited (PDE3A, Accession NM_000921). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE3A. LOC148254 (Accession XM_086121) is another VGAM2100 host target

gene. LOC148254 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148254, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148254 BINDING SITE, designated SEQ ID:38505, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73076] Another function of VGAM2100 is therefore inhibition of LOC148254 (Accession XM_086121). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148254. LOC256207 (Accession XM_170837) is another VGAM2100 host target gene. LOC256207 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256207, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256207 BINDING SITE, designated SEQ ID:45619, to the nucleotide sequence of VGAM2100 RNA, herein designated VGAM RNA, also designated SEQ ID:4811.

[73077] Another function of VGAM2100 is therefore inhibition of LOC256207 (Accession XM_170837). Accordingly, utilities of VGAM2100 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256207. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2101 (VGAM2101) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73078] VGAM2101 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2101 was detected is described hereinabove with reference to Figs. 1-8.

[73079] VGAM2101 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2101 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73080] VGAM2101 gene encodes a VGAM2101 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2101 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2101 precursor RNA is designated SEQ ID:2087, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2087 is located at position 171927 relative to the genome of Camelpox Virus.

[73081] VGAM2101 precursor RNA folds onto itself, forming VGAM2101 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73082] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2101 folded precursor RNA into VGAM2101 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2101 RNA is designated SEQ ID:4812, and is provided hereinbelow with reference to the sequence listing part.

[73083] VGAM2101 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2101 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2101 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73084] VGAM2101 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2101 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2101 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2101 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2101 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73085] The complementary binding of VGAM2101 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2101 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2101 host target RNA into VGAM2101 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73086] It is appreciated that VGAM2101 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2101 host target genes. The mRNA of each one of this plurality of VGAM2101 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2101 RNA, herein designated VGAM RNA, and which when bound by VGAM2101 RNA causes inhibition of translation of respective one or more VGAM2101 host target proteins.

[73087] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2101 gene, herein designated VGAM GENE, on one or more VGAM2101 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73088] It is yet further appreciated that a function of VGAM2101 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2101 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2101 correlate with, and may be deduced from, the identity of the host target genes which VGAM2101 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73089] Nucleotide sequences of the VGAM2101 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2101 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2101 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2101 are further described hereinbelow with reference to Table 1.

[73090] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2101 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2101 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[73091] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2101 gene, herein designated VGAM is inhibition of expression of VGAM2101 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2101 correlate with, and may be deduced from, the identity of the target genes which VGAM2101 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73092] BarH-like 1 (Drosophila) (BARHL1, Accession NM_020064) is a VGAM2101 host target gene. BARHL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BARHL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BARHL1 BINDING SITE, designated SEQ ID:21299, to the nucleotide sequence of VGAM2101 RNA, herein designated VGAM RNA, also designated SEQ ID:4812.

[73093] A function of VGAM2101 is therefore inhibition of BarH-like 1 (Drosophila) (BARHL1, Accession NM_020064), a gene which controls the expression of neural adhesion molecules. Accordingly, utilities of VGAM2101 include di-

agnosis, prevention and treatment of diseases and clinical conditions associated with BARHL1. The function of BARHL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1006.Collagen, Type I, Alpha 1 (COL1A1, Accession NM_000088) is another VGAM2101 host target gene. COL1A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL1A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL1A1 BINDING SITE, designated SEQ ID:5537, to the nucleotide sequence of VGAM2101 RNA, herein designated VGAM RNA, also designated SEQ ID:4812.

[73094] Another function of VGAM2101 is therefore inhibition of Collagen, Type I, Alpha 1 (COL1A1, Accession NM_000088). Accordingly, utilities of VGAM2101 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL1A1. SWI/SNF Related, Matrix Associated, Actin Dependent Regulator of Chromatin, Subfamily A, Member 3 (SMARCA3, Accession

NM_003071) is another VGAM2101 host target gene. SMARCA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMARCA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMARCA3 BINDING SITE, designated SEQ ID:9036, to the nucleotide sequence of VGAM2101 RNA, herein designated VGAM RNA, also designated SEQ ID:4812.

[73095] Another function of VGAM2101 is therefore inhibition of SWI/SNF Related, Matrix Associated, Actin Dependent Regulator of Chromatin, Subfamily A, Member 3 (SMARCA3, Accession NM_003071), a gene which is involved in chromatin assembly and remodeling. Accordingly, utilities of VGAM2101 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMARCA3. The function of SMARCA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1330.ABLIM (Accession NM_002313) is another VGAM2101 host target gene. ABLIM BINDING SITE1 and ABLIM BINDING SITE2 are HOST

TARGET binding sites found in untranslated regions of mRNA encoded by ABLIM, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABLIM BINDING SITE1 and ABLIM BINDING SITE2, designated SEQ ID:8109 and SEQ ID:13542 respectively, to the nucleotide sequence of VGAM2101 RNA, herein designated VGAM RNA, also designated SEQ ID:4812.

[73096] Another function of VGAM2101 is therefore inhibition of ABLIM (Accession NM_002313). Accordingly, utilities of VGAM2101 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABLIM. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2102 (VGAM2102) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73097] VGAM2102 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2102 was detected is described hereinabove with reference to Figs. 1-8.

[73098] VGAM2102 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2102 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73099] VGAM2102 gene encodes a VGAM2102 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2102 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2102 precursor RNA is designated SEQ ID:2088, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2088 is located at position 168981 relative to the genome of Camelpox Virus.

[73100] VGAM2102 precursor RNA folds onto itself, forming VGAM2102 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[73101] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2102 folded precursor RNA into VGAM2102 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2102 RNA is designated SEQ ID:4813, and is provided hereinbelow with reference to the sequence listing part.

[73102] VGAM2102 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2102 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2102 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73103] VGAM2102 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2102 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2102 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2102 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2102 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73104] The complementary binding of VGAM2102 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2102 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2102 host target RNA into VGAM2102 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73105] It is appreciated that VGAM2102 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2102 host target genes. The mRNA of each one of this plurality of VGAM2102 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2102 RNA, herein designated VGAM RNA, and which when bound by VGAM2102 RNA causes inhibition of translation of respective one or more VGAM2102 host target proteins.

[73106] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2102 gene, herein designated VGAM GENE, on one or more VGAM2102 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73107] It is yet further appreciated that a function of VGAM2102 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2102 correlate with, and may be deduced from, the identity of the host target genes which VGAM2102 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73108] Nucleotide sequences of the VGAM2102 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2102 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2102 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2102 are further described hereinbelow with reference to Table 1.

[73109] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2102 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2102 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73110] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2102 gene, herein designated VGAM is inhibition of expression of VGAM2102 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2102 correlate with, and may be deduced from, the identity of the target genes which VGAM2102 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73111] Heparan Sulfate 2-O-sulfotransferase 1 (HS2ST1, Accession NM_012262) is a VGAM2102 host target gene. HS2ST1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HS2ST1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of HS2ST1 BINDING SITE, designated SEQ ID:14578, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73112] A function of VGAM2102 is therefore inhibition of Heparan Sulfate 2-O-sulfotransferase 1 (HS2ST1, Accession NM_012262). Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HS2ST1. Pleiomorphic Adenoma Gene-like 1 (PLAGL1, Accession NM_002656) is another VGAM2102 host target gene. PLAGL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLAGL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLAGL1 BINDING SITE, designated SEQ ID:8529, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73113] Another function of VGAM2102 is therefore inhibition of Pleiomorphic Adenoma Gene-like 1 (PLAGL1, Accession NM_002656), a gene which regulates apoptosis and cell

cycle arrest. Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAGL1. The function of PLAGL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM89.Protein Phosphatase 1, Catalytic Subunit, Beta Isoform (PPP1CB, Accession NM_002709) is another VGAM2102 host target gene. PPP1CB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1CB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1CB BINDING SITE, designated SEQ ID:8555, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73114] Another function of VGAM2102 is therefore inhibition of Protein Phosphatase 1, Catalytic Subunit, Beta Isoform (PPP1CB, Accession NM_002709), a gene which is the catalytic subunit of protein phosphatase 1. Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with PPP1CB. The function of PPP1CB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM46.Protein Tyrosine Phosphatase, Receptor Type, J (PTPRJ, Accession NM_002843) is another VGAM2102 host target gene. PTPRJ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPRJ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRJ BINDING SITE, designated SEQ ID:8729, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73115] Another function of VGAM2102 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, J (PTPRJ, Accession NM_002843), a gene which Receptor-type protein tyrosine phosphatase J. Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRJ. The function of PTPRJ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM552.Tumor-associated Calcium Signal Transducer 2 (TACSTD2, Accession NM_002353) is another VGAM2102 host target gene. TACSTD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TACSTD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TACSTD2 BINDING SITE, designated SEQ ID:8159, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73116] Another function of VGAM2102 is therefore inhibition of Tumor-associated Calcium Signal Transducer 2 (TACSTD2, Accession NM_002353), a gene which belongs to ga733 tumor-associated antigen gene family and may function as growth factor receptors. Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TACSTD2. The function of TACSTD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM210.CAT56 (Accession NM_025263) is another VGAM2102 host target gene.

CAT56 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAT56, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAT56 BINDING SITE, designated SEQ ID:24933, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73117] Another function of VGAM2102 is therefore inhibition of CAT56 (Accession NM_025263). Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAT56. DKFZp761K1423 (Accession NM_018422) is another VGAM2102 host target gene. DKFZp761K1423 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761K1423, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761K1423 BINDING SITE, designated SEQ ID:20474, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ

ID:4813.

[73118] Another function of VGAM2102 is therefore inhibition of DKFZp761K1423 (Accession NM_018422). Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761K1423. KIAA0155 (Accession NM_014633) is another VGAM2102 host target gene. KIAA0155 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0155, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0155 BINDING SITE, designated SEQ ID:16004, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73119] Another function of VGAM2102 is therefore inhibition of KIAA0155 (Accession NM_014633). Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0155. KIAA1198 (Accession XM_032674) is another VGAM2102 host target gene. KIAA1198 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1198, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE, designated SEQ ID:31714, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73120] Another function of VGAM2102 is therefore inhibition of KIAA1198 (Accession XM_032674). Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1198. KIAA1915 (Accession XM_055481) is another VGAM2102 host target gene. KIAA1915 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1915, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1915 BINDING SITE, designated SEQ ID:36267, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73121] Another function of VGAM2102 is therefore inhibition of KIAA1915 (Accession XM_055481). Accordingly, utilities of VGAM2102 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1915. Zinc Finger Protein 387 (ZNF387, Accession NM_014682) is another VGAM2102 host target gene. ZNF387 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF387, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF387 BINDING SITE, designated SEQ ID:16173, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73122] Another function of VGAM2102 is therefore inhibition of Zinc Finger Protein 387 (ZNF387, Accession NM_014682). Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF387. LOC147343 (Accession XM_097225) is another VGAM2102 host target gene. LOC147343 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147343, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of LOC147343 BINDING SITE, designated SEQ ID:40832, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73123] Another function of VGAM2102 is therefore inhibition of LOC147343 (Accession XM_097225). Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147343. LOC164684 (Accession XM_092926) is another VGAM2102 host target gene. LOC164684 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC164684, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164684 BINDING SITE, designated SEQ ID:40161, to the nucleotide sequence of VGAM2102 RNA, herein designated VGAM RNA, also designated SEQ ID:4813.

[73124] Another function of VGAM2102 is therefore inhibition of LOC164684 (Accession XM_092926). Accordingly, utilities of VGAM2102 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164684. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2103 (VGAM2103) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73125] VGAM2103 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2103 was detected is described hereinabove with reference to Figs. 1-8.

[73126] VGAM2103 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2103 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73127] VGAM2103 gene encodes a VGAM2103 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2103 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2103 precursor RNA is designated SEQ ID:2089, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2089 is located at position 177859 relative to the genome of Camelpox Virus.

[73128] VGAM2103 precursor RNA folds onto itself, forming VGAM2103 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73129] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2103 folded precursor RNA into VGAM2103 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2103 RNA is designated SEQ ID:4814, and is provided hereinbelow with reference to the sequence listing part.

[73130] VGAM2103 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2103 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2103 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73131] VGAM2103 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2103 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2103 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2103 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2103 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73132] The complementary binding of VGAM2103 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2103 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2103 host target RNA into VGAM2103 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73133] It is appreciated that VGAM2103 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2103 host target genes. The mRNA of each one of this plurality of VGAM2103 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2103 RNA, herein designated VGAM RNA, and which when bound by VGAM2103 RNA causes inhibition of translation of respective one or more

VGAM2103 host target proteins.

[73134] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2103 gene, herein designated VGAM GENE, on one or more VGAM2103 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73135] It is yet further appreciated that a function of VGAM2103 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2103 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific

functions, and accordingly utilities, of VGAM2103 correlate with, and may be deduced from, the identity of the host target genes which VGAM2103 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73136] Nucleotide sequences of the VGAM2103 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2103 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2103 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2103 are further described hereinbelow with reference to Table 1.

[73137] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2103 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2103 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73138] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2103 gene, herein designated VGAM is inhibition of expression of VGAM2103 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2103 correlate with, and may be deduced from, the identity of the target genes which VGAM2103 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73139] Protocadherin 10 (PCDH10, Accession NM_032961) is a VGAM2103 host target gene. PCDH10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDH10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH10 BINDING SITE, designated SEQ ID:26771, to the nucleotide sequence of VGAM2103 RNA, herein designated VGAM RNA, also designated SEQ ID:4814.

[73140] A function of VGAM2103 is therefore inhibition of Protocadherin 10 (PCDH10, Accession NM_032961). Accordingly, utilities of VGAM2103 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH10. LOC150848 (Accession XM_097959) is another VGAM2103 host target gene. LOC150848 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150848, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150848 BINDING SITE, designated SEQ ID:41257, to the nucleotide sequence of VGAM2103 RNA, herein designated VGAM RNA, also designated SEQ ID:4814.

[73141] Another function of VGAM2103 is therefore inhibition of LOC150848 (Accession XM_097959). Accordingly, utilities of VGAM2103 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150848. LOC160414 (Accession XM_100898) is another VGAM2103 host target gene. LOC160414 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC160414, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC160414 BINDING SITE, designated SEQ ID:42105, to the nucleotide sequence of VGAM2103 RNA, herein designated VGAM RNA, also designated SEQ ID:4814.

[73142] Another function of VGAM2103 is therefore inhibition of LOC160414 (Accession XM_100898). Accordingly, utilities of VGAM2103 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC160414. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2104 (VGAM2104) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73143] VGAM2104 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2104 was detected is described hereinabove with reference to Figs. 1-8.

[73144] VGAM2104 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2104 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73145] VGAM2104 gene encodes a VGAM2104 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2104 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2104 precursor RNA is designated SEQ ID:2090, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2090 is located at position 161818 relative to the genome of Camelpox Virus.

[73146] VGAM2104 precursor RNA folds onto itself, forming VGAM2104 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73147] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2104 folded precursor RNA into VGAM2104 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2104 RNA is designated SEQ ID:4815, and is provided hereinbelow with reference to the sequence listing part.

[73148] VGAM2104 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2104 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2104 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73149] VGAM2104 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2104 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2104 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2104 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2104 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73150] The complementary binding of VGAM2104 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2104 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2104 host target RNA into VGAM2104 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73151] It is appreciated that VGAM2104 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2104 host target genes. The mRNA of each one of this plurality of VGAM2104 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2104 RNA, herein designated VGAM RNA, and which when bound by VGAM2104 RNA causes

inhibition of translation of respective one or more VGAM2104 host target proteins.

[73152] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2104 gene, herein designated VGAM GENE, on one or more VGAM2104 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73153] It is yet further appreciated that a function of VGAM2104 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2104 include diagnosis, prevention and

treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2104 correlate with, and may be deduced from, the identity of the host target genes which VGAM2104 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73154] Nucleotide sequences of the VGAM2104 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2104 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2104 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2104 are further described hereinbelow with reference to Table 1.

[73155] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2104 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2104 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73156] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2104 gene, herein designated VGAM is inhibition of expression of VGAM2104 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2104 correlate with, and may be deduced from, the identity of the target genes which VGAM2104 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73157] Catenin, Beta Interacting Protein 1 (CTNNBIP1, Accession NM_020248) is a VGAM2104 host target gene. CTNNBIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CTNNBIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTNNBIP1 BINDING SITE, designated SEQ ID:21542, to the nucleotide sequence of VGAM2104 RNA, herein designated VGAM RNA, also designated SEQ ID:4815.

[73158] A function of VGAM2104 is therefore inhibition of Catenin, Beta Interacting Protein 1 (CTNNBIP1, Accession NM_020248). Accordingly, utilities of VGAM2104 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTNNBIP1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred

to here as Viral Genomic Address Messenger 2105 (VGAM2105) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73159] VGAM2105 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2105 was detected is described hereinabove with reference to Figs. 1-8.

[73160] VGAM2105 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Grapevine Chrome Mosaic Virus. VGAM2105 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73161] VGAM2105 gene encodes a VGAM2105 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2105 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2105 precursor RNA is designated SEQ ID:2091, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2091 is located at position 3783 relative to the genome of Grapevine Chrome Mosaic Virus.

[73162] VGAM2105 precursor RNA folds onto itself, forming VGAM2105 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73163] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2105 folded precursor RNA into VGAM2105 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2105 RNA is designated SEQ ID:4816, and is provided hereinbelow with reference to the sequence listing part.

[73164] VGAM2105 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2105 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2105 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73165] VGAM2105 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2105 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2105 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2105 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2105 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73166] The complementary binding of VGAM2105 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2105 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2105 host target RNA into VGAM2105 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73167] It is appreciated that VGAM2105 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2105 host target genes. The mRNA of each one of this plurality of VGAM2105 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2105 RNA, herein designated VGAM RNA, and which when bound by VGAM2105 RNA causes inhibition of translation of respective one or more VGAM2105 host target proteins.

[73168] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2105 gene, herein designated VGAM GENE, on one or more VGAM2105 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73169] It is yet further appreciated that a function of VGAM2105 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2105 include diagnosis, prevention and treatment of viral infection by Grapevine Chrome Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2105 correlate with, and may be deduced from, the

identity of the host target genes which VGAM2105 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73170] Nucleotide sequences of the VGAM2105 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2105 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2105 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2105 are further described hereinbelow with reference to Table 1.

[73171] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2105 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2105 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73172] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2105 gene, herein designated VGAM is inhibition of expression of VGAM2105 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2105 correlate with, and may be deduced from, the identity of the target genes which VGAM2105

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73173] KIAA0459 (Accession XM_027862) is a VGAM2105 host target gene. KIAA0459 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:30571, to the nucleotide sequence of VGAM2105 RNA, herein designated VGAM RNA, also designated SEQ ID:4816.

[73174] A function of VGAM2105 is therefore inhibition of KIAA0459 (Accession XM_027862). Accordingly, utilities of VGAM2105 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2106 (VGAM2106) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73175] VGAM2106 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2106 was detected is described hereinabove with reference to Figs. 1-8.

[73176] VGAM2106 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Grapevine Chrome Mosaic Virus. VGAM2106 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73177] VGAM2106 gene encodes a VGAM2106 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2106 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2106 precursor RNA is designated SEQ ID:2092, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2092 is located at position 4094 relative to the genome of Grapevine Chrome Mosaic Virus.

[73178] VGAM2106 precursor RNA folds onto itself, forming VGAM2106 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73179] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2106 folded precursor RNA into VGAM2106 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2106 RNA is designated SEQ ID:4817, and is provided hereinbelow with reference to the sequence listing part.

[73180] VGAM2106 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2106 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2106 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[73181] VGAM2106 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2106 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2106 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2106 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2106 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73182] The complementary binding of VGAM2106 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2106 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2106 host target RNA into VGAM2106 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73183] It is appreciated that VGAM2106 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2106 host target genes. The mRNA of each one of this plurality of VGAM2106 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2106 RNA, herein designated VGAM RNA, and which when bound by VGAM2106 RNA causes inhibition of translation of respective one or more VGAM2106 host target proteins.

[73184] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2106 gene, herein designated VGAM GENE, on one or more VGAM2106 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73185] It is yet further appreciated that a function of VGAM2106 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2106 include diagnosis, prevention and treatment of viral infection by Grapevine Chrome Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2106 correlate with, and may be deduced from, the identity of the host target genes which VGAM2106 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73186] Nucleotide sequences of the VGAM2106 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2106 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2106 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2106 are further described hereinbelow with reference to Table 1.

[73187] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2106 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2106 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73188] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2106 gene, herein designated VGAM is inhibition of expression of VGAM2106 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2106 correlate with, and may be deduced from, the identity of the target genes which VGAM2106 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73189] Cystathionine-beta-synthase (CBS, Accession NM_000071) is a VGAM2106 host target gene. CBS BIND-

ING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CBS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBS BINDING SITE, designated SEQ ID:5517, to the nucleotide sequence of VGAM2106 RNA, herein designated VGAM RNA, also designated SEQ ID:4817.

[73190] A function of VGAM2106 is therefore inhibition of Cystathionine-beta-synthase (CBS, Accession NM_000071). Accordingly, utilities of VGAM2106 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBS. RAB6A, Member RAS Oncogene Family (RAB6A, Accession NM_002869) is another VGAM2106 host target gene. RAB6A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB6A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB6A BINDING SITE, designated SEQ ID:8776, to the nucleotide sequence of VGAM2106 RNA, herein designated VGAM RNA, also designated SEQ ID:4817.

[73191] Another function of VGAM2106 is therefore inhibition of RAB6A, Member RAS Oncogene Family (RAB6A, Accession NM_002869), a gene which is involved in protein trafficking. Accordingly, utilities of VGAM2106 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB6A. The function of RAB6A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM217.Sodium Channel, Voltage-gated, Type I, Alpha Polypeptide (SCN1A, Accession XM_114281) is another VGAM2106 host target gene. SCN1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCN1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCN1A BINDING SITE, designated SEQ ID:42835, to the nucleotide sequence of VGAM2106 RNA, herein designated VGAM RNA, also designated SEQ ID:4817.

[73192] Another function of VGAM2106 is therefore inhibition of Sodium Channel, Voltage-gated, Type I, Alpha Polypeptide (SCN1A, Accession XM_114281). Accordingly, utilities of

VGAM2106 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN1A. SEC14-like 2 (S. cerevisiae) (SEC14L2, Accession NM_012429) is another VGAM2106 host target gene. SEC14L2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC14L2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC14L2 BINDING SITE, designated SEQ ID:14807, to the nucleotide sequence of VGAM2106 RNA, herein designated VGAM RNA, also designated SEQ ID:4817.

[73193] Another function of VGAM2106 is therefore inhibition of SEC14-like 2 (S. cerevisiae) (SEC14L2, Accession NM_012429). Accordingly, utilities of VGAM2106 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC14L2. SEP15 (Accession NM_004261) is another VGAM2106 host target gene. SEP15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEP15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of SEP15 BINDING SITE, designated SEQ ID:10454, to the nucleotide sequence of VGAM2106 RNA, herein designated VGAM RNA, also designated SEQ ID:4817.

[73194] Another function of VGAM2106 is therefore inhibition of SEP15 (Accession NM_004261). Accordingly, utilities of VGAM2106 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEP15. LOC147514 (Accession XM_041564) is another VGAM2106 host target gene. LOC147514 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147514, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147514 BINDING SITE, designated SEQ ID:33547, to the nucleotide sequence of VGAM2106 RNA, herein designated VGAM RNA, also designated SEQ ID:4817.

[73195] Another function of VGAM2106 is therefore inhibition of LOC147514 (Accession XM_041564). Accordingly, utilities of VGAM2106 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC147514. LOC90625 (Accession XM_033004) is another VGAM2106 host target gene. LOC90625 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90625, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90625 BINDING SITE, designated SEQ ID:31818, to the nucleotide sequence of VGAM2106 RNA, herein designated VGAM RNA, also designated SEQ ID:4817.

[73196] Another function of VGAM2106 is therefore inhibition of LOC90625 (Accession XM_033004). Accordingly, utilities of VGAM2106 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90625. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2107 (VGAM2107) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73197] VGAM2107 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2107 was detected is described hereinabove with reference to Figs. 1-8.

[73198] VGAM2107 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Grapevine Chrome Mosaic Virus. VGAM2107 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73199] VGAM2107 gene encodes a VGAM2107 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2107 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2107 precursor RNA is designated SEQ ID:2093, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2093 is located at position 2929 relative to the genome of Grapevine Chrome Mosaic Virus.

[73200] VGAM2107 precursor RNA folds onto itself, forming VGAM2107 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73201] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2107 folded precursor RNA into VGAM2107 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2107 RNA is designated SEQ ID:4818, and is provided hereinbelow with reference to the sequence listing part.

[73202] VGAM2107 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2107 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2107 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73203] VGAM2107 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2107 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2107 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2107 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2107 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73204] The complementary binding of VGAM2107 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2107 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2107 host target RNA into VGAM2107 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73205] It is appreciated that VGAM2107 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2107 host target genes. The mRNA of each one of this plurality of VGAM2107 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2107 RNA, herein designated VGAM RNA, and which when bound by VGAM2107 RNA causes inhibition of translation of respective one or more VGAM2107 host target proteins.

[73206] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2107 gene, herein designated VGAM GENE, on one or more VGAM2107 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73207] It is yet further appreciated that a function of VGAM2107 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment of viral infection by Grapevine Chrome Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2107 correlate with, and may be deduced from, the identity of the host target genes which VGAM2107 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73208] Nucleotide sequences of the VGAM2107 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2107 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2107 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2107 are further described hereinbelow with reference to Table 1.

[73209] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2107 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2107 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73210] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2107 gene, herein designated VGAM is inhibition of expression of VGAM2107 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2107 correlate with, and may be deduced from, the identity of the target genes which VGAM2107 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73211] ATPase, Class VI, Type 11B (ATP11B, Accession XM_087254) is a VGAM2107 host target gene. ATP11B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP11B, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP11B BINDING SITE, designated SEQ ID:39146, to the nucleotide sequence of VGAM2107 RNA, herein designated VGAM RNA, also designated SEQ ID:4818.

[73212] A function of VGAM2107 is therefore inhibition of ATPase, Class VI, Type 11B (ATP11B, Accession XM_087254), a gene which is phosphorylated in their intermediate state, drives uphill transport of ions across membranes. Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP11B. The function of ATP11B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM665.Zinc Finger Protein 76 (expressed in testis) (ZNF76, Accession NM_003427) is another VGAM2107 host target gene. ZNF76 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF76, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF76 BIND-

ING SITE, designated SEQ ID:9477, to the nucleotide sequence of VGAM2107 RNA, herein designated VGAM RNA, also designated SEQ ID:4818.

[73213] Another function of VGAM2107 is therefore inhibition of Zinc Finger Protein 76 (expressed in testis) (ZNF76, Accession NM_003427). Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF76. Zinc Finger Protein 83 (HPF1) (ZNF83, Accession NM_018300) is another VGAM2107 host target gene. ZNF83 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF83, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF83 BINDING SITE, designated SEQ ID:20292, to the nucleotide sequence of VGAM2107 RNA, herein designated VGAM RNA, also designated SEQ ID:4818.

[73214] Another function of VGAM2107 is therefore inhibition of Zinc Finger Protein 83 (HPF1) (ZNF83, Accession NM_018300). Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF83. FLJ11608

(Accession NM_024557) is another VGAM2107 host target gene. FLJ11608 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11608, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11608 BINDING SITE, designated SEQ ID:23778, to the nucleotide sequence of VGAM2107 RNA, herein designated VGAM RNA, also designated SEQ ID:4818.

[73215] Another function of VGAM2107 is therefore inhibition of FLJ11608 (Accession NM_024557). Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11608. HEMK (Accession NM_016173) is another VGAM2107 host target gene. HEMK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HEMK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HEMK BINDING SITE, designated SEQ ID:18270, to the nucleotide sequence of VGAM2107 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4818.

[73216] Another function of VGAM2107 is therefore inhibition of HEMK (Accession NM_016173). Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEMK. KIAA0798 (Accession NM_014650) is another VGAM2107 host target gene. KIAA0798 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0798, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0798 BINDING SITE, designated SEQ ID:16069, to the nucleotide sequence of VGAM2107 RNA, herein designated VGAM RNA, also designated SEQ ID:4818.

[73217] Another function of VGAM2107 is therefore inhibition of KIAA0798 (Accession NM_014650). Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0798. KIAA1373 (Accession XM_048195) is another VGAM2107 host target gene. KIAA1373 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1373, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1373 BINDING SITE, designated SEQ ID:35125, to the nucleotide sequence of VGAM2107 RNA, herein designated VGAM RNA, also designated SEQ ID:4818.

[73218] Another function of VGAM2107 is therefore inhibition of KIAA1373 (Accession XM_048195). Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1373. MDS024 (Accession NM_021820) is another VGAM2107 host target gene. MDS024 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MDS024, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MDS024 BINDING SITE, designated SEQ ID:22398, to the nucleotide sequence of VGAM2107 RNA, herein designated VGAM RNA, also designated SEQ ID:4818.

[73219] Another function of VGAM2107 is therefore inhibition of MDS024 (Accession NM_021820). Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MDS024. LOC147976 (Accession XM_085980) is another VGAM2107 host target gene. LOC147976 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147976, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147976 BINDING SITE, designated SEQ ID:38425, to the nucleotide sequence of VGAM2107 RNA, herein designated VGAM RNA, also designated SEQ ID:4818.

[73220] Another function of VGAM2107 is therefore inhibition of LOC147976 (Accession XM_085980). Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147976. LOC254170 (Accession XM_170746) is another VGAM2107 host target gene. LOC254170 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254170, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254170 BINDING SITE, designated SEQ ID:45503, to

the nucleotide sequence of VGAM2107 RNA, herein designated VGAM RNA, also designated SEQ ID:4818.

[73221] Another function of VGAM2107 is therefore inhibition of LOC254170 (Accession XM_170746). Accordingly, utilities of VGAM2107 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254170. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2108 (VGAM2108) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73222] VGAM2108 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2108 was detected is described hereinabove with reference to Figs. 1-8.

[73223] VGAM2108 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Grapevine Chrome Mosaic Virus. VGAM2108 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73224] VGAM2108 gene encodes a VGAM2108 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2108 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2108 precursor RNA is designated SEQ ID:2094, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2094 is located at position 3193 relative to the genome of Grapevine Chrome Mosaic Virus.

[73225] VGAM2108 precursor RNA folds onto itself, forming VGAM2108 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73226] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2108 folded precursor RNA into VGAM2108 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2108 RNA is designated SEQ ID:4819, and is provided hereinbelow with reference to the sequence listing part.

[73227] VGAM2108 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2108 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2108 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73228] VGAM2108 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2108 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2108 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2108 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2108 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73229] The complementary binding of VGAM2108 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2108 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2108 host target RNA into VGAM2108 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73230] It is appreciated that VGAM2108 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2108 host target genes. The mRNA of each one of this plurality of VGAM2108 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2108 RNA, herein designated VGAM RNA, and which when bound by VGAM2108 RNA causes inhibition of translation of respective one or more VGAM2108 host target proteins.

[73231] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2108 gene, herein designated VGAM GENE, on one or more VGAM2108 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73232] It is yet further appreciated that a function of VGAM2108 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of viral infection by Grapevine Chrome Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2108 correlate with, and may be deduced from, the identity of the host target genes which VGAM2108 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73233] Nucleotide sequences of the VGAM2108 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2108 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2108 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2108 are further described hereinbelow with reference to Table 1.

[73234] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2108 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2108 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73235] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2108 gene, herein designated VGAM is inhibition of expression of VGAM2108 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2108 correlate with, and may be deduced from, the identity of the target genes which VGAM2108 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73236] X-prolyl Aminopeptidase (aminopeptidase P) 2, Membrane-bound (XPNPEP2, Accession NM_003399) is a VGAM2108 host target gene. XPNPEP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XPNPEP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XPNPEP2 BINDING SITE, designated SEQ ID:9434, to the nucleotide sequence of VGAM2108 RNA, herein designated VGAM RNA, also designated SEQ ID:4819.

[73237] A function of VGAM2108 is therefore inhibition of X-prolyl

Aminopeptidase (aminopeptidase P) 2, Membrane-bound (XPNPEP2, Accession NM_003399), a gene which is a membrane-associated X-prolyl metallopeptidase . Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XPNPEP2. The function of XPNPEP2 has been established by previous studies. Aminopeptidase P is a widely distributed hydrolase that is specific for N-terminal imido bonds, which are common to several collagen degradation products, neuropeptides, vasoactive peptides, and cytokines. Structurally, the enzyme is a member of the 'pita bread fold' family and occurs in mammalian tissues in both soluble and GPI-anchored membrane-bound forms. By RT-PCR using degenerate oligonucleotides based on the pig aminopeptidase P amino acid sequence, and by 5-prime and 3-prime RACE, Venema et al. (1997) isolated human kidney and lung cDNAs encoding XPNPEP2. The deduced XPNPEP2 protein has 673 amino acids and an estimated molecular mass of 75,490 Da. The authors stated that the human and pig XPNPEP2 amino acid sequences show significant evolutionary divergence, with 83% identity; 5 of 6 potential N-glycosylation sites, and 5 of 6 cysteine residues that are

potentially involved in disulfide bond formation, are conserved. Northern blot analysis detected a 3.5-kb XPNPEP2 transcript in human kidney, lung, heart, placenta, liver, small intestine, and colon, but not in brain, skeletal muscle, pancreas, spleen, thymus, prostate, testis, ovary, or leukocytes. Based on these results and on RT-PCR studies, Venema et al. (1997) suggested that the membrane-bound form and the soluble form, which is found in brain and leukocytes, are the products of 2 different genes or of alternative splicing of a single primary transcript. Women with balanced translocations between the long arm of the X chromosome and an autosome frequently suffer premature ovarian failure (POF; 311360). Two critical regions for POF which extend from Xq13 to Xq22 and from Xq22 to Xq26 have been identified by cytogenetic studies. To gain insight into the mechanism(s) responsible for ovarian failure in women with X/autosome translocations, Prueitt et al. (2000) molecularly characterized the translocation breakpoints of 9 X chromosomes. They mapped the breakpoints using somatic cell hybrids retaining the derivative autosome and densely spaced markers from the X-chromosome physical map. One of the POF-associated breakpoints in a critical region (Xq25) mapped to a se-

quenced PAC clone. The translocation disrupts XPNPEP2. XPNPEP2 mRNA was detected in fibroblasts that carried the translocation, suggesting that this gene at least partially escapes X inactivation. Although the physiologic substrates for the enzyme were not known, Prueitt et al. (2000) suggested that XPNPEP2 is a candidate gene for POF.

[73238] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[73239] Venema, R. C.; Ju, H.; Zou, R.; Venema, V. J.; Ryan, J. W. : Cloning and tissue distribution of human membrane-bound aminopeptidase P. Biochim. Biophys. Acta 1354: 45-48, 1997. ; and

[73240] Prueitt, R. L.; Ross, J. L.; Zinn, A. R. : Physical mapping of nine Xq translocation breakpoints and identification of XPNPEP2 as a premature ovarian failure candidate gene. Cytogenet.

[73241] Further studies establishing the function and utilities of XPNPEP2 are found in John Hopkins OMIM database record ID 300145, and in sited publications numbered 958-960 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.KIAA0429

(Accession NM_014751) is another VGAM2108 host target gene. KIAA0429 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0429, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0429 BINDING SITE, designated SEQ ID:16463, to the nucleotide sequence of VGAM2108 RNA, herein designated VGAM RNA, also designated SEQ ID:4819.

[73242] Another function of VGAM2108 is therefore inhibition of KIAA0429 (Accession NM_014751). Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0429. KIAA1553 (Accession XM_166320) is another VGAM2108 host target gene. KIAA1553 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1553, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1553 BINDING SITE, designated SEQ ID:44145, to the nucleotide sequence of VGAM2108 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4819.

[73243] Another function of VGAM2108 is therefore inhibition of KIAA1553 (Accession XM_166320). Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1553. Syndecan 3 (N-syndecan) (SDC3, Accession NM_014654) is another VGAM2108 host target gene. SDC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SDC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDC3 BINDING SITE, designated SEQ ID:16085, to the nucleotide sequence of VGAM2108 RNA, herein designated VGAM RNA, also designated SEQ ID:4819.

[73244] Another function of VGAM2108 is therefore inhibition of Syndecan 3 (N-syndecan) (SDC3, Accession NM_014654). Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDC3. Zinc Finger Protein 33a (KOX 31) (ZNF33A, Accession XM_166119) is another VGAM2108 host target gene. ZNF33A BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by ZNF33A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF33A BINDING SITE, designated SEQ ID:43898, to the nucleotide sequence of VGAM2108 RNA, herein designated VGAM RNA, also designated SEQ ID:4819.

[73245] Another function of VGAM2108 is therefore inhibition of Zinc Finger Protein 33a (KOX 31) (ZNF33A, Accession XM_166119). Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF33A. LOC149401 (Accession XM_086511) is another VGAM2108 host target gene. LOC149401 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149401, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149401 BINDING SITE, designated SEQ ID:38734, to the nucleotide sequence of VGAM2108 RNA, herein designated VGAM RNA, also designated SEQ ID:4819.

[73246] Another function of VGAM2108 is therefore inhibition of

LOC149401 (Accession XM_086511). Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149401. LOC150622 (Accession XM_086960) is another VGAM2108 host target gene. LOC150622 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150622, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150622 BINDING SITE, designated SEQ ID:38995, to the nucleotide sequence of VGAM2108 RNA, herein designated VGAM RNA, also designated SEQ ID:4819.

[73247] Another function of VGAM2108 is therefore inhibition of LOC150622 (Accession XM_086960). Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150622. LOC219621 (Accession XM_166148) is another VGAM2108 host target gene. LOC219621 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219621, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC219621 BINDING SITE, designated SEQ ID:43968, to the nucleotide sequence of VGAM2108 RNA, herein designated VGAM RNA, also designated SEQ ID:4819.

[73248] Another function of VGAM2108 is therefore inhibition of LOC219621 (Accession XM_166148). Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219621. LOC221477 (Accession XM_166397) is another VGAM2108 host target gene. LOC221477 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221477, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221477 BINDING SITE, designated SEQ ID:44255, to the nucleotide sequence of VGAM2108 RNA, herein designated VGAM RNA, also designated SEQ ID:4819.

[73249] Another function of VGAM2108 is therefore inhibition of LOC221477 (Accession XM_166397). Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221477. LOC255995 (Accession XM_173071) is an-

other VGAM2108 host target gene. LOC255995 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255995, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255995 BINDING SITE, designated SEQ ID:46325, to the nucleotide sequence of VGAM2108 RNA, herein designated VGAM RNA, also designated SEQ ID:4819.

[73250] Another function of VGAM2108 is therefore inhibition of LOC255995 (Accession XM_173071). Accordingly, utilities of VGAM2108 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255995. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2109 (VGAM2109) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73251] VGAM2109 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2109 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[73252] VGAM2109 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2109 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73253] VGAM2109 gene encodes a VGAM2109 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2109 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2109 precursor RNA is designated SEQ ID:2095, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2095 is located at position 22662 relative to the genome of Goatpox Virus.

[73254] VGAM2109 precursor RNA folds onto itself, forming VGAM2109 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73255] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2109 folded precursor RNA into VGAM2109 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2109 RNA is designated SEQ ID:4820, and is provided hereinbelow with reference to the sequence listing part.

[73256] VGAM2109 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2109 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2109 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73257] VGAM2109 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2109 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2109 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2109 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2109 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73258] The complementary binding of VGAM2109 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2109 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2109 host target RNA into VGAM2109 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73259] It is appreciated that VGAM2109 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2109 host target genes. The mRNA of each one of this plurality of VGAM2109 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2109 RNA, herein designated VGAM RNA, and which when bound by VGAM2109 RNA causes inhibition of translation of respective one or more VGAM2109 host target proteins.

[73260] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2109 gene, herein designated VGAM GENE, on one or more VGAM2109 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73261] It is yet further appreciated that a function of VGAM2109 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2109 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2109 correlate with, and may be deduced from, the identity of the host target genes which VGAM2109 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73262] Nucleotide sequences of the VGAM2109 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2109 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2109 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2109 are further described hereinbelow with reference to Table 1.

[73263] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2109 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2109 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73264] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2109 gene, herein designated VGAM is inhibition of expression of VGAM2109 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2109 correlate with, and may be deduced from, the identity of the target genes which VGAM2109 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73265] LOC91408 (Accession XM_038290) is a VGAM2109 host target gene. LOC91408 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91408, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91408 BINDING SITE, designated SEQ ID:32790, to the nucleotide sequence of VGAM2109 RNA, herein designated VGAM RNA, also designated SEQ ID:4820.

[73266] A function of VGAM2109 is therefore inhibition of LOC91408 (Accession XM_038290). Accordingly, utilities of VGAM2109 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91408. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2110 (VGAM2110) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73267] VGAM2110 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2110 was detected is described hereinabove with reference to Figs. 1-8.

[73268] VGAM2110 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Grapevine Chrome Mosaic Virus. VGAM2110 host target gene, herein designated

VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73269] VGAM2110 gene encodes a VGAM2110 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2110 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2110 precursor RNA is designated SEQ ID:2096, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2096 is located at position 1090 relative to the genome of Grapevine Chrome Mosaic Virus.

[73270] VGAM2110 precursor RNA folds onto itself, forming VGAM2110 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73271] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2110 folded precursor RNA into VGAM2110

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2110 RNA is designated SEQ ID:4821, and is provided hereinbelow with reference to the sequence listing part.

[73272] VGAM2110 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2110 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2110 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73273] VGAM2110 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2110 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2110 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2110 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2110 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73274] The complementary binding of VGAM2110 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2110 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2110 host target RNA into VGAM2110 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[73275] It is appreciated that VGAM2110 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2110 host target genes. The mRNA of each one of this plurality of VGAM2110 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2110 RNA, herein designated VGAM RNA, and which when bound by VGAM2110 RNA causes inhibition of translation of respective one or more VGAM2110 host target proteins.

[73276] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2110 gene, herein designated VGAM GENE, on one or more VGAM2110 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73277] It is yet further appreciated that a function of VGAM2110 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of viral infection by Grapevine Chrome Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2110 correlate with, and may be deduced from, the identity of the host target genes which VGAM2110 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73278] Nucleotide sequences of the VGAM2110 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2110 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2110 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2110 are further described hereinbelow with reference to Table 1.

[73279] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2110 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2110 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73280] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2110 gene, herein designated VGAM is inhibition of expression of VGAM2110 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2110 correlate with, and may be deduced from, the identity of the target genes which VGAM2110 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73281] Glypican 1 (GPC1, Accession NM_002081) is a VGAM2110 host target gene. GPC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPC1 BINDING SITE, designated SEQ ID:7869, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4821.

[73282] A function of VGAM2110 is therefore inhibition of Glypican 1 (GPC1, Accession NM_002081), a gene which may play a role in growth control and differentation. Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPC1. The function of GPC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM125.G Protein-coupled Receptor 44 (GPR44, Accession NM_004778) is another VGAM2110 host target gene. GPR44 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPR44, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR44 BINDING SITE, designated SEQ ID:11174, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73283] Another function of VGAM2110 is therefore inhibition of G Protein-coupled Receptor 44 (GPR44, Accession NM_004778), a gene which mediates signals to the inte-

rior of the cell via activation of heterotrimeric G proteins . Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR44. The function of GPR44 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1669.Islet Cell Autoantigen 1, 69kDa (ICA1, Accession NM_022308) is another VGAM2110 host target gene. ICA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ICA1 BINDING SITE, designated SEQ ID:22737, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73284] Another function of VGAM2110 is therefore inhibition of Islet Cell Autoantigen 1, 69kDa (ICA1, Accession NM_022308), a gene which Islet cell autoantigen 1. Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICA1. The function of ICA1 and its associ-

ation with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.LENG4 (Accession NM_024298) is another VGAM2110 host target gene. LENG4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LENG4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LENG4 BINDING SITE, designated SEQ ID:23583, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73285] Another function of VGAM2110 is therefore inhibition of LENG4 (Accession NM_024298), a gene which may be a transmembrane protein. Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LENG4. The function of LENG4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM259.PAIP2 (Accession NM_016480) is another VGAM2110 host target gene. PAIP2 BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by PAIP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAIP2 BINDING SITE, designated SEQ ID:18579, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73286] Another function of VGAM2110 is therefore inhibition of PAIP2 (Accession NM_016480). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAIP2. Secreted and Transmembrane 1 (SECTM1, Accession NM_003004) is another VGAM2110 host target gene. SECTM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SECTM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SECTM1 BINDING SITE, designated SEQ ID:8910, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73287] Another function of VGAM2110 is therefore inhibition of Secreted and Transmembrane 1 (SECTM1, Accession NM_003004). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SECTM1. Solute Carrier Family 30 (zinc transporter), Member 3 (SLC30A3, Accession NM_003459) is another VGAM2110 host target gene. SLC30A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC30A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC30A3 BINDING SITE, designated SEQ ID:9523, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73288] Another function of VGAM2110 is therefore inhibition of Solute Carrier Family 30 (zinc transporter), Member 3 (SLC30A3, Accession NM_003459). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC30A3. Solute Carrier Family 7 (cationic amino acid transporter, y+ system), Member 5 (SLC7A5, Accession

NM_003486) is another VGAM2110 host target gene. SLC7A5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC7A5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC7A5 BINDING SITE, designated SEQ ID:9575, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73289] Another function of VGAM2110 is therefore inhibition of Solute Carrier Family 7 (cationic amino acid transporter, y+ system), Member 5 (SLC7A5, Accession NM_003486), a gene which mediates transport of large and small neutral amino acids. Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC7A5. The function of SLC7A5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM430.START Domain Containing 4, Sterol Regulated (STARD4, Accession NM_139164) is another VGAM2110 host target gene. STARD4 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by STARD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STARD4 BINDING SITE, designated SEQ ID:29171, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73290] Another function of VGAM2110 is therefore inhibition of START Domain Containing 4, Sterol Regulated (STARD4, Accession NM_139164). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STARD4. Choline Kinase (CHK, Accession NM_001277) is another VGAM2110 host target gene. CHK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHK BINDING SITE, designated SEQ ID:6943, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73291] Another function of VGAM2110 is therefore inhibition of Choline Kinase (CHK, Accession NM_001277). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHK. DKFZP434N1817 (Accession XM_042930) is another VGAM2110 host target gene. DKFZP434N1817 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434N1817, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434N1817 BINDING SITE, designated SEQ ID:33814, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73292] Another function of VGAM2110 is therefore inhibition of DKFZP434N1817 (Accession XM_042930). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434N1817. H11 (Accession NM_014365) is another VGAM2110 host target gene. H11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by H11, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H11 BINDING SITE, designated SEQ ID:15692, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73293] Another function of VGAM2110 is therefore inhibition of H11 (Accession NM_014365). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H11. KIAA0329 (Accession NM_014844) is another VGAM2110 host target gene. KIAA0329 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0329, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0329 BINDING SITE, designated SEQ ID:16877, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73294] Another function of VGAM2110 is therefore inhibition of KIAA0329 (Accession NM_014844). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0329. KIAA0557 (Accession XM_085507) is another VGAM2110 host target gene. KIAA0557 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0557, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0557 BINDING SITE, designated SEQ ID:38204, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73295] Another function of VGAM2110 is therefore inhibition of KIAA0557 (Accession XM_085507). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0557. MGC4415 (Accession NM_031484) is another VGAM2110 host target gene. MGC4415 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4415, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4415 BINDING SITE, designated SEQ ID:25571, to the nucleotide

sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73296] Another function of VGAM2110 is therefore inhibition of MGC4415 (Accession NM_031484). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4415. Syntaphilin (SNPH, Accession NM_014723) is another VGAM2110 host target gene. SNPH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNPH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNPH BINDING SITE, designated SEQ ID:16291, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73297] Another function of VGAM2110 is therefore inhibition of Syntaphilin (SNPH, Accession NM_014723). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNPH. LOC150504 (Accession XM_001732) is another VGAM2110 host target gene. LOC150504 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by LOC150504, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150504 BINDING SITE, designated SEQ ID:29849, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73298] Another function of VGAM2110 is therefore inhibition of LOC150504 (Accession XM_001732). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150504. LOC151443 (Accession XM_087200) is another VGAM2110 host target gene. LOC151443 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151443, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151443 BINDING SITE, designated SEQ ID:39114, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73299] Another function of VGAM2110 is therefore inhibition of LOC151443 (Accession XM_087200). Accordingly, utilities

of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151443. LOC158236 (Accession XM_098898) is another VGAM2110 host target gene. LOC158236 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158236, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158236 BINDING SITE, designated SEQ ID:41926, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73300] Another function of VGAM2110 is therefore inhibition of LOC158236 (Accession XM_098898). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158236. LOC158376 (Accession XM_098934) is another VGAM2110 host target gene. LOC158376 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158376, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC158376 BINDING SITE, designated SEQ ID:41973, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73301] Another function of VGAM2110 is therefore inhibition of LOC158376 (Accession XM_098934). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158376. LOC158402 (Accession XM_098936) is another VGAM2110 host target gene. LOC158402 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158402, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158402 BINDING SITE, designated SEQ ID:41974, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73302] Another function of VGAM2110 is therefore inhibition of LOC158402 (Accession XM_098936). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158402. LOC199676 (Accession XM_117107) is another VGAM2110 host target gene. LOC199676 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199676, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199676 BINDING SITE, designated SEQ ID:43224, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73303] Another function of VGAM2110 is therefore inhibition of LOC199676 (Accession XM_117107). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199676. LOC254065 (Accession XM_173239) is another VGAM2110 host target gene. LOC254065 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254065, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254065 BINDING SITE, designated SEQ ID:46522, to the nucleotide sequence of VGAM2110 RNA, herein designated VGAM RNA, also designated SEQ ID:4821.

[73304] Another function of VGAM2110 is therefore inhibition of

LOC254065 (Accession XM_173239). Accordingly, utilities of VGAM2110 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254065. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2111 (VGAM2111) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73305] VGAM2111 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2111 was detected is described hereinabove with reference to Figs. 1-8.

[73306] VGAM2111 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sheeppox Virus. VGAM2111 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73307] VGAM2111 gene encodes a VGAM2111 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2111 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2111 precursor RNA is designated SEQ ID:2097, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2097 is located at position 6922 relative to the genome of Sheeppox Virus.

[73308] VGAM2111 precursor RNA folds onto itself, forming VGAM2111 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73309] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2111 folded precursor RNA into VGAM2111 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2111 RNA is designated SEQ ID:4822, and is provided hereinbelow with reference to the sequence listing part.

[73310] VGAM2111 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2111 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2111 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73311] VGAM2111 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2111 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2111 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2111 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2111 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73312] The complementary binding of VGAM2111 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2111 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2111 host target RNA into VGAM2111 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73313] It is appreciated that VGAM2111 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2111 host target genes. The mRNA of each one of this plurality of VGAM2111 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2111 RNA, herein designated VGAM RNA, and which when bound by VGAM2111 RNA causes inhibition of translation of respective one or more VGAM2111 host target proteins.

[73314] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2111 gene, herein designated VGAM GENE, on one or more VGAM2111 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73315] It is yet further appreciated that a function of VGAM2111

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of viral infection by Sheeppox Virus. Specific functions, and accordingly utilities, of VGAM2111 correlate with, and may be deduced from, the identity of the host target genes which VGAM2111 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73316] Nucleotide sequences of the VGAM2111 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2111 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2111 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2111 are further described hereinbelow with reference to Table 1.

[73317] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2111 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2111 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73318] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2111 gene, herein designated VGAM is inhibition of expression of VGAM2111 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2111 correlate with, and may be deduced from, the identity of the target genes which VGAM2111 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73319] Androgen Receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy; Kennedy disease) (AR, Accession NM_000044) is a VGAM2111 host target gene. AR BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AR BINDING SITE, designated SEQ ID:5485, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73320] A function of VGAM2111 is therefore inhibition of Androgen Receptor (dihydrotestosterone receptor; testicular feminization; spinal and bulbar muscular atrophy;

Kennedy disease) (AR, Accession NM_000044), a gene which are involved in the regulation of eukaryotic gene expression and affect cellular proliferation and differentiation in target tissues. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AR. The function of AR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1971.Cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1, Accession NM_053056) is another VGAM2111 host target gene. CCND1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CCND1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCND1 BINDING SITE, designated SEQ ID:27602, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73321] Another function of VGAM2111 is therefore inhibition of Cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1, Accession NM_053056), a gene which is involved in the

control of cell cycle and is required for Schwann cell proliferation to proceed normally during Wallerian degeneration. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCND1. The function of CCND1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM220.CD83 Antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83, Accession NM_004233) is another VGAM2111 host target gene. CD83 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD83, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD83 BINDING SITE, designated SEQ ID:10425, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73322] Another function of VGAM2111 is therefore inhibition of CD83 Antigen (activated B lymphocytes, immunoglobulin superfamily) (CD83, Accession NM_004233), a gene which may play a significant role in antigen presentation or the

cellular interactions that follow lymphocyte activation. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD83. The function of CD83 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1929.Chorea Acanthocytosis (CHAC, Accession NM_033305) is another VGAM2111 host target gene. CHAC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHAC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHAC BINDING SITE, designated SEQ ID:27137, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73323] Another function of VGAM2111 is therefore inhibition of Chorea Acanthocytosis (CHAC, Accession NM_033305), a gene which may regulate the cycling of proteins. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHAC. The function of CHAC and its association

with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM650.Cytochrome P450, Subfamily I (aromatic compound-inducible), Polypeptide 2 (CYP1A2, Accession NM_000761) is another VGAM2111 host target gene. CYP1A2 BINDING SITE1 and CYP1A2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CYP1A2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP1A2 BINDING SITE1 and CYP1A2 BINDING SITE2, designated SEQ ID:6410 and SEQ ID:34253 respectively, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73324] Another function of VGAM2111 is therefore inhibition of Cytochrome P450, Subfamily I (aromatic compound-inducible), Polypeptide 2 (CYP1A2, Accession NM_000761), a gene which intervenes in an NADPH-dependent electron transport pathway. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP1A2. The function of CYP1A2 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Desmocollin 2 (DSC2, Accession NM_004949) is another VGAM2111 host target gene. DSC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DSC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DSC2 BINDING SITE, designated SEQ ID:11391, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73325] Another function of VGAM2111 is therefore inhibition of Desmocollin 2 (DSC2, Accession NM_004949), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC2. The function of DSC2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM909.Dystrobrevin, Beta (DTNB, Accession NM_033147) is another VGAM2111 host target gene.

DTNB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DTNB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DTNB BINDING SITE, designated SEQ ID:27005, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73326] Another function of VGAM2111 is therefore inhibition of Dystrobrevin, Beta (DTNB, Accession NM_033147), a gene which is a part of a dystrophin-associated protein complex . Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DTNB. The function of DTNB has been established by previous studies. Dystrophin, a component of muscle that is defective in Duchenne muscular dystrophy (DMD; 310200), binds to a complex of proteins and glycoproteins, the dystrophin-associated protein complex (DPC), which effectively forms a transmembrane link between the extracellular matrix, and the cytoskeleton of the muscle fiber. The DPC can be divided into 3 subcomplexes: the dystroglycan complex, the sarcoglycan complex, and the cytoplasmic complex. The dystroglycan

complex consists of 2 proteins, alpha- and beta-dystroglycan (DAG1, 128239; DAG2, 600119), that bind to laminin and dystrophin, respectively. The sarcoglycan complex is composed of 4 transmembrane glycoproteins: alpha-, beta-, gamma-, and delta-sarcoglycan, and a 25-kD protein 25DAP. Mutations in all 4 sarcoglycan genes have been found in patients with different forms of limb-girdle muscular dystrophy. The cytoplasmic component of the DPC is composed of the syntrophin family of related proteins and the dystrophin-related protein, dystrobrevin. Peters et al. (1997) described beta-dystrobrevin. They cloned cDNAs from human liver libraries that encode a 627-amino acid polypeptide with a predicted molecular weight of 71 kD. The protein copurified with the dystrobrevin short form, Dp71. The mammalian dystrobrevin genes encode several protein isoforms that are expressed in different tissues, including brain and muscle. Blake et al. (1998) designated the isoform expressed in muscle as alpha-dystrobrevin and used the designation beta-dystrobrevin for the dystrophin-related protein they found to be abundantly expressed in brain and other tissues but not in muscle. Beta-dystrobrevin is encoded by a 2.5-kb alternatively spliced transcript that is

found throughout the brain. In common with dystrophin, beta-dystrobrevin is found in neurons of the cortex and hippocampal formation, but it is not found in the brain microvasculature. In the brain, beta-dystrobrevin coprecipitates with the dystrophin isoforms Dp71 and Dp140. The findings of Blake et al. (1998) indicated that the composition of the dystrophin-associated protein complex in the brain differs from that in muscle. Because beta-dystrobrevin and dystrophin are expressed in similar populations of neurons in the hippocampus and cortex, it is possible that beta-dystrobrevin interacts directly with dystrophin. If this is the case, then beta-dystrobrevin levels may be reduced in DMD patients similar to the reduction in sarcolemmal staining seen with other components of the DPC in dystrophic muscle. The findings may be relevant to the cognitive dysfunction affecting many patients with Duchenne muscular dystrophy.

[73327] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[73328] Blake, D. J.; Nawrotzki, R.; Loh, N. Y.; Gorecki, D. C.; Davies, K. E. : Beta-dystrobrevin, a member of the dystrophin-related protein family. Proc. Nat. Acad. Sci. 95:

241-246, 1998. ; and

[73329] Peters, M. F.; O'Brien, K. F.; Sadoulet-Puccio, H. M.; Kunkel, L. M.; Adams, M. E.; Froehner, S. C. : Beta-dystrobrevin, a new member of the dystrophin family: identification, cloning.

[73330] Further studies establishing the function and utilities of DTNB are found in John Hopkins OMIM database record ID 602415, and in sited publications numbered 284 and 1028 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Dishevelled, Dsh Homolog 3 (Drosophila) (DVL3, Accession NM_004423) is another VGAM2111 host target gene. DVL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DVL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DVL3 BINDING SITE, designated SEQ ID:10687, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73331] Another function of VGAM2111 is therefore inhibition of Dishevelled, Dsh Homolog 3 (Drosophila) (DVL3, Accession NM_004423), a gene which regulates cell prolifera-

tion. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DVL3. The function of DVL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM57.Exostoses (multiple)-like 2 (EXTL2, Accession NM_001439) is another VGAM2111 host target gene. EXTL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EXTL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EXTL2 BINDING SITE, designated SEQ ID:7159, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73332] Another function of VGAM2111 is therefore inhibition of Exostoses (multiple)-like 2 (EXTL2, Accession NM_001439), a gene which is homologous to the EXT and EXTL genes. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EXTL2. The function of EXTL2 and its association with various diseases and clini-

cal conditions, has been established by previous studies, as described hereinabove with reference to VGAM743.Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411) is another VGAM2111 host target gene. HLCS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HLCS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HLCS BINDING SITE, designated SEQ ID:5986, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73333] Another function of VGAM2111 is therefore inhibition of Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLCS. Hairy Homolog (Drosophila) (HRY, Accession NM_005524) is another VGAM2111 host target gene. HRY BINDING SITE is HOST TARGET binding

site found in the 5` untranslated region of mRNA encoded by HRY, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRY BINDING SITE, designated SEQ ID:12048, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73334] Another function of VGAM2111 is therefore inhibition of Hairy Homolog (Drosophila) (HRY, Accession NM_005524), a gene which may act as a negative regulator of myogenesis . Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRY. The function of HRY has been established by previous studies. By site-directed mutagenesis and overexpression of HRY in human fibroblasts, Yan et al. (2002) showed that HRY, as well as YY1 (OMIM Ref. No. 600013), functions as a transcriptional activator of acid alpha-glucosidase (GAA; 606800). Using gel shift assays, they found that HRY binds to a 25-bp enhancer element within the first intron of the GAA gene. In previous studies, Yan et al. (2001) had found that HRY, binding to the same element of the GAA gene in hepatoma cells,

acts as a GAA transcription silencer. Yan et al. (2002) noted that the dual function of HRY is likely to contribute to the subtle tissue-specific control of housekeeping genes such as GAA. Votruba et al. (1998) identified no mutations in the HRY gene in 36 patients from 18 pedigrees with OPA1. Using a polymorphism in the untranslated region of exon 2 of HRY, Votruba et al. (1998) found recombination between HRY and OPA1 in 1 pedigree.

[73335] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[73336] Yan, B.; Heus, J.; Lu, N.; Nichols, R. C.; Raben, N.; Plotz, P. H. : Transcriptional regulation of the human acid alpha-glucosidase gene: identification of a repressor element and its transcription factors Hes-1 and YY1. J. Biol. Chem. 276: 1789-1793, 2001. ; and

[73337] Yan, B.; Raben, N.; Plotz, P. H. : Hes-1, a known transcriptional repressor, acts as a transcriptional activator for the human acid alpha-glucosidase gene in human fibroblast cells. Bi.

[73338] Further studies establishing the function and utilities of HRY are found in John Hopkins OMIM database record ID 139605, and in sited publications numbered 3572-3575

listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Nuclear Receptor Subfamily 1, Group I, Member 2 (NR1I2, Accession NM_003889) is another VGAM2111 host target gene. NR1I2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NR1I2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR1I2 BINDING SITE, designated SEQ ID:9973, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73339] Another function of VGAM2111 is therefore inhibition of Nuclear Receptor Subfamily 1, Group I, Member 2 (NR1I2, Accession NM_003889), a gene which binds to a response element in the cyp3a4 gene promoter and activates its expression in response to a wide variety of endobiotics and xenobiotics. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR1I2. The function of NR1I2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM336.Nuclear Receptor Subfamily 4, Group A, Member 2 (NR4A2, Accession NM_006186) is another VGAM2111 host target gene. NR4A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NR4A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR4A2 BINDING SITE, designated SEQ ID:12856, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73340] Another function of VGAM2111 is therefore inhibition of Nuclear Receptor Subfamily 4, Group A, Member 2 (NR4A2, Accession NM_006186), a gene which may be a general coactivator of transcription. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR4A2. The function of NR4A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM127.P53AIP1 (Accession NM_022112) is another VGAM2111 host target gene. P53AIP1 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by P53AIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P53AIP1 BINDING SITE, designated SEQ ID:22657, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73341] Another function of VGAM2111 is therefore inhibition of P53AIP1 (Accession NM_022112). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P53AIP1. Protein Kinase, CGMP-dependent, Type I (PRKG1, Accession NM_006258) is another VGAM2111 host target gene. PRKG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKG1 BINDING SITE, designated SEQ ID:12935, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73342] Another function of VGAM2111 is therefore inhibition of

Protein Kinase, CGMP-dependent, Type I (PRKG1, Accession NM_006258), a gene which relaxes vascular smooth muscle and inhibits platelet aggregation. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKG1. The function of PRKG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1571.Protein Tyrosine Phosphatase, Non-receptor Type 2 (PTPN2, Accession NM_002828) is another VGAM2111 host target gene. PTPN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPN2 BINDING SITE, designated SEQ ID:8704, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73343] Another function of VGAM2111 is therefore inhibition of Protein Tyrosine Phosphatase, Non-receptor Type 2 (PTPN2, Accession NM_002828). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PTPN2. Synaptotagmin IV (SYT4, Accession XM_031162) is another VGAM2111 host target gene. SYT4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYT4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYT4 BINDING SITE, designated SEQ ID:31291, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73344] Another function of VGAM2111 is therefore inhibition of Synaptotagmin IV (SYT4, Accession XM_031162), a gene which may be involved in ca2+-dependent exocytosis of secretory vesicles or may serve as ca2+ sensors in the process of vesicular trafficking and exocytosis. Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT4. The function of SYT4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.X Kell Blood Group Precursor-related, Y-linked (XKRY, Accession NM_004677) is another

VGAM2111 host target gene. XKRY BINDING SITE1 and XKRY BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by XKRY, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XKRY BINDING SITE1 and XKRY BINDING SITE2, designated SEQ ID:11044 and SEQ ID:30153 respectively, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73345] Another function of VGAM2111 is therefore inhibition of X Kell Blood Group Precursor-related, Y-linked (XKRY, Accession NM_004677). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XKRY. Chromosome 6 Open Reading Frame 37 (C6orf37, Accession XM_041375) is another VGAM2111 host target gene. C6orf37 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C6orf37, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C6orf37 BINDING SITE, designated SEQ

ID:33506, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73346] Another function of VGAM2111 is therefore inhibition of Chromosome 6 Open Reading Frame 37 (C6orf37, Accession XM_041375). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf37. C6orf5 (Accession NM_015524) is another VGAM2111 host target gene. C6orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C6orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C6orf5 BINDING SITE, designated SEQ ID:17776, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73347] Another function of VGAM2111 is therefore inhibition of C6orf5 (Accession NM_015524). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf5. Calcium/calmodulin-dependent Protein Kinase Kinase 2,

Beta (CAMKK2, Accession NM_006549) is another VGAM2111 host target gene. CAMKK2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CAMKK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAMKK2 BINDING SITE, designated SEQ ID:13307, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73348] Another function of VGAM2111 is therefore inhibition of Calcium/calmodulin-dependent Protein Kinase Kinase 2, Beta (CAMKK2, Accession NM_006549). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMKK2. Collagen, Type XXI, Alpha 1 (COL21A1, Accession NM_030820) is another VGAM2111 host target gene. COL21A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL21A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL21A1 BINDING SITE, designated

SEQ ID:25149, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73349] Another function of VGAM2111 is therefore inhibition of Collagen, Type XXI, Alpha 1 (COL21A1, Accession NM_030820). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL21A1. Cysteine Sulfinic Acid Decarboxylase (CSAD, Accession NM_015989) is another VGAM2111 host target gene. CSAD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSAD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSAD BINDING SITE, designated SEQ ID:18081, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73350] Another function of VGAM2111 is therefore inhibition of Cysteine Sulfinic Acid Decarboxylase (CSAD, Accession NM_015989). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSAD. DKFZP547L112

(Accession XM_039353) is another VGAM2111 host target gene. DKFZP547L112 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP547L112, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP547L112 BINDING SITE, designated SEQ ID:33057, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73351] Another function of VGAM2111 is therefore inhibition of DKFZP547L112 (Accession XM_039353). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP547L112. FLJ12568 (Accession NM_024993) is another VGAM2111 host target gene. FLJ12568 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12568, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12568 BINDING SITE, designated SEQ ID:24554, to the nucleotide sequence of VGAM2111 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4822.

[73352] Another function of VGAM2111 is therefore inhibition of FLJ12568 (Accession NM_024993). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12568. FLJ13409 (Accession NM_024617) is another VGAM2111 host target gene. FLJ13409 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13409, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13409 BINDING SITE, designated SEQ ID:23879, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73353] Another function of VGAM2111 is therefore inhibition of FLJ13409 (Accession NM_024617). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13409. FLJ13841 (Accession NM_024702) is another VGAM2111 host target gene. FLJ13841 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13841, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13841 BINDING SITE, designated SEQ ID:24015, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73354] Another function of VGAM2111 is therefore inhibition of FLJ13841 (Accession NM_024702). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13841. FLJ20340 (Accession NM_017773) is another VGAM2111 host target gene. FLJ20340 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20340, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20340 BINDING SITE, designated SEQ ID:19395, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73355] Another function of VGAM2111 is therefore inhibition of FLJ20340 (Accession NM_017773). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20340. FLJ23058 (Accession NM_024696) is another VGAM2111 host target gene. FLJ23058 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23058, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23058 BINDING SITE, designated SEQ ID:24005, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73356] Another function of VGAM2111 is therefore inhibition of FLJ23058 (Accession NM_024696). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23058. FLJ23548 (Accession NM_024590) is another VGAM2111 host target gene. FLJ23548 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23548, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23548 BINDING SITE, designated SEQ ID:23826, to the nucleotide

sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73357] Another function of VGAM2111 is therefore inhibition of FLJ23548 (Accession NM_024590). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23548. GTP Binding Protein 5 (putative) (GTPBP5, Accession XM_037206) is another VGAM2111 host target gene. GTPBP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GTPBP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTPBP5 BINDING SITE, designated SEQ ID:32573, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73358] Another function of VGAM2111 is therefore inhibition of GTP Binding Protein 5 (putative) (GTPBP5, Accession XM_037206). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTPBP5. ICAP-1A (Accession NM_004763) is another VGAM2111 host target

gene. ICAP-1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICAP-1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ICAP-1A BINDING SITE, designated SEQ ID:11156, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73359] Another function of VGAM2111 is therefore inhibition of ICAP-1A (Accession NM_004763). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICAP-1A. KIAA0455 (Accession XM_051785) is another VGAM2111 host target gene. KIAA0455 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0455, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0455 BINDING SITE, designated SEQ ID:35880, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73360] Another function of VGAM2111 is therefore inhibition of KIAA0455 (Accession XM_051785). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0455. KIAA0471 (Accession NM_014857) is another VGAM2111 host target gene. KIAA0471 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0471, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0471 BINDING SITE, designated SEQ ID:16913, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73361] Another function of VGAM2111 is therefore inhibition of KIAA0471 (Accession NM_014857). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0471. KIAA1086 (Accession XM_047610) is another VGAM2111 host target gene. KIAA1086 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1086, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1086 BINDING SITE, designated SEQ ID:35011, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73362] Another function of VGAM2111 is therefore inhibition of KIAA1086 (Accession XM_047610). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1086. KIAA1260 (Accession XM_010461) is another VGAM2111 host target gene. KIAA1260 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1260, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1260 BINDING SITE, designated SEQ ID:30154, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73363] Another function of VGAM2111 is therefore inhibition of KIAA1260 (Accession XM_010461). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1260. KIAA1677 (Accession XM_040383) is another VGAM2111 host target gene. KIAA1677 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1677, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1677 BINDING SITE, designated SEQ ID:33289, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73364] Another function of VGAM2111 is therefore inhibition of KIAA1677 (Accession XM_040383). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1677. KIAA1829 (Accession XM_030378) is another VGAM2111 host target gene. KIAA1829 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1829, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1829 BINDING SITE, designated SEQ ID:31033, to the nucleotide sequence of VGAM2111 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4822.

[73365] Another function of VGAM2111 is therefore inhibition of KIAA1829 (Accession XM_030378). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1829. KIAA1866 (Accession XM_027658) is another VGAM2111 host target gene. KIAA1866 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1866, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1866 BINDING SITE, designated SEQ ID:30556, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73366] Another function of VGAM2111 is therefore inhibition of KIAA1866 (Accession XM_027658). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1866. MBLL39 (Accession NM_144778) is another VGAM2111 host target gene. MBLL39 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MBLL39, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MBLL39 BINDING SITE, designated SEQ ID:29574, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73367] Another function of VGAM2111 is therefore inhibition of MBLL39 (Accession NM_144778). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBLL39. MGC29891 (Accession NM_144618) is another VGAM2111 host target gene. MGC29891 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC29891, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC29891 BINDING SITE, designated SEQ ID:29436, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73368] Another function of VGAM2111 is therefore inhibition of MGC29891 (Accession NM_144618). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC29891. MOT8 (Accession NM_018836) is another VGAM2111 host target gene. MOT8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MOT8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MOT8 BINDING SITE, designated SEQ ID:20826, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73369] Another function of VGAM2111 is therefore inhibition of MOT8 (Accession NM_018836). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOT8. ODZ2 (Accession XM_047995) is another VGAM2111 host target gene. ODZ2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ODZ2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ODZ2 BINDING SITE, designated SEQ ID:35095, to the nucleotide sequence of VGAM2111 RNA,

herein designated VGAM RNA, also designated SEQ ID:4822.

[73370] Another function of VGAM2111 is therefore inhibition of ODZ2 (Accession XM_047995). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ODZ2. Proprotein Convertase Subtilisin/kexin Type 7 (PCSK7, Accession NM_004716) is another VGAM2111 host target gene. PCSK7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCSK7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCSK7 BINDING SITE, designated SEQ ID:11077, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73371] Another function of VGAM2111 is therefore inhibition of Proprotein Convertase Subtilisin/kexin Type 7 (PCSK7, Accession NM_004716). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCSK7. Pleckstrin Homology Domain Containing, Family A (phosphoinositide

binding specific) Member 3 (PLEKHA3, Accession NM_019091) is another VGAM2111 host target gene. PLEKHA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLEKHA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLEKHA3 BINDING SITE, designated SEQ ID:21166, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73372] Another function of VGAM2111 is therefore inhibition of Pleckstrin Homology Domain Containing, Family A (phosphoinositide binding specific) Member 3 (PLEKHA3, Accession NM_019091). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLEKHA3. PRO0478 (Accession NM_014129) is another VGAM2111 host target gene. PRO0478 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO0478, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-ING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PRO0478 BINDING SITE, designated SEQ ID:15396, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73373] Another function of VGAM2111 is therefore inhibition of PRO0478 (Accession NM_014129). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0478. RAB14, Member RAS Oncogene Family (RAB14, Accession NM_016322) is another VGAM2111 host target gene. RAB14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB14 BINDING SITE, designated SEQ ID:18445, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73374] Another function of VGAM2111 is therefore inhibition of RAB14, Member RAS Oncogene Family (RAB14, Accession NM_016322). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with RAB14. RICH1 (Accession NM_018054) is another VGAM2111 host target gene. RICH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RICH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RICH1 BINDING SITE, designated SEQ ID:19814, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73375] Another function of VGAM2111 is therefore inhibition of RICH1 (Accession NM_018054). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RICH1. Solute Carrier Family 11 (proton-coupled divalent metal ion transporters), Member 1 (SLC11A1, Accession XM_002585) is another VGAM2111 host target gene. SLC11A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC11A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of SLC11A1 BINDING SITE, designated SEQ ID:29901, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73376] Another function of VGAM2111 is therefore inhibition of Solute Carrier Family 11 (proton-coupled divalent metal ion transporters), Member 1 (SLC11A1, Accession XM_002585). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC11A1. LOC125434 (Accession XM_058921) is another VGAM2111 host target gene. LOC125434 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC125434, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC125434 BINDING SITE, designated SEQ ID:36795, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73377] Another function of VGAM2111 is therefore inhibition of LOC125434 (Accession XM_058921). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC125434. LOC145945 (Accession XM_096908) is another VGAM2111 host target gene. LOC145945 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145945, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145945 BINDING SITE, designated SEQ ID:40627, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73378] Another function of VGAM2111 is therefore inhibition of LOC145945 (Accession XM_096908). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145945. LOC146520 (Accession XM_085492) is another VGAM2111 host target gene. LOC146520 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146520, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146520 BINDING SITE, designated SEQ ID:38183, to

the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73379] Another function of VGAM2111 is therefore inhibition of LOC146520 (Accession XM_085492). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146520. LOC149127 (Accession XM_097584) is another VGAM2111 host target gene. LOC149127 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149127, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149127 BINDING SITE, designated SEQ ID:40951, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73380] Another function of VGAM2111 is therefore inhibition of LOC149127 (Accession XM_097584). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149127. LOC158427 (Accession NM_139246) is another VGAM2111 host target gene. LOC158427 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC158427, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158427 BINDING SITE, designated SEQ ID:29244, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73381] Another function of VGAM2111 is therefore inhibition of LOC158427 (Accession NM_139246). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158427. LOC199858 (Accession XM_114040) is another VGAM2111 host target gene. LOC199858 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199858, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199858 BINDING SITE, designated SEQ ID:42628, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73382] Another function of VGAM2111 is therefore inhibition of LOC199858 (Accession XM_114040). Accordingly, utilities

of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199858. LOC199923 (Accession XM_114057) is another VGAM2111 host target gene. LOC199923 BINDING SITE1 and LOC199923 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC199923, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199923 BINDING SITE1 and LOC199923 BINDING SITE2, designated SEQ ID:42663 and SEQ ID:42664 respectively, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73383] Another function of VGAM2111 is therefore inhibition of LOC199923 (Accession XM_114057). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199923. LOC219672 (Accession XM_166111) is another VGAM2111 host target gene. LOC219672 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219672, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219672 BINDING SITE, designated SEQ ID:43887, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73384] Another function of VGAM2111 is therefore inhibition of LOC219672 (Accession XM_166111). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219672. LOC221814 (Accession XM_168226) is another VGAM2111 host target gene. LOC221814 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221814, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221814 BINDING SITE, designated SEQ ID:45095, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73385] Another function of VGAM2111 is therefore inhibition of LOC221814 (Accession XM_168226). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221814. LOC221943 (Accession XM_168343) is another VGAM2111 host target gene. LOC221943 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221943, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221943 BINDING SITE, designated SEQ ID:45115, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73386] Another function of VGAM2111 is therefore inhibition of LOC221943 (Accession XM_168343). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221943. LOC253639 (Accession XM_171060) is another VGAM2111 host target gene. LOC253639 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253639, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253639 BINDING SITE, designated SEQ ID:45853, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73387] Another function of VGAM2111 is therefore inhibition of LOC253639 (Accession XM_171060). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC253639. LOC254659 (Accession XM_170822) is another VGAM2111 host target gene. LOC254659 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254659, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254659 BINDING SITE, designated SEQ ID:45598, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73388] Another function of VGAM2111 is therefore inhibition of LOC254659 (Accession XM_170822). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254659. LOC51141 (Accession XM_043953) is another VGAM2111 host target gene. LOC51141 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51141, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51141 BINDING SITE, designated SEQ ID:34045, to the nucleotide sequence of VGAM2111 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4822.

[73389] Another function of VGAM2111 is therefore inhibition of LOC51141 (Accession XM_043953). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51141. LOC56920 (Accession NM_020163) is another VGAM2111 host target gene. LOC56920 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC56920, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56920 BINDING SITE, designated SEQ ID:21379, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73390] Another function of VGAM2111 is therefore inhibition of LOC56920 (Accession NM_020163). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56920. LOC90155 (Accession XM_029487) is another VGAM2111 host target gene. LOC90155 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90155, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90155 BINDING SITE, designated SEQ ID:30898, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73391] Another function of VGAM2111 is therefore inhibition of LOC90155 (Accession XM_029487). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90155. LOC91496 (Accession XM_038788) is another VGAM2111 host target gene. LOC91496 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91496, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91496 BINDING SITE, designated SEQ ID:32919, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73392] Another function of VGAM2111 is therefore inhibition of LOC91496 (Accession XM_038788). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC91496. LOC92973 (Accession XM_048529) is another VGAM2111 host target gene. LOC92973 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92973, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92973 BINDING SITE, designated SEQ ID:35180, to the nucleotide sequence of VGAM2111 RNA, herein designated VGAM RNA, also designated SEQ ID:4822.

[73393] Another function of VGAM2111 is therefore inhibition of LOC92973 (Accession XM_048529). Accordingly, utilities of VGAM2111 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92973. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2112 (VGAM2112) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73394] VGAM2112 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2112 was detected is described hereinabove with reference to Figs. 1-8.

[73395] VGAM2112 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Grapevine Chrome Mosaic Virus. VGAM2112 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73396] VGAM2112 gene encodes a VGAM2112 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2112 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2112 precursor RNA is designated SEQ ID:2098, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2098 is located at position 1230 relative to the genome of Grapevine Chrome Mosaic Virus.

[73397] VGAM2112 precursor RNA folds onto itself, forming VGAM2112 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73398] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2112 folded precursor RNA into VGAM2112 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2112 RNA is designated SEQ ID:4823, and is provided hereinbelow with reference to the sequence listing part.

[73399] VGAM2112 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2112 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2112 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73400] VGAM2112 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2112 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2112 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2112 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2112 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73401] The complementary binding of VGAM2112 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2112 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2112 host target RNA into VGAM2112 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73402] It is appreciated that VGAM2112 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2112 host target genes. The mRNA of each one of this plurality of VGAM2112 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2112 RNA, herein designated VGAM RNA, and which when bound by VGAM2112 RNA causes inhibition of translation of respective one or more VGAM2112 host target proteins.

[73403] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2112 gene, herein designated VGAM GENE, on one or more VGAM2112 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73404] It is yet further appreciated that a function of VGAM2112 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2112 include diagnosis, prevention and treatment of viral infection by Grapevine Chrome Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2112 correlate with, and may be deduced from, the identity of the host target genes which VGAM2112 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73405] Nucleotide sequences of the VGAM2112 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2112 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2112 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2112 are further described hereinbelow with reference to Table 1.

[73406] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2112 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2112 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73407] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2112 gene, herein designated VGAM is inhibition of expression of VGAM2112 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2112 correlate with, and may be deduced from, the identity of the target genes which VGAM2112 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73408] Estrogen Receptor 1 (ESR1, Accession NM_000125) is a VGAM2112 host target gene. ESR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by ESR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESR1 BINDING SITE, designated SEQ ID:5600, to the nucleotide sequence of VGAM2112 RNA, herein designated VGAM RNA, also designated SEQ ID:4823.

[73409] A function of VGAM2112 is therefore inhibition of Estrogen Receptor 1 (ESR1, Accession NM_000125), a gene which involved in hormone-mediated inhibition of gene expression. Accordingly, utilities of VGAM2112 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESR1. The function of ESR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM695.Polycystic Kidney Disease 2-like 1 (PKD2L1, Accession NM_016112) is another VGAM2112 host target gene. PKD2L1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PKD2L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

PKD2L1 BINDING SITE, designated SEQ ID:18194, to the nucleotide sequence of VGAM2112 RNA, herein designated VGAM RNA, also designated SEQ ID:4823.

[73410] Another function of VGAM2112 is therefore inhibition of Polycystic Kidney Disease 2-like 1 (PKD2L1, Accession NM_016112). Accordingly, utilities of VGAM2112 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKD2L1. CGG Triplet Repeat Binding Protein 1 (CGGBP1, Accession NM_003663) is another VGAM2112 host target gene. CGGBP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CGGBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CGGBP1 BINDING SITE, designated SEQ ID:9739, to the nucleotide sequence of VGAM2112 RNA, herein designated VGAM RNA, also designated SEQ ID:4823.

[73411] Another function of VGAM2112 is therefore inhibition of CGG Triplet Repeat Binding Protein 1 (CGGBP1, Accession NM_003663). Accordingly, utilities of VGAM2112 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGGBP1. VRP (Accession

NM_007063) is another VGAM2112 host target gene. VRP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by VRP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VRP BINDING SITE, designated SEQ ID:13927, to the nucleotide sequence of VGAM2112 RNA, herein designated VGAM RNA, also designated SEQ ID:4823.

[73412] Another function of VGAM2112 is therefore inhibition of VRP (Accession NM_007063). Accordingly, utilities of VGAM2112 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VRP. LOC155382 (Accession XM_098713) is another VGAM2112 host target gene. LOC155382 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155382, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155382 BINDING SITE, designated SEQ ID:41763, to the nucleotide sequence of VGAM2112 RNA, herein designated VGAM RNA, also designated SEQ ID:4823.

[73413] Another function of VGAM2112 is therefore inhibition of LOC155382 (Accession XM_098713). Accordingly, utilities of VGAM2112 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155382. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2113 (VGAM2113) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73414] VGAM2113 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2113 was detected is described hereinabove with reference to Figs. 1-8.

[73415] VGAM2113 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Sheeppox Virus. VGAM2113 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73416] VGAM2113 gene encodes a VGAM2113 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2113 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2113 precursor RNA is designated SEQ ID:2099, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2099 is located at position 7750 relative to the genome of Sheeppox Virus.

[73417] VGAM2113 precursor RNA folds onto itself, forming VGAM2113 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73418] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2113 folded precursor RNA into VGAM2113 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2113 RNA is designated SEQ ID:4824, and is provided hereinbelow with reference to the sequence listing part.

[73419] VGAM2113 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2113 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2113 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73420] VGAM2113 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2113 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2113 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2113 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2113 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73421] The complementary binding of VGAM2113 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2113 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2113 host target RNA into VGAM2113 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73422] It is appreciated that VGAM2113 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2113 host target genes. The mRNA of each one of this plurality of VGAM2113 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2113 RNA, herein designated VGAM RNA, and which when bound by VGAM2113 RNA causes inhibition of translation of respective one or more VGAM2113 host target proteins.

[73423] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2113 gene, herein designated VGAM GENE, on one or more VGAM2113 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73424] It is yet further appreciated that a function of VGAM2113 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of viral infection by Sheeppox Virus. Specific functions, and accordingly utilities, of VGAM2113 correlate with, and may be deduced from, the identity of the host target genes which VGAM2113 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73425] Nucleotide sequences of the VGAM2113 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2113 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2113 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2113 are further described hereinbelow with reference to Table 1.

[73426] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2113 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2113 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[73427] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2113 gene, herein designated VGAM is inhibition of expression of VGAM2113 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2113 correlate with, and may be deduced from, the identity of the target genes which VGAM2113 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73428] ATP-binding Cassette, Sub-family D (ALD), Member 4 (ABCD4, Accession NM_020325) is a VGAM2113 host target gene. ABCD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCD4 BINDING SITE, designated SEQ ID:21586, to the nucleotide sequence of VGAM2113 RNA, herein designated VGAM RNA, also designated SEQ ID:4824.

[73429] A function of VGAM2113 is therefore inhibition of ATP-binding Cassette, Sub-family D (ALD), Member 4 (ABCD4, Accession NM_020325), a gene which Putative peroxiso-

mal ATP binding cassette transporter. Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCD4. The function of ABCD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1924.Eukaryotic Translation Initiation Factor 2C, 1 (EIF2C1, Accession NM_012199) is another VGAM2113 host target gene. EIF2C1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF2C1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF2C1 BINDING SITE, designated SEQ ID:14503, to the nucleotide sequence of VGAM2113 RNA, herein designated VGAM RNA, also designated SEQ ID:4824.

[73430] Another function of VGAM2113 is therefore inhibition of Eukaryotic Translation Initiation Factor 2C, 1 (EIF2C1, Accession NM_012199), a gene which plays an important role in the eukaryotic peptide chain initiation process. Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with EIF2C1. The function of EIF2C1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM118.Oculocerebrorenal Syndrome of Lowe (OCRL, Accession NM_001587) is another VGAM2113 host target gene. OCRL BINDING SITE1 and OCRL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by OCRL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OCRL BINDING SITE1 and OCRL BINDING SITE2, designated SEQ ID:7308 and SEQ ID:5821 respectively, to the nucleotide sequence of VGAM2113 RNA, herein designated VGAM RNA, also designated SEQ ID:4824.

[73431] Another function of VGAM2113 is therefore inhibition of Oculocerebrorenal Syndrome of Lowe (OCRL, Accession NM_001587). Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OCRL. SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9, Accession NM_000346) is another VGAM2113 host target gene. SOX9 BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX9 BINDING SITE, designated SEQ ID:5902, to the nucleotide sequence of VGAM2113 RNA, herein designated VGAM RNA, also designated SEQ ID:4824.

[73432] Another function of VGAM2113 is therefore inhibition of SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9, Accession NM_000346), a gene which regulates the expression of other genes involved in chondrogenesis. Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX9. The function of SOX9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM329.FLJ20211 (Accession NM_017713) is another VGAM2113 host target gene. FLJ20211 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20211, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20211 BINDING SITE, designated SEQ ID:19295, to the nucleotide sequence of VGAM2113 RNA, herein designated VGAM RNA, also designated SEQ ID:4824.

[73433] Another function of VGAM2113 is therefore inhibition of FLJ20211 (Accession NM_017713). Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20211. FLJ20574 (Accession NM_017886) is another VGAM2113 host target gene. FLJ20574 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20574, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20574 BINDING SITE, designated SEQ ID:19554, to the nucleotide sequence of VGAM2113 RNA, herein designated VGAM RNA, also designated SEQ ID:4824.

[73434] Another function of VGAM2113 is therefore inhibition of FLJ20574 (Accession NM_017886). Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20574. JM11 (Accession NM_033626) is another VGAM2113 host target gene. JM11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by JM11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JM11 BINDING SITE, designated SEQ ID:27332, to the nucleotide sequence of VGAM2113 RNA, herein designated VGAM RNA, also designated SEQ ID:4824.

[73435] Another function of VGAM2113 is therefore inhibition of JM11 (Accession NM_033626). Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JM11. KIAA0247 (Accession NM_014734) is another VGAM2113 host target gene. KIAA0247 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0247, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0247 BINDING SITE, designated SEQ ID:16380, to the nucleotide sequence of VGAM2113 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4824.

[73436] Another function of VGAM2113 is therefore inhibition of KIAA0247 (Accession NM_014734). Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0247. KIAA1024 (Accession XM_044580) is another VGAM2113 host target gene. KIAA1024 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1024, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1024 BINDING SITE, designated SEQ ID:34237, to the nucleotide sequence of VGAM2113 RNA, herein designated VGAM RNA, also designated SEQ ID:4824.

[73437] Another function of VGAM2113 is therefore inhibition of KIAA1024 (Accession XM_044580). Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1024. KIAA1819 (Accession XM_045716) is another VGAM2113 host target gene. KIAA1819 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1819, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1819 BINDING SITE, designated SEQ ID:34534, to the nucleotide sequence of VGAM2113 RNA, herein designated VGAM RNA, also designated SEQ ID:4824.

[73438] Another function of VGAM2113 is therefore inhibition of KIAA1819 (Accession XM_045716). Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1819. MEGF10 (Accession NM_032446) is another VGAM2113 host target gene. MEGF10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEGF10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEGF10 BINDING SITE, designated SEQ ID:26211, to the nucleotide sequence of VGAM2113 RNA, herein designated VGAM RNA, also designated SEQ ID:4824.

[73439] Another function of VGAM2113 is therefore inhibition of MEGF10 (Accession NM_032446). Accordingly, utilities of VGAM2113 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MEGF10. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2114 (VGAM2114) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73440] VGAM2114 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2114 was detected is described hereinabove with reference to Figs. 1-8.

[73441] VGAM2114 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2114 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73442] VGAM2114 gene encodes a VGAM2114 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2114 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2114 precursor RNA is desig-

nated SEQ ID:2100, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2100 is located at position 9163 relative to the genome of Cowpox Virus.

[73443] VGAM2114 precursor RNA folds onto itself, forming VGAM2114 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73444] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2114 folded precursor RNA into VGAM2114 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2114 RNA is designated SEQ ID:4825, and is provided hereinbelow with reference to the sequence

listing part.

[73445] VGAM2114 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2114 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2114 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73446] VGAM2114 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2114 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2114 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2114 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2114 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73447] The complementary binding of VGAM2114 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2114 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2114 host target RNA into VGAM2114 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73448] It is appreciated that VGAM2114 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2114 host target genes. The mRNA of each one of this plurality of VGAM2114 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2114 RNA, herein designated VGAM

RNA, and which when bound by VGAM2114 RNA causes inhibition of translation of respective one or more VGAM2114 host target proteins.

[73449] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2114 gene, herein designated VGAM GENE, on one or more VGAM2114 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73450] It is yet further appreciated that a function of VGAM2114 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2114 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2114 correlate with, and may be deduced from, the identity of the host target genes which VGAM2114 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73451] Nucleotide sequences of the VGAM2114 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2114 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2114 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2114 are further described hereinbelow with reference to Table 1.

[73452] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2114 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2114 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73453] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2114 gene, herein designated VGAM is

inhibition of expression of VGAM2114 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2114 correlate with, and may be deduced from, the identity of the target genes which VGAM2114 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73454] Mitogen-activated Protein Kinase 9 (MAPK9, Accession NM_002752) is a VGAM2114 host target gene. MAPK9 BINDING SITE1 through MAPK9 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MAPK9, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPK9 BINDING SITE1 through MAPK9 BINDING SITE4, designated SEQ ID:8631, SEQ ID:29136, SEQ ID:29138 and SEQ ID:29140 respectively, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73455] A function of VGAM2114 is therefore inhibition of Mitogen-activated Protein Kinase 9 (MAPK9, Accession NM_002752), a gene which Member of the MAP kinase family, regulates c-Jun in response to proinflammatory

cytokines and UV irradiation. Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK9. The function of MAPK9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Parkinson Disease (autosomal recessive, juvenile) 2, Parkin (PARK2, Accession NM_013987) is another VGAM2114 host target gene. PARK2 BINDING SITE1 through PARK2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PARK2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PARK2 BINDING SITE1 through PARK2 BINDING SITE3, designated SEQ ID:15153, SEQ ID:15160 and SEQ ID:8543 respectively, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73456] Another function of VGAM2114 is therefore inhibition of Parkinson Disease (autosomal recessive, juvenile) 2, Parkin (PARK2, Accession NM_013987). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PARK2. RAD52 Homolog (S. cerevisiae) (RAD52, Accession NM_134422) is another VGAM2114 host target gene. RAD52 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAD52, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE, designated SEQ ID:28643, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73457] Another function of VGAM2114 is therefore inhibition of RAD52 Homolog (S. cerevisiae) (RAD52, Accession NM_134422). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD52. Supervillin (SVIL, Accession NM_021738) is another VGAM2114 host target gene. SVIL BINDING SITE1 and SVIL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SVIL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementar-

ity of the nucleotide sequences of SVIL BINDING SITE1 and SVIL BINDING SITE2, designated SEQ ID:22345 and SEQ ID:9148 respectively, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73458] Another function of VGAM2114 is therefore inhibition of Supervillin (SVIL, Accession NM_021738), a gene which binds actin, links filamentous actin with the plasma membrane; and contains putative nuclear localization signals. Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SVIL. The function of SVIL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1459.C16orf5 (Accession NM_013399) is another VGAM2114 host target gene. C16orf5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C16orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C16orf5 BINDING SITE, designated SEQ ID:15051, to the nucleotide sequence of VGAM2114 RNA,

herein designated VGAM RNA, also designated SEQ ID:4825.

[73459] Another function of VGAM2114 is therefore inhibition of C16orf5 (Accession NM_013399). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C16orf5. DKFZp547M236 (Accession NM_018713) is another VGAM2114 host target gene. DKFZp547M236 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp547M236, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547M236 BINDING SITE, designated SEQ ID:20791, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73460] Another function of VGAM2114 is therefore inhibition of DKFZp547M236 (Accession NM_018713). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547M236. E74-like Factor 4 (ets domain transcription factor) (ELF4, Accession NM_001421) is another

VGAM2114 host target gene. ELF4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELF4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELF4 BINDING SITE, designated SEQ ID:7124, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73461] Another function of VGAM2114 is therefore inhibition of E74-like Factor 4 (ets domain transcription factor) (ELF4, Accession NM_001421). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELF4. Neuronal PAS Domain Protein 3 (NPAS3, Accession NM_022123) is another VGAM2114 host target gene. NPAS3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NPAS3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPAS3 BINDING SITE, designated SEQ ID:22667, to the nucleotide sequence of VGAM2114 RNA,

herein designated VGAM RNA, also designated SEQ ID:4825.

[73462] Another function of VGAM2114 is therefore inhibition of Neuronal PAS Domain Protein 3 (NPAS3, Accession NM_022123). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPAS3. Solute Carrier Family 11 (proton-coupled divalent metal ion transporters), Member 2 (SLC11A2, Accession NM_000617) is another VGAM2114 host target gene. SLC11A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC11A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC11A2 BINDING SITE, designated SEQ ID:6226, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73463] Another function of VGAM2114 is therefore inhibition of Solute Carrier Family 11 (proton-coupled divalent metal ion transporters), Member 2 (SLC11A2, Accession NM_000617). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with SLC11A2. Triple Homeobox 1 (TIX1, Accession XM_029734) is another VGAM2114 host target gene. TIX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIX1 BINDING SITE, designated SEQ ID:30927, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73464] Another function of VGAM2114 is therefore inhibition of Triple Homeobox 1 (TIX1, Accession XM_029734). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIX1. LOC143173 (Accession XM_016685) is another VGAM2114 host target gene. LOC143173 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143173, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143173 BINDING SITE, designated SEQ

ID:30271, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73465] Another function of VGAM2114 is therefore inhibition of LOC143173 (Accession XM_016685). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143173. LOC143915 (Accession XM_096502) is another VGAM2114 host target gene. LOC143915 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143915, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143915 BINDING SITE, designated SEQ ID:40379, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73466] Another function of VGAM2114 is therefore inhibition of LOC143915 (Accession XM_096502). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143915. LOC149302 (Accession XM_086489) is another VGAM2114 host target gene. LOC149302 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149302, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149302 BINDING SITE, designated SEQ ID:38702, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73467] Another function of VGAM2114 is therefore inhibition of LOC149302 (Accession XM_086489). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149302. LOC170082 (Accession XM_093092) is another VGAM2114 host target gene. LOC170082 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC170082, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC170082 BINDING SITE, designated SEQ ID:40170, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73468] Another function of VGAM2114 is therefore inhibition of

LOC170082 (Accession XM_093092). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170082. LOC221477 (Accession XM_166397) is another VGAM2114 host target gene. LOC221477 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221477, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221477 BINDING SITE, designated SEQ ID:44257, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73469] Another function of VGAM2114 is therefore inhibition of LOC221477 (Accession XM_166397). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221477. LOC221760 (Accession XM_168105) is another VGAM2114 host target gene. LOC221760 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221760, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC221760 BINDING SITE, designated SEQ ID:45031, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73470] Another function of VGAM2114 is therefore inhibition of LOC221760 (Accession XM_168105). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221760. LOC245806 (Accession XM_166309) is another VGAM2114 host target gene. LOC245806 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC245806, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC245806 BINDING SITE, designated SEQ ID:44131, to the nucleotide sequence of VGAM2114 RNA, herein designated VGAM RNA, also designated SEQ ID:4825.

[73471] Another function of VGAM2114 is therefore inhibition of LOC245806 (Accession XM_166309). Accordingly, utilities of VGAM2114 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC245806. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2115 (VGAM2115) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73472] VGAM2115 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2115 was detected is described hereinabove with reference to Figs. 1-8.

[73473] VGAM2115 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2115 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73474] VGAM2115 gene encodes a VGAM2115 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2115 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2115 precursor RNA is designated SEQ ID:2101, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2101 is located at position 211598 relative to the genome of Cowpox Virus.

[73475] VGAM2115 precursor RNA folds onto itself, forming VGAM2115 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73476] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2115 folded precursor RNA into VGAM2115 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2115 RNA is designated SEQ ID:4826, and is provided hereinbelow with reference to the sequence listing part.

[73477] VGAM2115 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2115 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2115 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73478] VGAM2115 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2115 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2115 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2115 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2115 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73479] The complementary binding of VGAM2115 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2115 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2115 host target RNA into VGAM2115 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73480] It is appreciated that VGAM2115 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2115 host target genes. The mRNA of each one of this plurality of VGAM2115 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2115 RNA, herein designated VGAM RNA, and which when bound by VGAM2115 RNA causes inhibition of translation of respective one or more

VGAM2115 host target proteins.

[73481] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2115 gene, herein designated VGAM GENE, on one or more VGAM2115 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73482] It is yet further appreciated that a function of VGAM2115 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2115 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific

functions, and accordingly utilities, of VGAM2115 correlate with, and may be deduced from, the identity of the host target genes which VGAM2115 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73483] Nucleotide sequences of the VGAM2115 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2115 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2115 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2115 are further described hereinbelow with reference to Table 1.

[73484] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2115 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2115 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73485] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2115 gene, herein designated VGAM is inhibition of expression of VGAM2115 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2115 correlate with, and may be deduced from, the identity of the target genes which VGAM2115 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73486] Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, Zeta Polypeptide (YWHAZ, Accession NM_003406) is a VGAM2115 host target gene. YWHAZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by YWHAZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YWHAZ BINDING SITE, designated SEQ ID:9445, to the nucleotide sequence of VGAM2115 RNA, herein designated VGAM RNA, also designated SEQ ID:4826.

[73487] A function of VGAM2115 is therefore inhibition of Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, Zeta Polypeptide (YWHAZ, Accession NM_003406), a gene which mediates signal transduction by binding to phosphorylated serine residues on a variety of signaling molecules. Accordingly, utilities of VGAM2115 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with YWHAZ. The function of YWHAZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM43.Parvin, Alpha (PARVA, Accession NM_018222) is another VGAM2115 host target gene. PARVA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PARVA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PARVA BINDING SITE, designated SEQ ID:20145, to the nucleotide sequence of VGAM2115 RNA, herein designated VGAM RNA, also designated SEQ ID:4826.

[73488] Another function of VGAM2115 is therefore inhibition of Parvin, Alpha (PARVA, Accession NM_018222). Accordingly, utilities of VGAM2115 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PARVA. LOC254251 (Accession XM_171088) is another VGAM2115 host target gene. LOC254251 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254251, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254251 BINDING SITE, designated SEQ ID:45894, to the nucleotide sequence of VGAM2115 RNA, herein designated VGAM RNA, also designated SEQ ID:4826.

[73489] Another function of VGAM2115 is therefore inhibition of LOC254251 (Accession XM_171088). Accordingly, utilities of VGAM2115 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254251. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2116 (VGAM2116) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73490] VGAM2116 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2116 was detected is described hereinabove with reference to Figs. 1-8.

[73491] VGAM2116 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus.

VGAM2116 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[73492] VGAM2116 gene encodes a VGAM2116 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2116 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2116 precursor RNA is designated SEQ ID:2102, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2102 is located at position 208834 relative to the genome of Cowpox Virus.

[73493] VGAM2116 precursor RNA folds onto itself, forming VGAM2116 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73494] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2116 folded precursor RNA into VGAM2116

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2116 RNA is designated SEQ ID:4827, and is provided hereinbelow with reference to the sequence listing part.

[73495] VGAM2116 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2116 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2116 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73496] VGAM2116 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2116 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2116 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2116 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2116 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73497] The complementary binding of VGAM2116 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2116 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2116 host target RNA into VGAM2116 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[73498] It is appreciated that VGAM2116 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2116 host target genes. The mRNA of each one of this plurality of VGAM2116 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2116 RNA, herein designated VGAM RNA, and which when bound by VGAM2116 RNA causes inhibition of translation of respective one or more VGAM2116 host target proteins.

[73499] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2116 gene, herein designated VGAM GENE, on one or more VGAM2116 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73500] It is yet further appreciated that a function of VGAM2116 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2116 correlate with, and may be deduced from, the identity of the host target genes which VGAM2116 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73501] Nucleotide sequences of the VGAM2116 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2116 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2116 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2116 are further described hereinbelow with reference to Table 1.

[73502] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2116 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2116 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73503] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2116 gene, herein designated VGAM is inhibition of expression of VGAM2116 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2116 correlate with, and may be deduced from, the identity of the target genes which VGAM2116 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73504] Aspartate Beta-hydroxylase (ASPH, Accession NM_032466) is a VGAM2116 host target gene. ASPH BINDING SITE1 and ASPH BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ASPH, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ASPH BINDING SITE1 and ASPH BINDING SITE2, designated SEQ ID:26222 and SEQ

ID:26227 respectively, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73505] A function of VGAM2116 is therefore inhibition of Aspartate Beta-hydroxylase (ASPH, Accession NM_032466), a gene which specifically hydroxylates the beta carbon of aspartic acid or asparagine residues in certain epidermal growth factor (EGF)-like domains of a number of proteins. Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASPH. The function of ASPH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM47.Tensin (TNS, Accession NM_022648) is another VGAM2116 host target gene. TNS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNS BINDING SITE, designated SEQ ID:22903, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73506] Another function of VGAM2116 is therefore inhibition of Tensin (TNS, Accession NM_022648). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNS. FLJ10656 (Accession NM_018170) is another VGAM2116 host target gene. FLJ10656 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10656, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10656 BINDING SITE, designated SEQ ID:19988, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73507] Another function of VGAM2116 is therefore inhibition of FLJ10656 (Accession NM_018170). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10656. GABA(A) Receptor-associated Protein Like 1 (GABARAPL1, Accession NM_031412) is another VGAM2116 host target gene. GABARAPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL1, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABARAPL1 BINDING SITE, designated SEQ ID:25392, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73508] Another function of VGAM2116 is therefore inhibition of GABA(A) Receptor-associated Protein Like 1 (GABARAPL1, Accession NM_031412). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL1. GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568) is another VGAM2116 host target gene. GABARAPL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABARAPL3 BINDING SITE, designated SEQ ID:26300, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73509] Another function of VGAM2116 is therefore inhibition of

GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL3. HT002 (Accession NM_014066) is another VGAM2116 host target gene. HT002 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HT002, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HT002 BINDING SITE, designated SEQ ID:15281, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73510] Another function of VGAM2116 is therefore inhibition of HT002 (Accession NM_014066). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HT002. KIAA0194 (Accession XM_038362) is another VGAM2116 host target gene. KIAA0194 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0194, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0194 BINDING SITE, designated SEQ ID:32825, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73511] Another function of VGAM2116 is therefore inhibition of KIAA0194 (Accession XM_038362). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0194. KIAA0435 (Accession NM_014801) is another VGAM2116 host target gene. KIAA0435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0435 BINDING SITE, designated SEQ ID:16721, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73512] Another function of VGAM2116 is therefore inhibition of KIAA0435 (Accession NM_014801). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0435. KIAA0475 (Accession NM_014864) is another VGAM2116 host target gene. KIAA0475 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:16949, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73513] Another function of VGAM2116 is therefore inhibition of KIAA0475 (Accession NM_014864). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0475. KIAA0542 (Accession XM_038520) is another VGAM2116 host target gene. KIAA0542 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0542, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0542 BINDING SITE, designated SEQ ID:32856, to the nucleotide sequence of VGAM2116 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4827.

[73514] Another function of VGAM2116 is therefore inhibition of KIAA0542 (Accession XM_038520). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0542. KIAA1301 (Accession XM_038999) is another VGAM2116 host target gene. KIAA1301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1301 BINDING SITE, designated SEQ ID:32974, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73515] Another function of VGAM2116 is therefore inhibition of KIAA1301 (Accession XM_038999). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1301. KIAA1323 (Accession XM_032146) is another VGAM2116 host target gene. KIAA1323 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1323, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1323 BINDING SITE, designated SEQ ID:31563, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73516] Another function of VGAM2116 is therefore inhibition of KIAA1323 (Accession XM_032146). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1323. Seizure Related 6 Homolog (mouse) (SEZ6, Accession XM_058869) is another VGAM2116 host target gene. SEZ6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEZ6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEZ6 BINDING SITE, designated SEQ ID:36774, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73517] Another function of VGAM2116 is therefore inhibition of Seizure Related 6 Homolog (mouse) (SEZ6, Accession XM_058869). Accordingly, utilities of VGAM2116 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with SEZ6. LOC132235 (Accession XM_072302) is another VGAM2116 host target gene. LOC132235 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC132235, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132235 BINDING SITE, designated SEQ ID:37483, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73518] Another function of VGAM2116 is therefore inhibition of LOC132235 (Accession XM_072302). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132235. LOC146895 (Accession XM_097120) is another VGAM2116 host target gene. LOC146895 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146895, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC146895 BINDING SITE, designated SEQ ID:40761, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73519] Another function of VGAM2116 is therefore inhibition of LOC146895 (Accession XM_097120). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146895. LOC152024 (Accession XM_087365) is another VGAM2116 host target gene. LOC152024 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152024, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152024 BINDING SITE, designated SEQ ID:39198, to the nucleotide sequence of VGAM2116 RNA, herein designated VGAM RNA, also designated SEQ ID:4827.

[73520] Another function of VGAM2116 is therefore inhibition of LOC152024 (Accession XM_087365). Accordingly, utilities of VGAM2116 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152024. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2117 (VGAM2117) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73521] VGAM2117 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2117 was detected is described hereinabove with reference to Figs. 1-8.

[73522] VGAM2117 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2117 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73523] VGAM2117 gene encodes a VGAM2117 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2117 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2117 precursor RNA is designated SEQ ID:2103, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2103 is located at position 206477 relative to the

genome of Cowpox Virus.

[73524] VGAM2117 precursor RNA folds onto itself, forming VGAM2117 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73525] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2117 folded precursor RNA into VGAM2117 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2117 RNA is designated SEQ ID:4828, and is provided hereinbelow with reference to the sequence listing part.

[73526] VGAM2117 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2117 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2117 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73527] VGAM2117 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2117 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2117 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2117 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2117 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73528] The complementary binding of VGAM2117 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2117 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2117 host target RNA into VGAM2117 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73529] It is appreciated that VGAM2117 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2117 host target genes. The mRNA of each one of this plurality of VGAM2117 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2117 RNA, herein designated VGAM RNA, and which when bound by VGAM2117 RNA causes inhibition of translation of respective one or more VGAM2117 host target proteins.

[73530] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2117 gene, herein designated VGAM GENE, on one or more VGAM2117 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73531] It is yet further appreciated that a function of VGAM2117 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2117 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2117 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2117 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73532] Nucleotide sequences of the VGAM2117 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2117 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2117 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2117 are further described hereinbelow with reference to Table 1.

[73533] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2117 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2117 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73534] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2117 gene, herein designated VGAM is inhibition of expression of VGAM2117 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2117 correlate with, and may be deduced

from, the identity of the target genes which VGAM2117 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73535] Coagulation Factor VIII, Procoagulant Component (hemophilia A) (F8, Accession NM_000132) is a VGAM2117 host target gene. F8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by F8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of F8 BINDING SITE, designated SEQ ID:5613, to the nucleotide sequence of VGAM2117 RNA, herein designated VGAM RNA, also designated SEQ ID:4828.

[73536] A function of VGAM2117 is therefore inhibition of Coagulation Factor VIII, Procoagulant Component (hemophilia A) (F8, Accession NM_000132). Accordingly, utilities of VGAM2117 include diagnosis, prevention and treatment of diseases and clinical conditions associated with F8. Microtubule-associated Protein, RP/EB Family, Member 1 (MAPRE1, Accession NM_012325) is another VGAM2117 host target gene. MAPRE1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by MAPRE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPRE1 BINDING SITE, designated SEQ ID:14706, to the nucleotide sequence of VGAM2117 RNA, herein designated VGAM RNA, also designated SEQ ID:4828.

[73537] Another function of VGAM2117 is therefore inhibition of Microtubule-associated Protein, RP/EB Family, Member 1 (MAPRE1, Accession NM_012325). Accordingly, utilities of VGAM2117 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPRE1. E2F Transcription Factor 5, P130-binding (E2F5, Accession NM_001951) is another VGAM2117 host target gene. E2F5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by E2F5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of E2F5 BINDING SITE, designated SEQ ID:7673, to the nucleotide sequence of VGAM2117 RNA, herein designated VGAM RNA, also designated SEQ ID:4828.

[73538] Another function of VGAM2117 is therefore inhibition of

E2F Transcription Factor 5, P130-binding (E2F5, Accession NM_001951). Accordingly, utilities of VGAM2117 include diagnosis, prevention and treatment of diseases and clinical conditions associated with E2F5. E74-like Factor 2 (ets domain transcription factor) (ELF2, Accession NM_006874) is another VGAM2117 host target gene. ELF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELF2 BINDING SITE, designated SEQ ID:13743, to the nucleotide sequence of VGAM2117 RNA, herein designated VGAM RNA, also designated SEQ ID:4828.

[73539] Another function of VGAM2117 is therefore inhibition of E74-like Factor 2 (ets domain transcription factor) (ELF2, Accession NM_006874). Accordingly, utilities of VGAM2117 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELF2. KIAA0252 (Accession XM_031646) is another VGAM2117 host target gene. KIAA0252 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0252, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0252 BINDING SITE, designated SEQ ID:31451, to the nucleotide sequence of VGAM2117 RNA, herein designated VGAM RNA, also designated SEQ ID:4828.

[73540] Another function of VGAM2117 is therefore inhibition of KIAA0252 (Accession XM_031646). Accordingly, utilities of VGAM2117 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0252. KIAA1855 (Accession XM_166453) is another VGAM2117 host target gene. KIAA1855 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1855, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1855 BINDING SITE, designated SEQ ID:44359, to the nucleotide sequence of VGAM2117 RNA, herein designated VGAM RNA, also designated SEQ ID:4828.

[73541] Another function of VGAM2117 is therefore inhibition of KIAA1855 (Accession XM_166453). Accordingly, utilities of VGAM2117 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1855. LOC152578 (Accession XM_098241) is another VGAM2117 host target gene. LOC152578 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152578, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152578 BINDING SITE, designated SEQ ID:41526, to the nucleotide sequence of VGAM2117 RNA, herein designated VGAM RNA, also designated SEQ ID:4828.

[73542] Another function of VGAM2117 is therefore inhibition of LOC152578 (Accession XM_098241). Accordingly, utilities of VGAM2117 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152578. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2118 (VGAM2118) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73543] VGAM2118 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2118 was detected is described hereinabove with reference to Figs. 1-8.

[73544] VGAM2118 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2118 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73545] VGAM2118 gene encodes a VGAM2118 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2118 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2118 precursor RNA is designated SEQ ID:2104, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2104 is located at position 6717 relative to the genome of Cowpox Virus.

[73546] VGAM2118 precursor RNA folds onto itself, forming VGAM2118 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73547] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2118 folded precursor RNA into VGAM2118 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2118 RNA is designated SEQ ID:4829, and is provided hereinbelow with reference to the sequence listing part.

[73548] VGAM2118 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2118 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2118 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73549] VGAM2118 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2118 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2118 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2118 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2118 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73550] The complementary binding of VGAM2118 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2118 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2118 host target RNA into VGAM2118 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73551] It is appreciated that VGAM2118 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2118 host target genes. The mRNA of each one of this plurality of VGAM2118 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2118 RNA, herein designated VGAM RNA, and which when bound by VGAM2118 RNA causes inhibition of translation of respective one or more VGAM2118 host target proteins.

[73552] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2118 gene, herein designated VGAM GENE, on one or more VGAM2118 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73553] It is yet further appreciated that a function of VGAM2118 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2118 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2118 correlate with, and may be deduced from, the identity of the host target genes which VGAM2118 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73554] Nucleotide sequences of the VGAM2118 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2118 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2118 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2118 are further described hereinbelow with reference to Table 1.

[73555] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2118 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2118 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73556] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2118 gene, herein designated VGAM is inhibition of expression of VGAM2118 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2118 correlate with, and may be deduced from, the identity of the target genes which VGAM2118 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73557] Kruppel-like Factor 8 (KLF8, Accession NM_007250) is a VGAM2118 host target gene. KLF8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region

of mRNA encoded by KLF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLF8 BINDING SITE, designated SEQ ID:14122, to the nucleotide sequence of VGAM2118 RNA, herein designated VGAM RNA, also designated SEQ ID:4829.

[73558] A function of VGAM2118 is therefore inhibition of Kruppel-like Factor 8 (KLF8, Accession NM_007250). Accordingly, utilities of VGAM2118 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF8. Tripartite Motif-containing 9 (TRIM9, Accession NM_052978) is another VGAM2118 host target gene. TRIM9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM9 BINDING SITE, designated SEQ ID:27548, to the nucleotide sequence of VGAM2118 RNA, herein designated VGAM RNA, also designated SEQ ID:4829.

[73559] Another function of VGAM2118 is therefore inhibition of

Tripartite Motif-containing 9 (TRIM9, Accession NM_052978), a gene which may function as a positive regulator for mannosylphosphate transferase and is required to mediate mannosylphosphate transfer in both the core and outer chain portions of n-linked. oligosaccharides. Accordingly, utilities of VGAM2118 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM9. The function of TRIM9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Transient Receptor Potential Cation Channel, Subfamily C, Member 1 (TRPC1, Accession NM_003304) is another VGAM2118 host target gene. TRPC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRPC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPC1 BINDING SITE, designated SEQ ID:9304, to the nucleotide sequence of VGAM2118 RNA, herein designated VGAM RNA, also designated SEQ ID:4829.

[73560] Another function of VGAM2118 is therefore inhibition of

Transient Receptor Potential Cation Channel, Subfamily C, Member 1 (TRPC1, Accession NM_003304), a gene which acts as a non-voltage-sensitive store-operated Ca2+ channel. Accordingly, utilities of VGAM2118 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPC1. The function of TRPC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Butyrophilin, Subfamily 3, Member A1 (BTN3A1, Accession NM_007048) is another VGAM2118 host target gene. BTN3A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTN3A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTN3A1 BINDING SITE, designated SEQ ID:13920, to the nucleotide sequence of VGAM2118 RNA, herein designated VGAM RNA, also designated SEQ ID:4829.

[73561] Another function of VGAM2118 is therefore inhibition of Butyrophilin, Subfamily 3, Member A1 (BTN3A1, Accession NM_007048). Accordingly, utilities of VGAM2118 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN3A1. DKFZp761J139 (Accession NM_032280) is another VGAM2118 host target gene. DKFZp761J139 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp761J139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761J139 BINDING SITE, designated SEQ ID:26034, to the nucleotide sequence of VGAM2118 RNA, herein designated VGAM RNA, also designated SEQ ID:4829.

[73562] Another function of VGAM2118 is therefore inhibition of DKFZp761J139 (Accession NM_032280). Accordingly, utilities of VGAM2118 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761J139. FLJ20147 (Accession NM_017687) is another VGAM2118 host target gene. FLJ20147 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20147, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

FLJ20147 BINDING SITE, designated SEQ ID:19241, to the nucleotide sequence of VGAM2118 RNA, herein designated VGAM RNA, also designated SEQ ID:4829.

[73563] Another function of VGAM2118 is therefore inhibition of FLJ20147 (Accession NM_017687). Accordingly, utilities of VGAM2118 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20147. MGC12466 (Accession XM_086336) is another VGAM2118 host target gene. MGC12466 BINDING SITE1 and MGC12466 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MGC12466, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC12466 BINDING SITE1 and MGC12466 BINDING SITE2, designated SEQ ID:38608 and SEQ ID:27066 respectively, to the nucleotide sequence of VGAM2118 RNA, herein designated VGAM RNA, also designated SEQ ID:4829.

[73564] Another function of VGAM2118 is therefore inhibition of MGC12466 (Accession XM_086336). Accordingly, utilities of VGAM2118 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC12466. LOC202934 (Accession XM_117486) is another VGAM2118 host target gene. LOC202934 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202934, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE, designated SEQ ID:43453, to the nucleotide sequence of VGAM2118 RNA, herein designated VGAM RNA, also designated SEQ ID:4829.

[73565] Another function of VGAM2118 is therefore inhibition of LOC202934 (Accession XM_117486). Accordingly, utilities of VGAM2118 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202934. LOC255465 (Accession XM_173206) is another VGAM2118 host target gene. LOC255465 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255465, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255465 BINDING SITE, designated SEQ ID:46447, to the nucleotide sequence of VGAM2118 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4829.

[73566] Another function of VGAM2118 is therefore inhibition of LOC255465 (Accession XM_173206). Accordingly, utilities of VGAM2118 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255465. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2119 (VGAM2119) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73567] VGAM2119 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2119 was detected is described hereinabove with reference to Figs. 1-8.

[73568] VGAM2119 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2119 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73569] VGAM2119 gene encodes a VGAM2119 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2119 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2119 precursor RNA is designated SEQ ID:2105, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2105 is located at position 206331 relative to the genome of Cowpox Virus.

[73570] VGAM2119 precursor RNA folds onto itself, forming VGAM2119 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73571] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2119 folded precursor RNA into VGAM2119 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2119 RNA is designated SEQ ID:4830, and is provided hereinbelow with reference to the sequence listing part.

[73572] VGAM2119 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2119 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2119 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73573] VGAM2119 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2119 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2119 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2119 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2119 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73574] The complementary binding of VGAM2119 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2119 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2119 host target RNA into VGAM2119 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73575] It is appreciated that VGAM2119 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2119 host target genes. The mRNA of

each one of this plurality of VGAM2119 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2119 RNA, herein designated VGAM RNA, and which when bound by VGAM2119 RNA causes inhibition of translation of respective one or more VGAM2119 host target proteins.

[73576] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2119 gene, herein designated VGAM GENE, on one or more VGAM2119 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[73577] It is yet further appreciated that a function of VGAM2119 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2119 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2119 correlate with, and may be deduced from, the identity of the host target genes which VGAM2119 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73578] Nucleotide sequences of the VGAM2119 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2119 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2119 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2119 are further described hereinbelow with reference to Table 1.

[73579] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2119 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2119 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73580] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2119 gene, herein designated VGAM is inhibition of expression of VGAM2119 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2119 correlate with, and may be deduced from, the identity of the target genes which VGAM2119 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73581] PRO2435 (Accession NM_018527) is a VGAM2119 host target gene. PRO2435 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2435 BINDING SITE, designated SEQ ID:20598, to the nucleotide sequence of VGAM2119 RNA, herein designated VGAM RNA, also designated SEQ ID:4830.

[73582] A function of VGAM2119 is therefore inhibition of PRO2435 (Accession NM_018527). Accordingly, utilities of VGAM2119 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PRO2435. LOC143425 (Accession XM_113695) is another VGAM2119 host target gene. LOC143425 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143425, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143425 BINDING SITE, designated SEQ ID:42354, to the nucleotide sequence of VGAM2119 RNA, herein designated VGAM RNA, also designated SEQ ID:4830.

[73583] Another function of VGAM2119 is therefore inhibition of LOC143425 (Accession XM_113695). Accordingly, utilities of VGAM2119 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143425. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2120 (VGAM2120) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73584] VGAM2120 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2120 was detected is described hereinabove with reference to Figs. 1-8.

[73585] VGAM2120 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2120 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73586] VGAM2120 gene encodes a VGAM2120 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2120 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2120 precursor RNA is designated SEQ ID:2106, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2106 is located at position 214751 relative to the genome of Cowpox Virus.

[73587] VGAM2120 precursor RNA folds onto itself, forming VGAM2120 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73588] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2120 folded precursor RNA into VGAM2120 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2120 RNA is designated SEQ ID:4831, and is provided hereinbelow with reference to the sequence listing part.

[73589] VGAM2120 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2120 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2120 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73590] VGAM2120 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2120 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2120 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2120 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2120 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73591] The complementary binding of VGAM2120 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2120 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2120 host target RNA into VGAM2120 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73592] It is appreciated that VGAM2120 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2120 host target genes. The mRNA of each one of this plurality of VGAM2120 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2120 RNA, herein designated VGAM RNA, and which when bound by VGAM2120 RNA causes inhibition of translation of respective one or more VGAM2120 host target proteins.

[73593] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2120 gene, herein designated VGAM GENE, on one or more VGAM2120 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73594] It is yet further appreciated that a function of VGAM2120 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2120 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2120 correlate with, and may be deduced from, the identity of the host target genes which VGAM2120 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73595] Nucleotide sequences of the VGAM2120 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2120 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2120 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2120 are further described hereinbelow with reference to Table 1.

[73596] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2120 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2120 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73597] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2120 gene, herein designated VGAM is inhibition of expression of VGAM2120 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2120 correlate with, and may be deduced from, the identity of the target genes which VGAM2120 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73598] ATP-binding Cassette, Sub-family A (ABC1), Member 1 (ABCA1, Accession NM_005502) is a VGAM2120 host target gene. ABCA1 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by ABCA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCA1 BINDING SITE, designated SEQ ID:12012, to the nucleotide sequence of VGAM2120 RNA, herein designated VGAM RNA, also designated SEQ ID:4831.

[73599] A function of VGAM2120 is therefore inhibition of ATP-binding Cassette, Sub-family A (ABC1), Member 1 (ABCA1, Accession NM_005502), a gene which camp-dependent and sulfonylurea-sensitive anion transporter. Accordingly, utilities of VGAM2120 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCA1. The function of ABCA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1956.Ret Proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease) (RET, Accession NM_000323) is another VGAM2120 host target gene. RET BINDING SITE1 through RET BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA

encoded by RET, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RET BINDING SITE1 through RET BINDING SITE4, designated SEQ ID:5866, SEQ ID:21780, SEQ ID:21782 and SEQ ID:21959 respectively, to the nucleotide sequence of VGAM2120 RNA, herein designated VGAM RNA, also designated SEQ ID:4831.

[73600] Another function of VGAM2120 is therefore inhibition of Ret Proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease) (RET, Accession NM_000323), a gene which transduces signals for cell growth and differentiation. Accordingly, utilities of VGAM2120 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RET. The function of RET and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.KIAA1023 (Accession NM_017604) is another VGAM2120 host target gene. KIAA1023 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1023, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1023 BINDING SITE, designated SEQ ID:19086, to the nucleotide sequence of VGAM2120 RNA, herein designated VGAM RNA, also designated SEQ ID:4831.

[73601] Another function of VGAM2120 is therefore inhibition of KIAA1023 (Accession NM_017604). Accordingly, utilities of VGAM2120 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1023. Uronyl-2-sulfotransferase (UST, Accession NM_005715) is another VGAM2120 host target gene. UST BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UST, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UST BINDING SITE, designated SEQ ID:12269, to the nucleotide sequence of VGAM2120 RNA, herein designated VGAM RNA, also designated SEQ ID:4831.

[73602] Another function of VGAM2120 is therefore inhibition of Uronyl-2-sulfotransferase (UST, Accession NM_005715). Accordingly, utilities of VGAM2120 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with UST. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2121 (VGAM2121) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73603] VGAM2121 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2121 was detected is described hereinabove with reference to Figs. 1-8.

[73604] VGAM2121 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2121 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73605] VGAM2121 gene encodes a VGAM2121 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2121 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2121 precursor RNA is designated SEQ ID:2107, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2107 is located at position 6122 relative to the genome of Cowpox Virus.

[73606] VGAM2121 precursor RNA folds onto itself, forming VGAM2121 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73607] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2121 folded precursor RNA into VGAM2121 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2121 RNA is designated SEQ ID:4832, and is provided hereinbelow with reference to the sequence listing part.

[73608] VGAM2121 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2121 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2121 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73609] VGAM2121 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2121 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2121 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2121 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2121 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73610] The complementary binding of VGAM2121 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2121 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2121 host target RNA into VGAM2121 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73611] It is appreciated that VGAM2121 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2121 host target genes. The mRNA of each one of this plurality of VGAM2121 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2121 RNA, herein designated VGAM RNA, and which when bound by VGAM2121 RNA causes

inhibition of translation of respective one or more VGAM2121 host target proteins.

[73612] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2121 gene, herein designated VGAM GENE, on one or more VGAM2121 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73613] It is yet further appreciated that a function of VGAM2121 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2121 include diagnosis, prevention and

treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2121 correlate with, and may be deduced from, the identity of the host target genes which VGAM2121 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73614] Nucleotide sequences of the VGAM2121 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2121 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2121 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2121 are further described hereinbelow with reference to Table 1.

[73615] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2121 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2121 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73616] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2121 gene, herein designated VGAM is inhibition of expression of VGAM2121 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2121 correlate with, and may be deduced from, the identity of the target genes which VGAM2121 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73617] FYVE and Coiled-coil Domain Containing 1 (FYCO1, Accession NM_024513) is a VGAM2121 host target gene. FYCO1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FYCO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FYCO1 BINDING SITE, designated SEQ ID:23712, to the nucleotide sequence of VGAM2121 RNA, herein designated VGAM RNA, also designated SEQ ID:4832.

[73618] A function of VGAM2121 is therefore inhibition of FYVE and Coiled-coil Domain Containing 1 (FYCO1, Accession NM_024513). Accordingly, utilities of VGAM2121 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FYCO1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to

here as Viral Genomic Address Messenger 2122 (VGAM2122) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73619] VGAM2122 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2122 was detected is described hereinabove with reference to Figs. 1-8.

[73620] VGAM2122 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2122 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73621] VGAM2122 gene encodes a VGAM2122 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2122 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2122 precursor RNA is designated SEQ ID:2108, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2108 is located at position 5631 relative to the genome of Cowpox Virus.

[73622] VGAM2122 precursor RNA folds onto itself, forming VGAM2122 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73623] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2122 folded precursor RNA into VGAM2122 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of VGAM2122 RNA is designated SEQ ID:4833, and is provided hereinbelow with reference to the sequence listing part.

[73624] VGAM2122 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2122 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2122 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73625] VGAM2122 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2122 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2122 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2122 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2122 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73626] The complementary binding of VGAM2122 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2122 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2122 host target RNA into VGAM2122 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73627] It is appreciated that VGAM2122 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2122 host target genes. The mRNA of each one of this plurality of VGAM2122 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2122 RNA, herein designated VGAM RNA, and which when bound by VGAM2122 RNA causes inhibition of translation of respective one or more VGAM2122 host target proteins.

[73628] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2122 gene, herein designated VGAM GENE, on one or more VGAM2122 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73629] It is yet further appreciated that a function of VGAM2122 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2122 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2122 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2122 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73630] Nucleotide sequences of the VGAM2122 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2122 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2122 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2122 are further described hereinbelow with reference to Table 1.

[73631] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2122 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2122 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73632] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2122 gene, herein designated VGAM is inhibition of expression of VGAM2122 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2122 correlate with, and may be deduced from, the identity of the target genes which VGAM2122

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73633] Enoyl Coenzyme A Hydratase 1, Peroxisomal (ECH1, Accession XM_008904) is a VGAM2122 host target gene. ECH1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ECH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ECH1 BINDING SITE, designated SEQ ID:30097, to the nucleotide sequence of VGAM2122 RNA, herein designated VGAM RNA, also designated SEQ ID:4833.

[73634] A function of VGAM2122 is therefore inhibition of Enoyl Coenzyme A Hydratase 1, Peroxisomal (ECH1, Accession XM_008904). Accordingly, utilities of VGAM2122 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ECH1. LOC203317 (Accession XM_114683) is another VGAM2122 host target gene. LOC203317 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203317, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of LOC203317 BINDING SITE, designated SEQ ID:43030, to the nucleotide sequence of VGAM2122 RNA, herein designated VGAM RNA, also designated SEQ ID:4833.

[73635] Another function of VGAM2122 is therefore inhibition of LOC203317 (Accession XM_114683). Accordingly, utilities of VGAM2122 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203317. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2123 (VGAM2123) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73636] VGAM2123 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2123 was detected is described hereinabove with reference to Figs. 1-8.

[73637] VGAM2123 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2123 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[73638] VGAM2123 gene encodes a VGAM2123 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2123 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2123 precursor RNA is designated SEQ ID:2109, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2109 is located at position 208014 relative to the genome of Cowpox Virus.

[73639] VGAM2123 precursor RNA folds onto itself, forming VGAM2123 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73640] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2123 folded precursor RNA into VGAM2123 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2123 RNA is designated SEQ ID:4834, and is provided hereinbelow with reference to the sequence listing part.

[73641] VGAM2123 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2123 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2123 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73642] VGAM2123 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2123 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2123 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2123 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2123 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73643] The complementary binding of VGAM2123 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2123 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2123 host target RNA into VGAM2123 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73644] It is appreciated that VGAM2123 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2123 host target genes. The mRNA of each one of this plurality of VGAM2123 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2123 RNA, herein designated VGAM RNA, and which when bound by VGAM2123 RNA causes inhibition of translation of respective one or more VGAM2123 host target proteins.

[73645] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2123 gene, herein designated VGAM GENE, on one or more VGAM2123 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73646] It is yet further appreciated that a function of VGAM2123 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2123 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2123 correlate with, and may be deduced from, the identity of the host target genes which VGAM2123 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73647] Nucleotide sequences of the VGAM2123 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2123 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2123 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2123 are further described hereinbelow with reference to Table 1.

[73648] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2123 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2123 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73649] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2123 gene, herein designated VGAM is inhibition of expression of VGAM2123 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2123 correlate with, and may be deduced from, the identity of the target genes which VGAM2123 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73650] Dachshund Homolog (Drosophila) (DACH, Accession NM_080759) is a VGAM2123 host target gene. DACH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DACH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DACH BINDING SITE, designated SEQ ID:28042, to the nucleotide sequence of VGAM2123 RNA, herein designated VGAM RNA, also designated SEQ ID:4834.

[73651] A function of VGAM2123 is therefore inhibition of Dachshund Homolog (Drosophila) (DACH, Accession NM_080759), a gene which regulates early progenitor cell proliferation during retinogenesis and pituitary development . Accordingly, utilities of VGAM2123 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DACH. The function of DACH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM260.Fragile X Mental Retardation 1 (FMR1, Accession NM_002024) is another VGAM2123 host target gene. FMR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FMR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FMR1 BINDING SITE, designated SEQ ID:7776, to the nucleotide sequence of VGAM2123 RNA, herein designated VGAM RNA, also designated SEQ ID:4834.

[73652] Another function of VGAM2123 is therefore inhibition of Fragile X Mental Retardation 1 (FMR1, Accession NM_002024). Accordingly, utilities of VGAM2123 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with FMR1. Maltase-glucoamylase (alpha-glucosidase) (MGAM, Accession XM_051351) is another VGAM2123 host target gene. MGAM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGAM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGAM BINDING SITE, designated SEQ ID:35822, to the nucleotide sequence of VGAM2123 RNA, herein designated VGAM RNA, also designated SEQ ID:4834.

[73653] Another function of VGAM2123 is therefore inhibition of Maltase-glucoamylase (alpha-glucosidase) (MGAM, Accession XM_051351), a gene which plays a role in the final steps of digestion of starch. Accordingly, utilities of VGAM2123 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGAM. The function of MGAM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM791.MHC Class II Transactivator (MHC2TA, Ac-

cession NM_000246) is another VGAM2123 host target gene. MHC2TA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MHC2TA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MHC2TA BINDING SITE, designated SEQ ID:5784, to the nucleotide sequence of VGAM2123 RNA, herein designated VGAM RNA, also designated SEQ ID:4834.

[73654] Another function of VGAM2123 is therefore inhibition of MHC Class II Transactivator (MHC2TA, Accession NM_000246). Accordingly, utilities of VGAM2123 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MHC2TA. Reserved (C8orf13, Accession XM_088377) is another VGAM2123 host target gene. C8orf13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C8orf13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C8orf13 BINDING SITE, designated SEQ ID:39657, to the nucleotide sequence of

VGAM2123 RNA, herein designated VGAM RNA, also designated SEQ ID:4834.

[73655] Another function of VGAM2123 is therefore inhibition of Reserved (C8orf13, Accession XM_088377). Accordingly, utilities of VGAM2123 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf13. FLJ11827 (Accession NM_025093) is another VGAM2123 host target gene. FLJ11827 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11827, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11827 BINDING SITE, designated SEQ ID:24723, to the nucleotide sequence of VGAM2123 RNA, herein designated VGAM RNA, also designated SEQ ID:4834.

[73656] Another function of VGAM2123 is therefore inhibition of FLJ11827 (Accession NM_025093). Accordingly, utilities of VGAM2123 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11827. KIAA0472 (Accession XM_050147) is another VGAM2123 host target gene. KIAA0472 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by KIAA0472, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0472 BINDING SITE, designated SEQ ID:35583, to the nucleotide sequence of VGAM2123 RNA, herein designated VGAM RNA, also designated SEQ ID:4834.

[73657] Another function of VGAM2123 is therefore inhibition of KIAA0472 (Accession XM_050147). Accordingly, utilities of VGAM2123 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0472. SRY (sex determining region Y)-box 6 (SOX6, Accession NM_033326) is another VGAM2123 host target gene. SOX6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX6 BINDING SITE, designated SEQ ID:27159, to the nucleotide sequence of VGAM2123 RNA, herein designated VGAM RNA, also designated SEQ ID:4834.

[73658] Another function of VGAM2123 is therefore inhibition of SRY (sex determining region Y)-box 6 (SOX6, Accession

NM_033326). Accordingly, utilities of VGAM2123 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX6. LOC149276 (Accession XM_097621) is another VGAM2123 host target gene. LOC149276 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149276, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149276 BINDING SITE, designated SEQ ID:40977, to the nucleotide sequence of VGAM2123 RNA, herein designated VGAM RNA, also designated SEQ ID:4834.

[73659] Another function of VGAM2123 is therefore inhibition of LOC149276 (Accession XM_097621). Accordingly, utilities of VGAM2123 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149276. LOC153910 (Accession XM_087801) is another VGAM2123 host target gene. LOC153910 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153910, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC153910 BINDING SITE, designated SEQ ID:39441, to the nucleotide sequence of VGAM2123 RNA, herein designated VGAM RNA, also designated SEQ ID:4834.

[73660] Another function of VGAM2123 is therefore inhibition of LOC153910 (Accession XM_087801). Accordingly, utilities of VGAM2123 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153910. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2124 (VGAM2124) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73661] VGAM2124 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2124 was detected is described hereinabove with reference to Figs. 1-8.

[73662] VGAM2124 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2124 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[73663] VGAM2124 gene encodes a VGAM2124 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2124 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2124 precursor RNA is designated SEQ ID:2110, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2110 is located at position 205910 relative to the genome of Cowpox Virus.

[73664] VGAM2124 precursor RNA folds onto itself, forming VGAM2124 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73665] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2124 folded precursor RNA into VGAM2124 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2124 RNA is designated SEQ ID:4835, and is provided hereinbelow with reference to the sequence listing part.

[73666] VGAM2124 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2124 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2124 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73667] VGAM2124 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2124 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2124 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2124 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2124 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73668] The complementary binding of VGAM2124 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2124 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2124 host target RNA into VGAM2124 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73669] It is appreciated that VGAM2124 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2124 host target genes. The mRNA of each one of this plurality of VGAM2124 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2124 RNA, herein designated VGAM RNA, and which when bound by VGAM2124 RNA causes inhibition of translation of respective one or more VGAM2124 host target proteins.

[73670] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2124 gene, herein designated VGAM GENE, on one or more VGAM2124 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73671] It is yet further appreciated that a function of VGAM2124 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2124 correlate with, and may be deduced from, the identity of the host target genes which VGAM2124 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73672] Nucleotide sequences of the VGAM2124 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2124 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2124 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2124 are further described hereinbelow with reference to Table 1.

[73673] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2124 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2124 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73674] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2124 gene, herein designated VGAM is inhibition of expression of VGAM2124 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2124 correlate with, and may be deduced from, the identity of the target genes which VGAM2124 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73675] Elongation of Very Long Chain Fatty Acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4 (ELOVL4, Accession NM_022726) is a VGAM2124 host target gene. ELOVL4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELOVL4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELOVL4 BINDING SITE, designated SEQ ID:22928, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM

RNA, also designated SEQ ID:4835.

[73676] A function of VGAM2124 is therefore inhibition of Elongation of Very Long Chain Fatty Acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4 (ELOVL4, Accession NM_022726). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELOVL4. Glutaminase (GLS, Accession NM_014905) is another VGAM2124 host target gene. GLS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GLS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GLS BINDING SITE, designated SEQ ID:17110, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73677] Another function of VGAM2124 is therefore inhibition of Glutaminase (GLS, Accession NM_014905). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLS. Homeo Box C5 (HOXC5, Accession NM_018953) is another VGAM2124 host target gene. HOXC5 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by HOXC5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOXC5 BINDING SITE, designated SEQ ID:21022, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73678] Another function of VGAM2124 is therefore inhibition of Homeo Box C5 (HOXC5, Accession NM_018953). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXC5. Insulin-like Growth Factor Binding Protein 3 (IGFBP3, Accession NM_000598) is another VGAM2124 host target gene. IGFBP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IGFBP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IGFBP3 BINDING SITE, designated SEQ ID:6199, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73679] Another function of VGAM2124 is therefore inhibition of

Insulin-like Growth Factor Binding Protein 3 (IGFBP3, Accession NM_000598). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IGFBP3. Lamin B Receptor (LBR, Accession XM_001795) is another VGAM2124 host target gene. LBR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LBR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LBR BINDING SITE, designated SEQ ID:29851, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73680] Another function of VGAM2124 is therefore inhibition of Lamin B Receptor (LBR, Accession XM_001795). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LBR. PR Domain Containing 2, with ZNF Domain (PRDM2, Accession NM_015866) is another VGAM2124 host target gene. PRDM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRDM2, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRDM2 BINDING SITE, designated SEQ ID:18007, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73681] Another function of VGAM2124 is therefore inhibition of PR Domain Containing 2, with ZNF Domain (PRDM2, Accession NM_015866), a gene which plays a role in transcriptional regulation during neuronal differentiation and pathogenesis of retinoblastoma. Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDM2. The function of PRDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM120.Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 7 (SLC4A7, Accession NM_003615) is another VGAM2124 host target gene. SLC4A7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC4A7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of SLC4A7 BINDING SITE, designated SEQ ID:9673, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73682] Another function of VGAM2124 is therefore inhibition of Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 7 (SLC4A7, Accession NM_003615), a gene which mediates the coupled movement of sodium and bicarbonate ions across the plasma membrane. Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC4A7. The function of SLC4A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM66.Sorting Nexin 6 (SNX6, Accession NM_021249) is another VGAM2124 host target gene. SNX6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNX6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNX6 BINDING SITE, designated SEQ

ID:22219, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73683] Another function of VGAM2124 is therefore inhibition of Sorting Nexin 6 (SNX6, Accession NM_021249). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX6. Thymidine Kinase 2, Mitochondrial (TK2, Accession NM_004614) is another VGAM2124 host target gene. TK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TK2 BINDING SITE, designated SEQ ID:10960, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73684] Another function of VGAM2124 is therefore inhibition of Thymidine Kinase 2, Mitochondrial (TK2, Accession NM_004614), a gene which phosphorylates thymidine, deoxycytidine, deoxyuridine, and also anti-viral and anti-cancer nucleoside analogs. Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with TK2. The function of TK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM210.Tropomodulin 2 (neuronal) (TMOD2, Accession NM_014548) is another VGAM2124 host target gene. TMOD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TMOD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMOD2 BINDING SITE, designated SEQ ID:15860, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73685] Another function of VGAM2124 is therefore inhibition of Tropomodulin 2 (neuronal) (TMOD2, Accession NM_014548), a gene which is an actin-capping protein for the slow-growing end of filamentous actin. Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMOD2. The function of TMOD2 and its association with various diseases and clinical conditions, has been es-

tablished by previous studies, as described hereinabove with reference to VGAM791.WAS Protein Family, Member 3 (WASF3, Accession NM_006646) is another VGAM2124 host target gene. WASF3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by WASF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WASF3 BINDING SITE, designated SEQ ID:13445, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73686] Another function of VGAM2124 is therefore inhibition of WAS Protein Family, Member 3 (WASF3, Accession NM_006646), a gene which stimulates actin polymerization. Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WASF3. The function of WASF3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1692.Chromosome 11 Open Reading Frame 21 (C11orf21, Accession NM_014144) is another VGAM2124

host target gene. C11orf21 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf21, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf21 BINDING SITE, designated SEQ ID:15428, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73687] Another function of VGAM2124 is therefore inhibition of Chromosome 11 Open Reading Frame 21 (C11orf21, Accession NM_014144). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf21. DnaJ (Hsp40) Homolog, Subfamily A, Member 3 (DNAJA3, Accession XM_017984) is another VGAM2124 host target gene. DNAJA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DNAJA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNAJA3 BINDING SITE, designated SEQ ID:30335, to the nucleotide sequence of VGAM2124 RNA,

herein designated VGAM RNA, also designated SEQ ID:4835.

[73688] Another function of VGAM2124 is therefore inhibition of DnaJ (Hsp40) Homolog, Subfamily A, Member 3 (DNAJA3, Accession XM_017984). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAJA3. FLJ12761 (Accession NM_024545) is another VGAM2124 host target gene. FLJ12761 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12761, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12761 BINDING SITE, designated SEQ ID:23758, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73689] Another function of VGAM2124 is therefore inhibition of FLJ12761 (Accession NM_024545). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12761. FLJ12788 (Accession NM_022492) is another VGAM2124 host target gene. FLJ12788 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12788, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12788 BINDING SITE, designated SEQ ID:22874, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73690] Another function of VGAM2124 is therefore inhibition of FLJ12788 (Accession NM_022492). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12788. FLJ20783 (Accession NM_017958) is another VGAM2124 host target gene. FLJ20783 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20783, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20783 BINDING SITE, designated SEQ ID:19672, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73691] Another function of VGAM2124 is therefore inhibition of

FLJ20783 (Accession NM_017958). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20783. KIAA0179 (Accession XM_035973) is another VGAM2124 host target gene. KIAA0179 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0179, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0179 BINDING SITE, designated SEQ ID:32368, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73692] Another function of VGAM2124 is therefore inhibition of KIAA0179 (Accession XM_035973). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0179. KIAA1209 (Accession XM_027307) is another VGAM2124 host target gene. KIAA1209 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1209, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1209 BINDING SITE, designated SEQ ID:30474, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73693] Another function of VGAM2124 is therefore inhibition of KIAA1209 (Accession XM_027307). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1209. KIAA1432 (Accession XM_039698) is another VGAM2124 host target gene. KIAA1432 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1432, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1432 BINDING SITE, designated SEQ ID:33156, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73694] Another function of VGAM2124 is therefore inhibition of KIAA1432 (Accession XM_039698). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1432. KIAA1582 (Accession XM_037262) is another

VGAM2124 host target gene. KIAA1582 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1582, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1582 BINDING SITE, designated SEQ ID:32592, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73695] Another function of VGAM2124 is therefore inhibition of KIAA1582 (Accession XM_037262). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1582. KIAA1804 (Accession XM_045864) is another VGAM2124 host target gene. KIAA1804 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1804, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1804 BINDING SITE, designated SEQ ID:34590, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73696] Another function of VGAM2124 is therefore inhibition of KIAA1804 (Accession XM_045864). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1804. MGC21636 (Accession NM_145032) is another VGAM2124 host target gene. MGC21636 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC21636, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC21636 BINDING SITE, designated SEQ ID:29648, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73697] Another function of VGAM2124 is therefore inhibition of MGC21636 (Accession NM_145032). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21636. MGC5149 (Accession XM_051200) is another VGAM2124 host target gene. MGC5149 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC5149, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5149 BINDING SITE, designated SEQ ID:35785, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73698] Another function of VGAM2124 is therefore inhibition of MGC5149 (Accession XM_051200). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5149. Ring Finger Protein (C3HC4 type) 8 (RNF8, Accession NM_003958) is another VGAM2124 host target gene. RNF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF8 BINDING SITE, designated SEQ ID:10098, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73699] Another function of VGAM2124 is therefore inhibition of Ring Finger Protein (C3HC4 type) 8 (RNF8, Accession NM_003958). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with RNF8. Sema Domain, Immunoglobulin Domain (Ig), Short Basic Domain, Secreted, (semaphorin) 3C (SEMA3C, Accession NM_006379) is another VGAM2124 host target gene. SEMA3C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEMA3C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEMA3C BINDING SITE, designated SEQ ID:13075, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73700] Another function of VGAM2124 is therefore inhibition of Sema Domain, Immunoglobulin Domain (Ig), Short Basic Domain, Secreted, (semaphorin) 3C (SEMA3C, Accession NM_006379). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA3C. SHAPY (Accession NM_138793) is another VGAM2124 host target gene. SHAPY BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SHAPY, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of SHAPY BINDING SITE, designated SEQ ID:29017, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73701] Another function of VGAM2124 is therefore inhibition of SHAPY (Accession NM_138793). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHAPY. Stromal Antigen 2 (STAG2, Accession XM_047285) is another VGAM2124 host target gene. STAG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STAG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAG2 BINDING SITE, designated SEQ ID:34930, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73702] Another function of VGAM2124 is therefore inhibition of Stromal Antigen 2 (STAG2, Accession XM_047285). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with STAG2. Yes-associated Protein 1, 65kDa (YAP1, Accession NM_006106) is another VGAM2124 host target gene. YAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by YAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YAP1 BINDING SITE, designated SEQ ID:12755, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73703] Another function of VGAM2124 is therefore inhibition of Yes-associated Protein 1, 65kDa (YAP1, Accession NM_006106). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YAP1. Zinc Finger RNA Binding Protein (ZFR, Accession NM_016107) is another VGAM2124 host target gene. ZFR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZFR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZFR BINDING SITE, desig-

nated SEQ ID:18189, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73704] Another function of VGAM2124 is therefore inhibition of Zinc Finger RNA Binding Protein (ZFR, Accession NM_016107). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFR. Zinc Finger Protein 294 (ZNF294, Accession XM_047829) is another VGAM2124 host target gene. ZNF294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF294 BINDING SITE, designated SEQ ID:35057, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73705] Another function of VGAM2124 is therefore inhibition of Zinc Finger Protein 294 (ZNF294, Accession XM_047829). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF294. LOC118706 (Accession

XM_058336) is another VGAM2124 host target gene. LOC118706 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC118706, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC118706 BINDING SITE, designated SEQ ID:36597, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73706] Another function of VGAM2124 is therefore inhibition of LOC118706 (Accession XM_058336). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118706. LOC127428 (Accession XM_059144) is another VGAM2124 host target gene. LOC127428 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC127428, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127428 BINDING SITE, designated SEQ ID:36898, to the nucleotide sequence of VGAM2124 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4835.

[73707] Another function of VGAM2124 is therefore inhibition of LOC127428 (Accession XM_059144). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127428. LOC133686 (Accession XM_059667) is another VGAM2124 host target gene. LOC133686 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC133686, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133686 BINDING SITE, designated SEQ ID:37057, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73708] Another function of VGAM2124 is therefore inhibition of LOC133686 (Accession XM_059667). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133686. LOC143158 (Accession XM_084445) is another VGAM2124 host target gene. LOC143158 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143158, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143158 BINDING SITE, designated SEQ ID:37592, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73709] Another function of VGAM2124 is therefore inhibition of LOC143158 (Accession XM_084445). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143158. LOC144438 (Accession XM_084860) is another VGAM2124 host target gene. LOC144438 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144438, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144438 BINDING SITE, designated SEQ ID:37739, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73710] Another function of VGAM2124 is therefore inhibition of LOC144438 (Accession XM_084860). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC144438. LOC145820 (Accession XM_085246) is another VGAM2124 host target gene. LOC145820 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145820, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145820 BINDING SITE, designated SEQ ID:37993, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73711] Another function of VGAM2124 is therefore inhibition of LOC145820 (Accession XM_085246). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145820. LOC147160 (Accession XM_097202) is another VGAM2124 host target gene. LOC147160 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147160 BINDING SITE, designated SEQ ID:40809, to

the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73712] Another function of VGAM2124 is therefore inhibition of LOC147160 (Accession XM_097202). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147160. LOC147463 (Accession XM_085799) is another VGAM2124 host target gene. LOC147463 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147463, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147463 BINDING SITE, designated SEQ ID:38342, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73713] Another function of VGAM2124 is therefore inhibition of LOC147463 (Accession XM_085799). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147463. LOC159053 (Accession XM_099021) is another VGAM2124 host target gene. LOC159053 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC159053, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159053 BINDING SITE, designated SEQ ID:42060, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73714] Another function of VGAM2124 is therefore inhibition of LOC159053 (Accession XM_099021). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159053. LOC201931 (Accession XM_114407) is another VGAM2124 host target gene. LOC201931 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201931, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201931 BINDING SITE, designated SEQ ID:42930, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73715] Another function of VGAM2124 is therefore inhibition of LOC201931 (Accession XM_114407). Accordingly, utilities

of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201931. LOC220466 (Accession XM_058363) is another VGAM2124 host target gene. LOC220466 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220466, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220466 BINDING SITE, designated SEQ ID:36611, to the nucleotide sequence of VGAM2124 RNA, herein designated VGAM RNA, also designated SEQ ID:4835.

[73716] Another function of VGAM2124 is therefore inhibition of LOC220466 (Accession XM_058363). Accordingly, utilities of VGAM2124 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220466. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2125 (VGAM2125) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73717] VGAM2125 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2125 was detected is described hereinabove with reference to Figs. 1-8.

[73718] VGAM2125 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline Herpesvirus 3. VGAM2125 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73719] VGAM2125 gene encodes a VGAM2125 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2125 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2125 precursor RNA is designated SEQ ID:2111, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2111 is located at position 18618 relative to the genome of Ateline Herpesvirus 3.

[73720] VGAM2125 precursor RNA folds onto itself, forming VGAM2125 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73721] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2125 folded precursor RNA into VGAM2125 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2125 RNA is designated SEQ ID:4836, and is provided hereinbelow with reference to the sequence listing part.

[73722] VGAM2125 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2125 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2125 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[73723] VGAM2125 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2125 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2125 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2125 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2125 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73724] The complementary binding of VGAM2125 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2125 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2125 host target RNA into VGAM2125 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73725] It is appreciated that VGAM2125 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2125 host target genes. The mRNA of each one of this plurality of VGAM2125 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2125 RNA, herein designated VGAM RNA, and which when bound by VGAM2125 RNA causes inhibition of translation of respective one or more VGAM2125 host target proteins.

[73726] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2125 gene, herein designated VGAM GENE, on one or more VGAM2125 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73727] It is yet further appreciated that a function of VGAM2125 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2125 correlate with, and may be deduced from, the identity of the host target genes which VGAM2125 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73728] Nucleotide sequences of the VGAM2125 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2125 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2125 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2125 are further described hereinbelow with reference to Table 1.

[73729] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2125 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2125 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73730] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2125 gene, herein designated VGAM is inhibition of expression of VGAM2125 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2125 correlate with, and may be deduced from, the identity of the target genes which VGAM2125 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73731] Angiotensin I Converting Enzyme (peptidyl-dipeptidase A) 2 (ACE2, Accession NM_021804) is a VGAM2125 host tar-

get gene. ACE2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ACE2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACE2 BINDING SITE, designated SEQ ID:22356, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73732] A function of VGAM2125 is therefore inhibition of Angiotensin I Converting Enzyme (peptidyl-dipeptidase A) 2 (ACE2, Accession NM_021804), a gene which converts angiotensin i to angiotensin ii by release of the terminal his-leu. Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACE2. The function of ACE2 has been established by previous studies. By EST database searching for sequences showing homology to the zinc metalloprotease angiotensin I converting enzyme (ACE; 106180) and by screening a human lymphoma cDNA library, Tipnis et al. (2000) cloned a full-length ACE2 cDNA, which they called ACEH, encoding a deduced 805-amino acid protein that shares approximately 40% identity with the N- and C-terminal domains of ACE. ACE2 contains a

potential 17-amino acid N-terminal signal peptide and a putative 22-amino acid C-terminal membrane anchor. It has a conserved zinc metalloprotease consensus sequence (HEXXH) and a conserved glutamine residue that is predicted to serve as a third zinc ligand. Northern blot analysis detected high expression of ACE2 in kidney, testis, and heart, and moderate expression in colon, small intestine, and ovary. Expression in CHO cells of a soluble, truncated form of ACE2, lacking transmembrane and cytosolic domains, produced a glycosylated protein that is able to cleave angiotensin I and angiotensin II but not bradykinin. In the hydrolysis of the angiotensins, ACE2 functions exclusively as a carboxypeptidase. Tipnis et al. (2000) showed that ACE2 is not inhibited by benzylsuccinate, a carboxypeptidase A inhibitor, or by other ACE inhibitors such as lisinopril. Tipnis et al. (2000) mapped the ACE2 gene by sequence similarity to a sequence in GenBank (AC003669) mapping to Xp22. Animal model experiments lend further support to the function of ACE2. Crackower et al. (2002) demonstrated that Ace2 maps to a defined quantitative trait locus (QTL) on the X chromosome in 3 different rat models of hypertension. In all hypertensive rat strains, Ace2 mRNA and protein expression were

markedly reduced, suggesting that Ace2 is a candidate gene for this QTL.

[73733] It is appreciated that the abovementioned animal model for ACE2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[73734] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[73735] Tipnis, S. R.; Hooper, N. M.; Hyde, R.; Karran, E.; Christie, G.; Turner, A. J. : A human homolog of angiotensin-converting enzyme: cloning and functional expression as a captopril-insensitive carboxypeptidase. J. Biol. Chem. 275: 33238-33243, 2000. ; and

[73736] Crackower, M. A.; Sarao, R.; Oudit, G. Y.; Yagil, C.; Kozieradzki, I.; Scanga, S. E.; Oliveira-dos-Santos, A. J.; da Costa, J.; Zhang, L.; Pei, Y.; Scholey, J.; Ferrario, C. M.; Manouki.

[73737] Further studies establishing the function and utilities of ACE2 are found in John Hopkins OMIM database record ID 300335, and in sited publications numbered 9447 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Mitogen-activated Pro-

tein Kinase Kinase Kinase 5 (MAP3K5, Accession NM_005923) is another VGAM2125 host target gene. MAP3K5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K5 BINDING SITE, designated SEQ ID:12546, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73738] Another function of VGAM2125 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 5 (MAP3K5, Accession NM_005923), a gene which phosphorylates and activates two different subgroups of map kinase kinases, mkk4/sek1 and mkk3/mapkk6 (or mkk6) .overexpression induces apoptotic cell death. Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K5. The function of MAP3K5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1622.Aminopeptidase Puromycin

Sensitive (NPEPPS, Accession NM_006310) is another VGAM2125 host target gene. NPEPPS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NPEPPS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPEPPS BINDING SITE, designated SEQ ID:12996, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73739] Another function of VGAM2125 is therefore inhibition of Aminopeptidase Puromycin Sensitive (NPEPPS, Accession NM_006310), a gene which is puromycin-sensitive aminopeptidase and has metallopeptidase activity. Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPEPPS. The function of NPEPPS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM83.Protein Kinase, AMP-activated, Alpha 2 Catalytic Subunit (PRKAA2, Accession NM_006252) is another VGAM2125 host target gene. PRKAA2 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by PRKAA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKAA2 BINDING SITE, designated SEQ ID:12927, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73740] Another function of VGAM2125 is therefore inhibition of Protein Kinase, AMP-activated, Alpha 2 Catalytic Subunit (PRKAA2, Accession NM_006252), a gene which are responsible for the regulation of fatty acid synthesis by phosphorylation of acetyl-coa carboxylase. Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKAA2. The function of PRKAA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1544.Prostaglandin-endoperoxide Synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2, Accession NM_000963) is another VGAM2125 host target gene. PTGS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by PTGS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTGS2 BINDING SITE, designated SEQ ID:6681, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73741] Another function of VGAM2125 is therefore inhibition of Prostaglandin-endoperoxide Synthase 2 (prostaglandin G/H synthase and cyclooxygenase) (PTGS2, Accession NM_000963), a gene which may have a role as a major mediator of inflammation and/or a role for prostanoid signaling in activity-dependent plasticity. Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGS2. The function of PTGS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM292.Chromosome 6 Open Reading Frame 35 (C6orf35, Accession NM_018452) is another VGAM2125 host target gene. C6orf35 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C6orf35, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C6orf35 BINDING SITE, designated SEQ ID:20526, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73742] Another function of VGAM2125 is therefore inhibition of Chromosome 6 Open Reading Frame 35 (C6orf35, Accession NM_018452). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf35. FLJ20730 (Accession NM_017945) is another VGAM2125 host target gene. FLJ20730 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20730, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20730 BINDING SITE, designated SEQ ID:19639, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73743] Another function of VGAM2125 is therefore inhibition of FLJ20730 (Accession NM_017945). Accordingly, utilities of

VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20730. FLJ22833 (Accession NM_022837) is another VGAM2125 host target gene. FLJ22833 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22833, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22833 BINDING SITE, designated SEQ ID:23119, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73744] Another function of VGAM2125 is therefore inhibition of FLJ22833 (Accession NM_022837). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22833. FLJ23462 (Accession NM_024843) is another VGAM2125 host target gene. FLJ23462 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23462, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23462

BINDING SITE, designated SEQ ID:24258, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73745] Another function of VGAM2125 is therefore inhibition of FLJ23462 (Accession NM_024843). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23462. MADP-1 (Accession NM_033114) is another VGAM2125 host target gene. MADP-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MADP-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MADP-1 BINDING SITE, designated SEQ ID:26961, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73746] Another function of VGAM2125 is therefore inhibition of MADP-1 (Accession NM_033114). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADP-1. MCM10 Minichromosome Maintenance Deficient 10 (S. cerevisiae) (MCM10, Accession NM_018518) is another

VGAM2125 host target gene. MCM10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MCM10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MCM10 BINDING SITE, designated SEQ ID:20591, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73747] Another function of VGAM2125 is therefore inhibition of MCM10 Minichromosome Maintenance Deficient 10 (S. cerevisiae) (MCM10, Accession NM_018518). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCM10. Phospholipase C-like 1 (PLCL1, Accession NM_006226) is another VGAM2125 host target gene. PLCL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLCL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLCL1 BINDING SITE, designated SEQ ID:12888, to the nucleotide sequence of VGAM2125 RNA,

herein designated VGAM RNA, also designated SEQ ID:4836.

[73748] Another function of VGAM2125 is therefore inhibition of Phospholipase C-like 1 (PLCL1, Accession NM_006226). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLCL1. LOC151473 (Accession XM_087215) is another VGAM2125 host target gene. LOC151473 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151473, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151473 BINDING SITE, designated SEQ ID:39117, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73749] Another function of VGAM2125 is therefore inhibition of LOC151473 (Accession XM_087215). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151473. LOC162461 (Accession XM_091568) is another VGAM2125 host target gene. LOC162461 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC162461, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162461 BINDING SITE, designated SEQ ID:40056, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73750] Another function of VGAM2125 is therefore inhibition of LOC162461 (Accession XM_091568). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162461. LOC220776 (Accession XM_043388) is another VGAM2125 host target gene. LOC220776 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220776, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220776 BINDING SITE, designated SEQ ID:33926, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73751] Another function of VGAM2125 is therefore inhibition of

LOC220776 (Accession XM_043388). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220776. LOC253019 (Accession XM_170907) is another VGAM2125 host target gene. LOC253019 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253019, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253019 BINDING SITE, designated SEQ ID:45665, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73752] Another function of VGAM2125 is therefore inhibition of LOC253019 (Accession XM_170907). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253019. LOC253975 (Accession XM_171130) is another VGAM2125 host target gene. LOC253975 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253975, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC253975 BINDING SITE, designated SEQ ID:45932, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73753] Another function of VGAM2125 is therefore inhibition of LOC253975 (Accession XM_171130). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253975. LOC85479 (Accession NM_033105) is another VGAM2125 host target gene. LOC85479 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC85479, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC85479 BINDING SITE, designated SEQ ID:26955, to the nucleotide sequence of VGAM2125 RNA, herein designated VGAM RNA, also designated SEQ ID:4836.

[73754] Another function of VGAM2125 is therefore inhibition of LOC85479 (Accession NM_033105). Accordingly, utilities of VGAM2125 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC85479. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2126 (VGAM2126) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73755] VGAM2126 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2126 was detected is described hereinabove with reference to Figs. 1-8.

[73756] VGAM2126 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline Herpesvirus 3. VGAM2126 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73757] VGAM2126 gene encodes a VGAM2126 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2126 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2126 precursor RNA is designated SEQ ID:2112, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2112 is located at position 6412 relative to the genome of Ateline Herpesvirus 3.

[73758] VGAM2126 precursor RNA folds onto itself, forming VGAM2126 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73759] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2126 folded precursor RNA into VGAM2126 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2126 RNA is designated SEQ ID:4837, and is provided hereinbelow with reference to the sequence listing part.

[73760] VGAM2126 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2126 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2126 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73761] VGAM2126 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2126 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2126 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2126 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2126 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73762] The complementary binding of VGAM2126 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2126 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2126 host target RNA into VGAM2126 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73763] It is appreciated that VGAM2126 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2126 host target genes. The mRNA of each one of this plurality of VGAM2126 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2126 RNA, herein designated VGAM RNA, and which when bound by VGAM2126 RNA causes inhibition of translation of respective one or more

VGAM2126 host target proteins.

[73764] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2126 gene, herein designated VGAM GENE, on one or more VGAM2126 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73765] It is yet further appreciated that a function of VGAM2126 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2126 include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Spe-

cific functions, and accordingly utilities, of VGAM2126 correlate with, and may be deduced from, the identity of the host target genes which VGAM2126 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73766] Nucleotide sequences of the VGAM2126 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2126 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2126 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2126 are further described hereinbelow with reference to Table 1.

[73767] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2126 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2126 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73768] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2126 gene, herein designated VGAM is inhibition of expression of VGAM2126 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2126 correlate with, and may be deduced from, the identity of the target genes which VGAM2126 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73769] Amyloid Beta Precursor Protein (cytoplasmic tail) Binding Protein 2 (APPBP2, Accession NM_006380) is a VGAM2126 host target gene. APPBP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APPBP2 BINDING SITE, designated SEQ ID:13083, to the nucleotide sequence of VGAM2126 RNA, herein designated VGAM RNA, also designated SEQ ID:4837.

[73770] A function of VGAM2126 is therefore inhibition of Amyloid Beta Precursor Protein (cytoplasmic tail) Binding Protein 2 (APPBP2, Accession NM_006380), a gene which interacts with the basolateral sorting signal of amyloid precursor protein. Accordingly, utilities of VGAM2126 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APPBP2. The function of APPBP2 and its association with various diseases and clin-

ical conditions, has been established by previous studies, as described hereinabove with reference to VGAM525.Aquaporin 6, Kidney Specific (AQP6, Accession NM_001652) is another VGAM2126 host target gene. AQP6 BINDING SITE1 and AQP6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AQP6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE1 and AQP6 BINDING SITE2, designated SEQ ID:7360 and SEQ ID:27617 respectively, to the nucleotide sequence of VGAM2126 RNA, herein designated VGAM RNA, also designated SEQ ID:4837.

[73771] Another function of VGAM2126 is therefore inhibition of Aquaporin 6, Kidney Specific (AQP6, Accession NM_001652), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid-base metabolism. Accordingly, utilities of VGAM2126 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6. The function of AQP6 and its association with various diseases and clinical conditions, has been established

by previous studies, as described hereinabove with reference to VGAM340.RPP30 (Accession NM_006413) is another VGAM2126 host target gene. RPP30 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPP30, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPP30 BINDING SITE, designated SEQ ID:13122, to the nucleotide sequence of VGAM2126 RNA, herein designated VGAM RNA, also designated SEQ ID:4837.

[73772] Another function of VGAM2126 is therefore inhibition of RPP30 (Accession NM_006413), a gene which is a component of ribonuclease p that processes 5' ends of precursor tRNAs. Accordingly, utilities of VGAM2126 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPP30. The function of RPP30 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM230.Kell Blood Group Precursor (McLeod phenotype) (XK, Accession NM_021083) is another VGAM2126 host target gene. XK BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by XK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XK BINDING SITE, designated SEQ ID:22064, to the nucleotide sequence of VGAM2126 RNA, herein designated VGAM RNA, also designated SEQ ID:4837.

[73773] Another function of VGAM2126 is therefore inhibition of Kell Blood Group Precursor (McLeod phenotype) (XK, Accession NM_021083). Accordingly, utilities of VGAM2126 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XK. HCA4 (Accession XM_085287) is another VGAM2126 host target gene. HCA4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCA4 BINDING SITE, designated SEQ ID:38029, to the nucleotide sequence of VGAM2126 RNA, herein designated VGAM RNA, also designated SEQ ID:4837.

[73774] Another function of VGAM2126 is therefore inhibition of HCA4 (Accession XM_085287). Accordingly, utilities of

VGAM2126 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCA4. KIAA0635 (Accession NM_014645) is another VGAM2126 host target gene. KIAA0635 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0635, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0635 BINDING SITE, designated SEQ ID:16058, to the nucleotide sequence of VGAM2126 RNA, herein designated VGAM RNA, also designated SEQ ID:4837.

[73775] Another function of VGAM2126 is therefore inhibition of KIAA0635 (Accession NM_014645). Accordingly, utilities of VGAM2126 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0635. LOC158219 (Accession XM_088514) is another VGAM2126 host target gene. LOC158219 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC158219 BINDING SITE, designated SEQ ID:39763, to the nucleotide sequence of VGAM2126 RNA, herein designated VGAM RNA, also designated SEQ ID:4837.

[73776] Another function of VGAM2126 is therefore inhibition of LOC158219 (Accession XM_088514). Accordingly, utilities of VGAM2126 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158219. LOC158434 (Accession XM_098939) is another VGAM2126 host target gene. LOC158434 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158434, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158434 BINDING SITE, designated SEQ ID:41989, to the nucleotide sequence of VGAM2126 RNA, herein designated VGAM RNA, also designated SEQ ID:4837.

[73777] Another function of VGAM2126 is therefore inhibition of LOC158434 (Accession XM_098939). Accordingly, utilities of VGAM2126 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158434. LOC221337 (Accession XM_166387) is another VGAM2126 host target gene. LOC221337 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221337, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221337 BINDING SITE, designated SEQ ID:44237, to the nucleotide sequence of VGAM2126 RNA, herein designated VGAM RNA, also designated SEQ ID:4837.

[73778] Another function of VGAM2126 is therefore inhibition of LOC221337 (Accession XM_166387). Accordingly, utilities of VGAM2126 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221337. LOC256021 (Accession XM_172884) is another VGAM2126 host target gene. LOC256021 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256021, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256021 BINDING SITE, designated SEQ ID:46165, to the nucleotide sequence of VGAM2126 RNA, herein designated VGAM RNA, also designated SEQ ID:4837.

[73779] Another function of VGAM2126 is therefore inhibition of

LOC256021 (Accession XM_172884). Accordingly, utilities of VGAM2126 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256021. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2127 (VGAM2127) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73780] VGAM2127 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2127 was detected is described hereinabove with reference to Figs. 1-8.

[73781] VGAM2127 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline Herpesvirus 3. VGAM2127 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73782] VGAM2127 gene encodes a VGAM2127 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2127 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2127 precursor RNA is designated SEQ ID:2113, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2113 is located at position 22317 relative to the genome of Ateline Herpesvirus 3.

[73783] VGAM2127 precursor RNA folds onto itself, forming VGAM2127 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73784] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2127 folded precursor RNA into VGAM2127 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide se-

quence of VGAM2127 RNA is designated SEQ ID:4838, and is provided hereinbelow with reference to the sequence listing part.

[73785] VGAM2127 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2127 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2127 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73786] VGAM2127 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2127 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2127 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2127 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2127 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73787] The complementary binding of VGAM2127 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2127 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2127 host target RNA into VGAM2127 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73788] It is appreciated that VGAM2127 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2127 host target genes. The mRNA of each one of this plurality of VGAM2127 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2127 RNA, herein designated VGAM RNA, and which when bound by VGAM2127 RNA causes inhibition of translation of respective one or more VGAM2127 host target proteins.

[73789] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2127 gene, herein designated VGAM GENE, on one or more VGAM2127 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73790] It is yet further appreciated that a function of VGAM2127

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2127 correlate with, and may be deduced from, the identity of the host target genes which VGAM2127 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73791] Nucleotide sequences of the VGAM2127 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2127 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2127 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2127 are further described hereinbelow with reference to Table 1.

[73792] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2127 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2127 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73793] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2127 gene, herein designated VGAM is inhibition of expression of VGAM2127 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2127 correlate with, and may be deduced from, the identity of the target genes which VGAM2127 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73794] FLJ21615 (Accession NM_032205) is a VGAM2127 host target gene. FLJ21615 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21615, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21615 BINDING SITE, designated SEQ ID:25909, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73795] A function of VGAM2127 is therefore inhibition of FLJ21615 (Accession NM_032205). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21615. GABA(A) Receptors Associated Protein Like 3

(GABARAPL3, Accession NM_032568) is another VGAM2127 host target gene. GABARAPL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABARAPL3 BINDING SITE, designated SEQ ID:26296, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73796] Another function of VGAM2127 is therefore inhibition of GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL3. KIAA0077 (Accession XM_040158) is another VGAM2127 host target gene. KIAA0077 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0077, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0077 BINDING SITE, designated SEQ ID:33267, to the

nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73797] Another function of VGAM2127 is therefore inhibition of KIAA0077 (Accession XM_040158). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0077. KIAA0923 (Accession NM_014021) is another VGAM2127 host target gene. KIAA0923 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0923, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0923 BINDING SITE, designated SEQ ID:15240, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73798] Another function of VGAM2127 is therefore inhibition of KIAA0923 (Accession NM_014021). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0923. LAT1-3TM (Accession XM_043976) is another VGAM2127 host target gene. LAT1-3TM BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by LAT1-3TM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAT1-3TM BINDING SITE, designated SEQ ID:34053, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73799] Another function of VGAM2127 is therefore inhibition of LAT1-3TM (Accession XM_043976). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAT1-3TM. MGC13071 (Accession NM_032689) is another VGAM2127 host target gene. MGC13071 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC13071, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13071 BINDING SITE, designated SEQ ID:26407, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73800] Another function of VGAM2127 is therefore inhibition of MGC13071 (Accession NM_032689). Accordingly, utilities

of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13071. VEZATIN (Accession NM_017599) is another VGAM2127 host target gene. VEZATIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VEZATIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VEZATIN BINDING SITE, designated SEQ ID:19070, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73801] Another function of VGAM2127 is therefore inhibition of VEZATIN (Accession NM_017599). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VEZATIN. LOC116236 (Accession XM_057674) is another VGAM2127 host target gene. LOC116236 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC116236, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC116236 BINDING SITE, designated SEQ ID:36541, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73802] Another function of VGAM2127 is therefore inhibition of LOC116236 (Accession XM_057674). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116236. LOC122786 (Accession XM_058660) is another VGAM2127 host target gene. LOC122786 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC122786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122786 BINDING SITE, designated SEQ ID:36696, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73803] Another function of VGAM2127 is therefore inhibition of LOC122786 (Accession XM_058660). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122786. LOC145371 (Accession XM_085123) is another VGAM2127 host target gene. LOC145371 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145371, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145371 BINDING SITE, designated SEQ ID:37842, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73804] Another function of VGAM2127 is therefore inhibition of LOC145371 (Accession XM_085123). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145371. LOC162239 (Accession XM_091439) is another VGAM2127 host target gene. LOC162239 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC162239, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162239 BINDING SITE, designated SEQ ID:40055, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73805] Another function of VGAM2127 is therefore inhibition of

LOC162239 (Accession XM_091439). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162239. LOC169026 (Accession XM_095471) is another VGAM2127 host target gene. LOC169026 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC169026, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169026 BINDING SITE, designated SEQ ID:40268, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73806] Another function of VGAM2127 is therefore inhibition of LOC169026 (Accession XM_095471). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169026. LOC222070 (Accession XM_168433) is another VGAM2127 host target gene. LOC222070 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222070, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC222070 BINDING SITE, designated SEQ ID:45176, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73807] Another function of VGAM2127 is therefore inhibition of LOC222070 (Accession XM_168433). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222070. LOC93333 (Accession XM_050624) is another VGAM2127 host target gene. LOC93333 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93333 BINDING SITE, designated SEQ ID:35664, to the nucleotide sequence of VGAM2127 RNA, herein designated VGAM RNA, also designated SEQ ID:4838.

[73808] Another function of VGAM2127 is therefore inhibition of LOC93333 (Accession XM_050624). Accordingly, utilities of VGAM2127 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93333. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2128 (VGAM2128) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73809] VGAM2128 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2128 was detected is described hereinabove with reference to Figs. 1-8.

[73810] VGAM2128 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline Herpesvirus 3. VGAM2128 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73811] VGAM2128 gene encodes a VGAM2128 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2128 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2128 precursor RNA is designated SEQ ID:2114, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2114 is located at position 22124 relative to the genome of Ateline Herpesvirus 3.

[73812] VGAM2128 precursor RNA folds onto itself, forming VGAM2128 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73813] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2128 folded precursor RNA into VGAM2128 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2128 RNA is designated SEQ ID:4839, and is provided hereinbelow with reference to the sequence listing part.

[73814] VGAM2128 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2128 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2128 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73815] VGAM2128 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2128 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2128 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2128 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2128 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73816] The complementary binding of VGAM2128 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2128 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2128 host target RNA into VGAM2128 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73817] It is appreciated that VGAM2128 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2128 host target genes. The mRNA of each one of this plurality of VGAM2128 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2128 RNA, herein designated VGAM RNA, and which when bound by VGAM2128 RNA causes inhibition of translation of respective one or more

VGAM2128 host target proteins.

[73818] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2128 gene, herein designated VGAM GENE, on one or more VGAM2128 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73819] It is yet further appreciated that a function of VGAM2128 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2128 include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Spe-

cific functions, and accordingly utilities, of VGAM2128 correlate with, and may be deduced from, the identity of the host target genes which VGAM2128 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73820] Nucleotide sequences of the VGAM2128 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2128 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2128 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2128 are further described hereinbelow with reference to Table 1.

[73821] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2128 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2128 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73822] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2128 gene, herein designated VGAM is inhibition of expression of VGAM2128 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2128 correlate with, and may be deduced from, the identity of the target genes which VGAM2128 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73823] Discs, Large (Drosophila) Homolog 5 (DLG5, Accession XM_096398) is a VGAM2128 host target gene. DLG5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DLG5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLG5 BINDING SITE, designated SEQ ID:40339, to the nucleotide sequence of VGAM2128 RNA, herein designated VGAM RNA, also designated SEQ ID:4839.

[73824] A function of VGAM2128 is therefore inhibition of Discs, Large (Drosophila) Homolog 5 (DLG5, Accession XM_096398), a gene which may transmit extracellular signals to inhibit cell proliferation. Accordingly, utilities of VGAM2128 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLG5. The function of DLG5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM444.MGC23937 (Accession NM_145052) is another VGAM2128 host target gene. MGC23937 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC23937, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC23937 BINDING SITE, designated SEQ ID:29682, to the nucleotide sequence of VGAM2128 RNA, herein designated VGAM RNA, also designated SEQ ID:4839.

[73825] Another function of VGAM2128 is therefore inhibition of MGC23937 (Accession NM_145052). Accordingly, utilities of VGAM2128 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC23937. LOC158969 (Accession XM_088728) is another VGAM2128 host target gene. LOC158969 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158969, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158969 BINDING SITE, designated SEQ ID:39922, to the nucleotide sequence of VGAM2128 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4839.

[73826] Another function of VGAM2128 is therefore inhibition of LOC158969 (Accession XM_088728). Accordingly, utilities of VGAM2128 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158969. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2129 (VGAM2129) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73827] VGAM2129 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2129 was detected is described hereinabove with reference to Figs. 1-8.

[73828] VGAM2129 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline Herpesvirus 3. VGAM2129 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73829] VGAM2129 gene encodes a VGAM2129 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2129 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2129 precursor RNA is designated SEQ ID:2115, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2115 is located at position 9401 relative to the genome of Ateline Herpesvirus 3.

[73830] VGAM2129 precursor RNA folds onto itself, forming VGAM2129 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73831] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2129 folded precursor RNA into VGAM2129 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2129 RNA is designated SEQ ID:4840, and is provided hereinbelow with reference to the sequence listing part.

[73832] VGAM2129 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2129 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2129 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73833] VGAM2129 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2129 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2129 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2129 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2129 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73834] The complementary binding of VGAM2129 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2129 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2129 host target RNA into VGAM2129 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73835] It is appreciated that VGAM2129 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2129 host target genes. The mRNA of

each one of this plurality of VGAM2129 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2129 RNA, herein designated VGAM RNA, and which when bound by VGAM2129 RNA causes inhibition of translation of respective one or more VGAM2129 host target proteins.

[73836] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2129 gene, herein designated VGAM GENE, on one or more VGAM2129 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[73837] It is yet further appreciated that a function of VGAM2129 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2129 correlate with, and may be deduced from, the identity of the host target genes which VGAM2129 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73838] Nucleotide sequences of the VGAM2129 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2129 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2129 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2129 are further described hereinbelow with reference to Table 1.

[73839] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2129 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2129 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73840] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2129 gene, herein designated VGAM is inhibition of expression of VGAM2129 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2129 correlate with, and may be deduced from, the identity of the target genes which VGAM2129 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73841] Cysteine-rich Motor Neuron 1 (CRIM1, Accession NM_016441) is a VGAM2129 host target gene. CRIM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRIM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRIM1 BINDING SITE, designated SEQ ID:18558, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73842] A function of VGAM2129 is therefore inhibition of Cysteine-rich Motor Neuron 1 (CRIM1, Accession NM_016441). Accordingly, utilities of VGAM2129 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with CRIM1. Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_001879) is another VGAM2129 host target gene. MASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MASP1 BINDING SITE, designated SEQ ID:7605, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73843] Another function of VGAM2129 is therefore inhibition of Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_001879), a gene which a complement-dependent bactericidal factor . Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MASP1. The function of MASP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM566.Rho-associated, Coiled-coil Containing Protein Kinase 2 (ROCK2, Accession XM_038377) is another VGAM2129 host target gene. ROCK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ROCK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ROCK2 BINDING SITE, designated SEQ ID:32839, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73844] Another function of VGAM2129 is therefore inhibition of Rho-associated, Coiled-coil Containing Protein Kinase 2 (ROCK2, Accession XM_038377), a gene which regulates cytokinesis, smooth muscle contraction, the formation of actin stress fibers and focal adhesions. Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ROCK2. The function of ROCK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM273.CASPR3 (Accession NM_033655) is another VGAM2129 host target gene.

CASPR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CASPR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASPR3 BINDING SITE, designated SEQ ID:27386, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73845] Another function of VGAM2129 is therefore inhibition of CASPR3 (Accession NM_033655). Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASPR3. FHR5 (Accession NM_030787) is another VGAM2129 host target gene. FHR5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FHR5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FHR5 BINDING SITE, designated SEQ ID:25083, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73846] Another function of VGAM2129 is therefore inhibition of FHR5 (Accession NM_030787). Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHR5. FLJ11726 (Accession NM_024971) is another VGAM2129 host target gene. FLJ11726 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11726, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11726 BINDING SITE, designated SEQ ID:24526, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73847] Another function of VGAM2129 is therefore inhibition of FLJ11726 (Accession NM_024971). Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11726. FLJ20085 (Accession NM_017660) is another VGAM2129 host target gene. FLJ20085 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20085, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20085 BINDING SITE, designated SEQ ID:19185, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73848] Another function of VGAM2129 is therefore inhibition of FLJ20085 (Accession NM_017660). Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20085. KIAA0475 (Accession NM_014864) is another VGAM2129 host target gene. KIAA0475 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:16948, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73849] Another function of VGAM2129 is therefore inhibition of KIAA0475 (Accession NM_014864). Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0475. RAB40A, Member RAS Oncogene Family (RAB40A, Accession XM_088733) is another VGAM2129 host target gene. RAB40A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAB40A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB40A BINDING SITE, designated SEQ ID:39929, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73850] Another function of VGAM2129 is therefore inhibition of RAB40A, Member RAS Oncogene Family (RAB40A, Accession XM_088733). Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB40A. TUSP (Accession NM_020245) is another VGAM2129 host target gene. TUSP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUSP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUSP BINDING SITE, designated SEQ ID:21523,

to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73851] Another function of VGAM2129 is therefore inhibition of TUSP (Accession NM_020245). Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUSP. Ubiquitin Specific Protease 2 (USP2, Accession NM_004205) is another VGAM2129 host target gene. USP2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by USP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP2 BINDING SITE, designated SEQ ID:10400, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73852] Another function of VGAM2129 is therefore inhibition of Ubiquitin Specific Protease 2 (USP2, Accession NM_004205). Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP2. LOC219920 (Accession XM_167787) is another VGAM2129 host target gene. LOC219920 BINDING SITE is HOST TARGET binding

site found in the 5` untranslated region of mRNA encoded by LOC219920, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219920 BINDING SITE, designated SEQ ID:44806, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73853] Another function of VGAM2129 is therefore inhibition of LOC219920 (Accession XM_167787). Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219920. LOC255589 (Accession XM_173060) is another VGAM2129 host target gene. LOC255589 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255589, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255589 BINDING SITE, designated SEQ ID:46314, to the nucleotide sequence of VGAM2129 RNA, herein designated VGAM RNA, also designated SEQ ID:4840.

[73854] Another function of VGAM2129 is therefore inhibition of

LOC255589 (Accession XM_173060). Accordingly, utilities of VGAM2129 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255589. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2130 (VGAM2130) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73855] VGAM2130 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2130 was detected is described hereinabove with reference to Figs. 1-8.

[73856] VGAM2130 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline Herpesvirus 3. VGAM2130 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73857] VGAM2130 gene encodes a VGAM2130 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2130 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2130 precursor RNA is designated SEQ ID:2116, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2116 is located at position 23005 relative to the genome of Ateline Herpesvirus 3.

[73858] VGAM2130 precursor RNA folds onto itself, forming VGAM2130 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73859] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2130 folded precursor RNA into VGAM2130 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2130 RNA is designated SEQ ID:4841, and is provided hereinbelow with reference to the sequence listing part.

[73860] VGAM2130 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2130 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2130 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73861] VGAM2130 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2130 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2130 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2130 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2130 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73862] The complementary binding of VGAM2130 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2130 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2130 host target RNA into VGAM2130 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73863] It is appreciated that VGAM2130 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2130 host target genes. The mRNA of each one of this plurality of VGAM2130 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2130 RNA, herein designated VGAM RNA, and which when bound by VGAM2130 RNA causes inhibition of translation of respective one or more VGAM2130 host target proteins.

[73864] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2130 gene, herein designated VGAM GENE, on one or more VGAM2130 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73865] It is yet further appreciated that a function of VGAM2130

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2130 include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2130 correlate with, and may be deduced from, the identity of the host target genes which VGAM2130 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73866] Nucleotide sequences of the VGAM2130 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2130 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2130 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2130 are further described hereinbelow with reference to Table 1.

[73867] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2130 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2130 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73868] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2130 gene, herein designated VGAM is inhibition of expression of VGAM2130 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2130 correlate with, and may be deduced from, the identity of the target genes which VGAM2130 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73869] Actinin, Alpha 2 (ACTN2, Accession NM_001103) is a VGAM2130 host target gene. ACTN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ACTN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACTN2 BINDING SITE, designated SEQ ID:6755, to the nucleotide sequence of VGAM2130 RNA, herein designated VGAM RNA, also designated SEQ ID:4841.

[73870] A function of VGAM2130 is therefore inhibition of Actinin, Alpha 2 (ACTN2, Accession NM_001103), a gene which an actin-binding protein with multiple roles in different cell types. Accordingly, utilities of VGAM2130 include diagnosis, prevention and treatment of diseases and clinical con-

ditions associated with ACTN2. The function of ACTN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM88.Eukaryotic Translation Initiation Factor 2C, 1 (EIF2C1, Accession NM_012199) is another VGAM2130 host target gene. EIF2C1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF2C1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF2C1 BINDING SITE, designated SEQ ID:14500, to the nucleotide sequence of VGAM2130 RNA, herein designated VGAM RNA, also designated SEQ ID:4841.

[73871] Another function of VGAM2130 is therefore inhibition of Eukaryotic Translation Initiation Factor 2C, 1 (EIF2C1, Accession NM_012199), a gene which plays an important role in the eukaryotic peptide chain initiation process. Accordingly, utilities of VGAM2130 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF2C1. The function of EIF2C1 and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to VGAM118.PRO2000 (Accession NM_014109) is another VGAM2130 host target gene. PRO2000 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2000, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2000 BINDING SITE, designated SEQ ID:15337, to the nucleotide sequence of VGAM2130 RNA, herein designated VGAM RNA, also designated SEQ ID:4841.

[73872] Another function of VGAM2130 is therefore inhibition of PRO2000 (Accession NM_014109). Accordingly, utilities of VGAM2130 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2000. LOC150383 (Accession XM_086905) is another VGAM2130 host target gene. LOC150383 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150383, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC150383 BINDING SITE, designated SEQ ID:38945, to the nucleotide sequence of VGAM2130 RNA, herein designated VGAM RNA, also designated SEQ ID:4841.

[73873] Another function of VGAM2130 is therefore inhibition of LOC150383 (Accession XM_086905). Accordingly, utilities of VGAM2130 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150383. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2131 (VGAM2131) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73874] VGAM2131 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2131 was detected is described hereinabove with reference to Figs. 1-8.

[73875] VGAM2131 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline Herpesvirus 3. VGAM2131 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73876] VGAM2131 gene encodes a VGAM2131 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2131 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2131 precursor RNA is designated SEQ ID:2117, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2117 is located at position 9609 relative to the genome of Ateline Herpesvirus 3.

[73877] VGAM2131 precursor RNA folds onto itself, forming VGAM2131 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73878] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2131 folded precursor RNA into VGAM2131 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2131 RNA is designated SEQ ID:4842, and is provided hereinbelow with reference to the sequence listing part.

[73879] VGAM2131 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2131 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2131 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73880] VGAM2131 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2131 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2131 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2131 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2131 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73881] The complementary binding of VGAM2131 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2131 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2131 host target RNA into VGAM2131 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73882] It is appreciated that VGAM2131 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2131 host target genes. The mRNA of each one of this plurality of VGAM2131 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2131 RNA, herein designated VGAM RNA, and which when bound by VGAM2131 RNA causes inhibition of translation of respective one or more VGAM2131 host target proteins.

[73883] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2131 gene, herein designated VGAM GENE, on one or more VGAM2131 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73884] It is yet further appreciated that a function of VGAM2131 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2131 include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2131 correlate with, and may be deduced from, the identity of the host target genes which VGAM2131 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73885] Nucleotide sequences of the VGAM2131 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2131 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2131 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2131 are further described hereinbelow with reference to Table 1.

[73886] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2131 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2131 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73887] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2131 gene, herein designated VGAM is inhibition of expression of VGAM2131 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2131 correlate with, and may be deduced from, the identity of the target genes which VGAM2131 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73888] Adrenergic, Beta, Receptor Kinase 2 (ADRBK2, Accession NM_005160) is a VGAM2131 host target gene. ADRBK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADRBK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADRBK2 BINDING SITE, designated SEQ ID:11642, to the nucleotide sequence of VGAM2131 RNA, herein designated VGAM RNA, also designated SEQ ID:4842.

[73889] A function of VGAM2131 is therefore inhibition of Adrenergic, Beta, Receptor Kinase 2 (ADRBK2, Accession NM_005160), a gene which regulates desensitization of G protein-coupled receptors. Accordingly, utilities of VGAM2131 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADRBK2. The function of ADRBK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM806.TRAM (Accession NM_014294) is another VGAM2131 host target gene. TRAM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRAM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRAM BINDING SITE, designated SEQ ID:15589, to the nucleotide sequence of VGAM2131 RNA, herein designated VGAM RNA, also designated SEQ ID:4842.

[73890] Another function of VGAM2131 is therefore inhibition of TRAM (Accession NM_014294). Accordingly, utilities of VGAM2131 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAM.

Coenzyme Q7 Homolog, Ubiquinone (yeast) (COQ7, Accession NM_016138) is another VGAM2131 host target gene. COQ7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COQ7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COQ7 BINDING SITE, designated SEQ ID:18221, to the nucleotide sequence of VGAM2131 RNA, herein designated VGAM RNA, also designated SEQ ID:4842.

[73891] Another function of VGAM2131 is therefore inhibition of Coenzyme Q7 Homolog, Ubiquinone (yeast) (COQ7, Accession NM_016138). Accordingly, utilities of VGAM2131 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COQ7. FLJ22965 (Accession NM_022101) is another VGAM2131 host target gene. FLJ22965 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22965, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22965 BINDING SITE, designated SEQ ID:22642, to the nucleotide sequence of VGAM2131

RNA, herein designated VGAM RNA, also designated SEQ ID:4842.

[73892] Another function of VGAM2131 is therefore inhibition of FLJ22965 (Accession NM_022101). Accordingly, utilities of VGAM2131 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22965. SMOC1 (Accession NM_022137) is another VGAM2131 host target gene. SMOC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMOC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMOC1 BINDING SITE, designated SEQ ID:22697, to the nucleotide sequence of VGAM2131 RNA, herein designated VGAM RNA, also designated SEQ ID:4842.

[73893] Another function of VGAM2131 is therefore inhibition of SMOC1 (Accession NM_022137). Accordingly, utilities of VGAM2131 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMOC1. LOC155072 (Accession XM_098661) is another VGAM2131 host target gene. LOC155072 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC155072, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155072 BINDING SITE, designated SEQ ID:41758, to the nucleotide sequence of VGAM2131 RNA, herein designated VGAM RNA, also designated SEQ ID:4842.

[73894] Another function of VGAM2131 is therefore inhibition of LOC155072 (Accession XM_098661). Accordingly, utilities of VGAM2131 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155072. LOC202868 (Accession XM_117477) is another VGAM2131 host target gene. LOC202868 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202868, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202868 BINDING SITE, designated SEQ ID:43445, to the nucleotide sequence of VGAM2131 RNA, herein designated VGAM RNA, also designated SEQ ID:4842.

[73895] Another function of VGAM2131 is therefore inhibition of LOC202868 (Accession XM_117477). Accordingly, utilities

of VGAM2131 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202868. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2132 (VGAM2132) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73896] VGAM2132 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2132 was detected is described hereinabove with reference to Figs. 1-8.

[73897] VGAM2132 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline Herpesvirus 3. VGAM2132 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73898] VGAM2132 gene encodes a VGAM2132 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2132 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2132 precursor RNA is designated SEQ ID:2118, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2118 is located at position 17602 relative to the genome of Ateline Herpesvirus 3.

[73899] VGAM2132 precursor RNA folds onto itself, forming VGAM2132 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73900] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2132 folded precursor RNA into VGAM2132 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2132 RNA is designated SEQ ID:4843, and

is provided hereinbelow with reference to the sequence listing part.

[73901] VGAM2132 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2132 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2132 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73902] VGAM2132 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2132 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2132 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2132 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2132 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73903] The complementary binding of VGAM2132 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2132 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2132 host target RNA into VGAM2132 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73904] It is appreciated that VGAM2132 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2132 host target genes. The mRNA of each one of this plurality of VGAM2132 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2132 RNA, herein designated VGAM RNA, and which when bound by VGAM2132 RNA causes inhibition of translation of respective one or more VGAM2132 host target proteins.

[73905] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2132 gene, herein designated VGAM GENE, on one or more VGAM2132 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73906] It is yet further appreciated that a function of VGAM2132 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2132 include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2132 correlate with, and may be deduced from, the identity of the host target genes which VGAM2132 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73907] Nucleotide sequences of the VGAM2132 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2132 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2132 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2132 are further described hereinbelow with reference to Table 1.

[73908] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2132 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2132 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73909] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2132 gene, herein designated VGAM is inhibition of expression of VGAM2132 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2132 correlate with, and may be deduced from, the identity of the target genes which VGAM2132 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73910] Mel Transforming Oncogene (derived from cell line NK14)- RAB8 Homolog (MEL, Accession NM_005370) is a VGAM2132 host target gene. MEL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEL BINDING SITE, designated SEQ ID:11846, to the nucleotide sequence of VGAM2132 RNA, herein designated VGAM RNA, also designated SEQ ID:4843.

[73911] A function of VGAM2132 is therefore inhibition of Mel Transforming Oncogene (derived from cell line NK14)-RAB8 Homolog (MEL, Accession NM_005370), a gene which may be involved in vesicular trafficking and neurotransmitter release. Accordingly, utilities of VGAM2132

include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEL. The function of MEL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM40.Multiple Endocrine Neoplasia I (MEN1, Accession NM_130799) is another VGAM2132 host target gene. MEN1 BINDING SITE1 through MEN1 BINDING SITE7 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MEN1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEN1 BINDING SITE1 through MEN1 BINDING SITE7, designated SEQ ID:28288, SEQ ID:28290, SEQ ID:28292, SEQ ID:28294, SEQ ID:28297, SEQ ID:28301 and SEQ ID:5774 respectively, to the nucleotide sequence of VGAM2132 RNA, herein designated VGAM RNA, also designated SEQ ID:4843.

[73912] Another function of VGAM2132 is therefore inhibition of Multiple Endocrine Neoplasia I (MEN1, Accession NM_130799). Accordingly, utilities of VGAM2132 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEN1. LOC115795

(Accession XM_056738) is another VGAM2132 host target gene. LOC115795 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC115795, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115795 BINDING SITE, designated SEQ ID:36418, to the nucleotide sequence of VGAM2132 RNA, herein designated VGAM RNA, also designated SEQ ID:4843.

[73913] Another function of VGAM2132 is therefore inhibition of LOC115795 (Accession XM_056738). Accordingly, utilities of VGAM2132 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115795. LOC130813 (Accession XM_065904) is another VGAM2132 host target gene. LOC130813 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC130813, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130813 BINDING SITE, designated SEQ ID:37315, to the nucleotide sequence of VGAM2132 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4843.

[73914] Another function of VGAM2132 is therefore inhibition of LOC130813 (Accession XM_065904). Accordingly, utilities of VGAM2132 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130813. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2133 (VGAM2133) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73915] VGAM2133 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2133 was detected is described hereinabove with reference to Figs. 1-8.

[73916] VGAM2133 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline Herpesvirus 3. VGAM2133 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73917] VGAM2133 gene encodes a VGAM2133 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2133 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2133 precursor RNA is designated SEQ ID:2119, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2119 is located at position 4296 relative to the genome of Ateline Herpesvirus 3.

[73918] VGAM2133 precursor RNA folds onto itself, forming VGAM2133 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73919] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2133 folded precursor RNA into VGAM2133 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2133 RNA is designated SEQ ID:4844, and is provided hereinbelow with reference to the sequence listing part.

[73920] VGAM2133 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2133 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2133 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73921] VGAM2133 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2133 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2133 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2133 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2133 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73922] The complementary binding of VGAM2133 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2133 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2133 host target RNA into VGAM2133 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73923] It is appreciated that VGAM2133 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2133 host target genes. The mRNA of

each one of this plurality of VGAM2133 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2133 RNA, herein designated VGAM RNA, and which when bound by VGAM2133 RNA causes inhibition of translation of respective one or more VGAM2133 host target proteins.

[73924] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2133 gene, herein designated VGAM GENE, on one or more VGAM2133 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[73925] It is yet further appreciated that a function of VGAM2133 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2133 correlate with, and may be deduced from, the identity of the host target genes which VGAM2133 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73926] Nucleotide sequences of the VGAM2133 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2133 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2133 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2133 are further described hereinbelow with reference to Table 1.

[73927] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2133 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2133 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73928] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2133 gene, herein designated VGAM is inhibition of expression of VGAM2133 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2133 correlate with, and may be deduced from, the identity of the target genes which VGAM2133 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73929] Adaptor-related Protein Complex 2, Beta 1 Subunit (AP2B1, Accession NM_001282) is a VGAM2133 host target gene. AP2B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP2B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP2B1 BINDING SITE, designated SEQ ID:6949, to the nucleotide sequence of VGAM2133 RNA, herein designated VGAM RNA, also designated SEQ ID:4844.

[73930] A function of VGAM2133 is therefore inhibition of Adaptor-related Protein Complex 2, Beta 1 Subunit (AP2B1, Ac-

cession NM_001282), a gene which links clathrin to receptors in coated vesicles. Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP2B1. The function of AP2B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1126.B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898) is another VGAM2133 host target gene. BCL11B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL11B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL11B BINDING SITE, designated SEQ ID:23161, to the nucleotide sequence of VGAM2133 RNA, herein designated VGAM RNA, also designated SEQ ID:4844.

[73931] Another function of VGAM2133 is therefore inhibition of B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898). Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

BCL11B. Cytochrome P450, Subfamily XIX (aromatization of androgens) (CYP19, Accession NM_031226) is another VGAM2133 host target gene. CYP19 BINDING SITE1 and CYP19 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CYP19, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP19 BINDING SITE1 and CYP19 BINDING SITE2, designated SEQ ID:25270 and SEQ ID:5560 respectively, to the nucleotide sequence of VGAM2133 RNA, herein designated VGAM RNA, also designated SEQ ID:4844.

[73932] Another function of VGAM2133 is therefore inhibition of Cytochrome P450, Subfamily XIX (aromatization of androgens) (CYP19, Accession NM_031226), a gene which catalyzes the last steps of estrogen biosynthesis. Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP19. The function of CYP19 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM508.VAMP

(vesicle-associated membrane protein)-associated Protein B and C (VAPB, Accession NM_004738) is another VGAM2133 host target gene. VAPB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VAPB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VAPB BINDING SITE, designated SEQ ID:11131, to the nucleotide sequence of VGAM2133 RNA, herein designated VGAM RNA, also designated SEQ ID:4844.

[73933] Another function of VGAM2133 is therefore inhibition of VAMP (vesicle-associated membrane protein)-associated Protein B and C (VAPB, Accession NM_004738). Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VAPB. Chromosome 21 Open Reading Frame 25 (C21orf25, Accession XM_032945) is another VGAM2133 host target gene. C21orf25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C21orf25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of C21orf25 BINDING SITE, designated SEQ ID:31799, to the nucleotide sequence of VGAM2133 RNA, herein designated VGAM RNA, also designated SEQ ID:4844.

[73934] Another function of VGAM2133 is therefore inhibition of Chromosome 21 Open Reading Frame 25 (C21orf25, Accession XM_032945). Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf25. FLJ14735 (Accession NM_032832) is another VGAM2133 host target gene. FLJ14735 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14735, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14735 BINDING SITE, designated SEQ ID:26608, to the nucleotide sequence of VGAM2133 RNA, herein designated VGAM RNA, also designated SEQ ID:4844.

[73935] Another function of VGAM2133 is therefore inhibition of FLJ14735 (Accession NM_032832). Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ14735. Methyl-CpG Binding Domain Protein 2 (MBD2, Accession NM_015832) is another VGAM2133 host target gene. MBD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MBD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MBD2 BINDING SITE, designated SEQ ID:17944, to the nucleotide sequence of VGAM2133 RNA, herein designated VGAM RNA, also designated SEQ ID:4844.

[73936] Another function of VGAM2133 is therefore inhibition of Methyl-CpG Binding Domain Protein 2 (MBD2, Accession NM_015832). Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBD2. MGC21738 (Accession NM_145044) is another VGAM2133 host target gene. MGC21738 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC21738, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC21738 BINDING SITE, designated SEQ ID:29676, to the nucleotide sequence of

VGAM2133 RNA, herein designated VGAM RNA, also designated SEQ ID:4844.

[73937] Another function of VGAM2133 is therefore inhibition of MGC21738 (Accession NM_145044). Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21738. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 1A (PPP1R1A, Accession NM_006741) is another VGAM2133 host target gene. PPP1R1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R1A BINDING SITE, designated SEQ ID:13590, to the nucleotide sequence of VGAM2133 RNA, herein designated VGAM RNA, also designated SEQ ID:4844.

[73938] Another function of VGAM2133 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 1A (PPP1R1A, Accession NM_006741). Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R1A. LOC203248 (Accession XM_114659) is another

VGAM2133 host target gene. LOC203248 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203248, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203248 BINDING SITE, designated SEQ ID:43016, to the nucleotide sequence of VGAM2133 RNA, herein designated VGAM RNA, also designated SEQ ID:4844.

[73939] Another function of VGAM2133 is therefore inhibition of LOC203248 (Accession XM_114659). Accordingly, utilities of VGAM2133 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203248. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2134 (VGAM2134) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73940] VGAM2134 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2134 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[73941] VGAM2134 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline Herpesvirus 3. VGAM2134 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73942] VGAM2134 gene encodes a VGAM2134 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2134 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2134 precursor RNA is designated SEQ ID:2120, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2120 is located at position 20245 relative to the genome of Ateline Herpesvirus 3.

[73943] VGAM2134 precursor RNA folds onto itself, forming VGAM2134 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73944] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2134 folded precursor RNA into VGAM2134 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM2134 RNA is designated SEQ ID:4845, and is provided hereinbelow with reference to the sequence listing part.

[73945] VGAM2134 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2134 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2134 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73946] VGAM2134 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2134 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2134 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2134 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2134 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73947] The complementary binding of VGAM2134 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2134 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2134 host target RNA into VGAM2134 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73948] It is appreciated that VGAM2134 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2134 host target genes. The mRNA of each one of this plurality of VGAM2134 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2134 RNA, herein designated VGAM RNA, and which when bound by VGAM2134 RNA causes inhibition of translation of respective one or more VGAM2134 host target proteins.

[73949] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2134 gene, herein designated VGAM GENE, on one or more VGAM2134 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73950] It is yet further appreciated that a function of VGAM2134 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2134 correlate with, and may be deduced from, the identity of the host target genes which VGAM2134 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73951] Nucleotide sequences of the VGAM2134 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2134 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2134 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2134 are further described hereinbelow with reference to Table 1.

[73952] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2134 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2134 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73953] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2134 gene, herein designated VGAM is inhibition of expression of VGAM2134 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2134 correlate with, and may be deduced from, the identity of the target genes which VGAM2134 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73954] Catenin (cadherin-associated protein), Alpha 1, 102kDa (CTNNA1, Accession XM_038221) is a VGAM2134 host target gene. CTNNA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CTNNA1, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTNNA1 BINDING SITE, designated SEQ ID:32785, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73955] A function of VGAM2134 is therefore inhibition of Catenin (cadherin-associated protein), Alpha 1, 102kDa (CTNNA1, Accession XM_038221), a gene which is a transmembrane glycoprotein responsible for physical connection of epithelial cells. Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTNNA1. The function of CTNNA1 has been established by previous studies. E-cadherin is a transmembrane glycoprotein responsible for physical connection of epithelial cells through Ca(2+)-binding regions in its extracellular domain. E-cadherin-mediated cell-cell adhesion is effected by 3 cytoplasmic proteins known as catenins alpha, beta (see OMIM Ref. No. 116806), and gamma. These catenins are thought to work as connectors that anchor the E-cadherin to the cytoskeletal actin bundle through the cadherin cytoplasmic domain. Dysfunction of this adhesion complex

causes dissociation of cancer cells from primary tumor nodules, thus possibly contributing to cancer invasion and metastasis. Herrenknecht et al. (1991) and Nagafuchi et al. (1991) isolated a murine cDNA encoding the 102-kD alpha-catenin (OMIM Ref. No. CAP102). Oda et al. (1993) cloned and sequenced human alpha-catenin. They found that it shows extensive homology with that of the mouse. Hirano et al. (1992) and Shimoyama et al. (1992) showed that a human lung cancer cell line, PC9, which expresses E-cadherin but only a small quantity of abnormal-sized alpha-catenin, grew initially as isolated cells and then re-gained its cell-cell adhesion potential when transfected with alpha-catenin. Oda et al. (1993) found 2 abnormal mRNA sequences of alpha-catenin in PC9; one was a 957-bp deletion resulting in a 319-amino acid deletion and another was a 761-bp deletion resulting in a frameshift. The deletions were thought to be responsible for the loss of alpha-catenin expression. Vasioukhin et al. (2001) examined the consequences of alpha-catenin protein ablation in otherwise normal newborn mice. When surface epithelium alpha-catenin was ablated, hair follicle development was blocked and epidermal morphogenesis was dramatically affected, with defects in adherens junc-

tion formation, intercellular adhesion, and epithelial polarity. Differentiation occurred, but epidermis displayed hyperproliferation, suprabasal mitoses, and multinucleated cells. In vitro, alpha-catenin null keratinocytes were poorly contact inhibited and grew rapidly. These differences were not dependent upon intercellular adhesion and were in marked contrast to keratinocytes conditionally null for another essential intercellular adhesion protein, desmoplakin (DSP; 125647). Knockout keratinocytes exhibited sustained activation of the Ras-MAPK cascade due to aberrations in growth factor responses. The authors concluded that features of precancerous lesions often attributed to defects in cell cycle regulatory genes can be generated by compromising the function of alpha-catenin

[73956] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[73957] Oda, T.; Kanai, Y.; Shimoyama, Y.; Nagafuchi, A.; Tsukita, S.; Hirohashi, S. : Cloning of the human alpha-catenin cDNA and its aberrant mRNA in a human cancer cell line. Biochem. Biophys. Res. Commun. 193: 897-904, 1993. ; and

[73958] Vasioukhin, V.; Bauer, C.; Degenstein, L.; Wise, B.; Fuchs,

E. : Hyperproliferation and defects in epithelial polarity upon conditional ablation of alpha-catenin in skin. Cell 104: 605-.

[73959] Further studies establishing the function and utilities of CTNNA1 are found in John Hopkins OMIM database record ID 116805, and in sited publications numbered 2025, 1072 and 11656-2033 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Leucine-rich, Glioma Inactivated 1 (LGI1, Accession NM_005097) is another VGAM2134 host target gene. LGI1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LGI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LGI1 BINDING SITE, designated SEQ ID:11564, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73960] Another function of VGAM2134 is therefore inhibition of Leucine-rich, Glioma Inactivated 1 (LGI1, Accession NM_005097). Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LGI1. Regulator of G-

protein Signalling 16 (RGS16, Accession NM_002928) is another VGAM2134 host target gene. RGS16 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RGS16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RGS16 BINDING SITE, designated SEQ ID:8834, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73961] Another function of VGAM2134 is therefore inhibition of Regulator of G-protein Signalling 16 (RGS16, Accession NM_002928), a gene which inhibits signal transduction. Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS16. The function of RGS16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1843.Formin Homology 2 Domain Containing 2 (FHOD2, Accession XM_057927) is another VGAM2134 host target gene. FHOD2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

FHOD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FHOD2 BINDING SITE, designated SEQ ID:36553, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73962] Another function of VGAM2134 is therefore inhibition of Formin Homology 2 Domain Containing 2 (FHOD2, Accession XM_057927). Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHOD2. FLJ12409 (Accession NM_025105) is another VGAM2134 host target gene. FLJ12409 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12409, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12409 BINDING SITE, designated SEQ ID:24754, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73963] Another function of VGAM2134 is therefore inhibition of

FLJ12409 (Accession NM_025105). Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12409. FLJ20445 (Accession NM_017824) is another VGAM2134 host target gene. FLJ20445 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20445 BINDING SITE, designated SEQ ID:19482, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73964] Another function of VGAM2134 is therefore inhibition of FLJ20445 (Accession NM_017824). Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20445. FLJ20739 (Accession XM_042197) is another VGAM2134 host target gene. FLJ20739 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20739, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ20739 BINDING SITE, designated SEQ ID:33705, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73965] Another function of VGAM2134 is therefore inhibition of FLJ20739 (Accession XM_042197). Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20739. FLJ30567 (Accession NM_145022) is another VGAM2134 host target gene. FLJ30567 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ30567, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ30567 BINDING SITE, designated SEQ ID:29630, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73966] Another function of VGAM2134 is therefore inhibition of FLJ30567 (Accession NM_145022). Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30567. KIAA0266 (Accession NM_021645) is another

VGAM2134 host target gene. KIAA0266 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0266 BINDING SITE, designated SEQ ID:22311, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73967] Another function of VGAM2134 is therefore inhibition of KIAA0266 (Accession NM_021645). Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0266. KIAA1336 (Accession XM_051306) is another VGAM2134 host target gene. KIAA1336 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1336, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1336 BINDING SITE, designated SEQ ID:35804, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73968] Another function of VGAM2134 is therefore inhibition of KIAA1336 (Accession XM_051306). Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1336. SKIP (Accession NM_130766) is another VGAM2134 host target gene. SKIP BINDING SITE1 and SKIP BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SKIP, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SKIP BINDING SITE1 and SKIP BINDING SITE2, designated SEQ ID:28265 and SEQ ID:18601 respectively, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73969] Another function of VGAM2134 is therefore inhibition of SKIP (Accession NM_130766). Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SKIP. LOC144231 (Accession XM_096561) is another VGAM2134 host target gene. LOC144231 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144231, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144231 BINDING SITE, designated SEQ ID:40394, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73970] Another function of VGAM2134 is therefore inhibition of LOC144231 (Accession XM_096561). Accordingly, utilities of VGAM2134 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144231. LOC154215 (Accession XM_087875) is another VGAM2134 host target gene. LOC154215 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154215, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154215 BINDING SITE, designated SEQ ID:39464, to the nucleotide sequence of VGAM2134 RNA, herein designated VGAM RNA, also designated SEQ ID:4845.

[73971] Another function of VGAM2134 is therefore inhibition of LOC154215 (Accession XM_087875). Accordingly, utilities of VGAM2134 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC154215. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2135 (VGAM2135) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[73972] VGAM2135 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2135 was detected is described hereinabove with reference to Figs. 1-8.

[73973] VGAM2135 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ateline Herpesvirus 3. VGAM2135 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73974] VGAM2135 gene encodes a VGAM2135 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2135 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2135 precursor RNA is desig-

nated SEQ ID:2121, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2121 is located at position 17990 relative to the genome of Ateline Herpesvirus 3.

[73975] VGAM2135 precursor RNA folds onto itself, forming VGAM2135 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73976] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2135 folded precursor RNA into VGAM2135 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2135 RNA is designated SEQ ID:4846, and is provided hereinbelow with reference to the sequence

listing part.

[73977] VGAM2135 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2135 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2135 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73978] VGAM2135 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2135 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2135 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2135 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2135 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[73979] The complementary binding of VGAM2135 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2135 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2135 host target RNA into VGAM2135 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73980] It is appreciated that VGAM2135 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2135 host target genes. The mRNA of each one of this plurality of VGAM2135 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2135 RNA, herein designated VGAM

RNA, and which when bound by VGAM2135 RNA causes inhibition of translation of respective one or more VGAM2135 host target proteins.

[73981] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2135 gene, herein designated VGAM GENE, on one or more VGAM2135 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[73982] It is yet further appreciated that a function of VGAM2135 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2135 include diagnosis, prevention and treatment of viral infection by Ateline Herpesvirus 3. Specific functions, and accordingly utilities, of VGAM2135 correlate with, and may be deduced from, the identity of the host target genes which VGAM2135 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[73983] Nucleotide sequences of the VGAM2135 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2135 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2135 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2135 are further described hereinbelow with reference to Table 1.

[73984] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2135 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2135 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[73985] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2135 gene, herein designated VGAM is

inhibition of expression of VGAM2135 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2135 correlate with, and may be deduced from, the identity of the target genes which VGAM2135 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[73986] Brain-specific Angiogenesis Inhibitor 3 (BAI3, Accession NM_001704) is a VGAM2135 host target gene. BAI3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAI3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAI3 BINDING SITE, designated SEQ ID:7427, to the nucleotide sequence of VGAM2135 RNA, herein designated VGAM RNA, also designated SEQ ID:4846.

[73987] A function of VGAM2135 is therefore inhibition of Brain-specific Angiogenesis Inhibitor 3 (BAI3, Accession NM_001704). Accordingly, utilities of VGAM2135 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAI3. KIAA0210 (Accession NM_014744) is another VGAM2135 host target gene. KIAA0210 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by KIAA0210, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0210 BINDING SITE, designated SEQ ID:16424, to the nucleotide sequence of VGAM2135 RNA, herein designated VGAM RNA, also designated SEQ ID:4846.

[73988] Another function of VGAM2135 is therefore inhibition of KIAA0210 (Accession NM_014744). Accordingly, utilities of VGAM2135 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0210. KIAA1204 (Accession XM_045011) is another VGAM2135 host target gene. KIAA1204 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1204, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1204 BINDING SITE, designated SEQ ID:34311, to the nucleotide sequence of VGAM2135 RNA, herein designated VGAM RNA, also designated SEQ ID:4846.

[73989] Another function of VGAM2135 is therefore inhibition of

KIAA1204 (Accession XM_045011). Accordingly, utilities of VGAM2135 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1204. LOC219988 (Accession XM_166223) is another VGAM2135 host target gene. LOC219988 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219988, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219988 BINDING SITE, designated SEQ ID:44045, to the nucleotide sequence of VGAM2135 RNA, herein designated VGAM RNA, also designated SEQ ID:4846.

[73990] Another function of VGAM2135 is therefore inhibition of LOC219988 (Accession XM_166223). Accordingly, utilities of VGAM2135 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219988. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2136 (VGAM2136) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[73991] VGAM2136 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2136 was detected is described hereinabove with reference to Figs. 1-8.

[73992] VGAM2136 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2136 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[73993] VGAM2136 gene encodes a VGAM2136 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2136 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2136 precursor RNA is designated SEQ ID:2122, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2122 is located at position 176642 relative to the genome of Ectromelia Virus.

[73994] VGAM2136 precursor RNA folds onto itself, forming VGAM2136 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[73995] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2136 folded precursor RNA into VGAM2136 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of VGAM2136 RNA is designated SEQ ID:4847, and is provided hereinbelow with reference to the sequence listing part.

[73996] VGAM2136 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2136 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2136 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[73997] VGAM2136 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2136 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2136 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2136 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2136 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[73998] The complementary binding of VGAM2136 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2136 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2136 host target RNA into VGAM2136 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[73999] It is appreciated that VGAM2136 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2136 host target genes. The mRNA of each one of this plurality of VGAM2136 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2136 RNA, herein designated VGAM RNA, and which when bound by VGAM2136 RNA causes inhibition of translation of respective one or more VGAM2136 host target proteins.

[74000] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2136 gene, herein designated VGAM GENE, on one

or more VGAM2136 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74001] It is yet further appreciated that a function of VGAM2136 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2136 correlate with, and may be deduced from, the identity of the host target genes which VGAM2136 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74002] Nucleotide sequences of the VGAM2136 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2136 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2136 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2136 are further described hereinbelow with reference to Table 1.

[74003] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2136 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2136 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74004] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2136 gene, herein designated VGAM is inhibition of expression of VGAM2136 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2136 correlate with, and may be deduced from, the identity of the target genes which VGAM2136 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74005] ADP-ribosyltransferase (NAD+; poly (ADP-ribose) Poly-

merase) (ADPRT, Accession NM_001618) is a VGAM2136 host target gene. ADPRT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADPRT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADPRT BINDING SITE, designated SEQ ID:7327, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74006] A function of VGAM2136 is therefore inhibition of ADP-ribosyltransferase (NAD+; poly (ADP-ribose) Polymerase) (ADPRT, Accession NM_001618), a gene which catalyzes addition of mono-ADP-ribose to arginine residues of proteins, inhibits Pol II transcription. Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADPRT. The function of ADPRT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM506.Cadherin 19, Type 2 (CDH19, Accession NM_021153) is another VGAM2136 host target gene. CDH19 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by CDH19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDH19 BINDING SITE, designated SEQ ID:22127, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74007] Another function of VGAM2136 is therefore inhibition of Cadherin 19, Type 2 (CDH19, Accession NM_021153), a gene which is a calcium dependent cell adhesion protein. Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH19. The function of CDH19 has been established by previous studies. In EST database searches for cadherin sequences, Kools et al. (2000) identified a partial CDH19 cDNA, which they called CDH7L2. CDH19 encodes a 772-amino acid protein predicted to contain 5 EC (extracellular calcium-binding) repeats, a transmembrane domain, and a cytoplasmic tail. Kools et al. (2000) classified CDH19 as an atypical (type II) cadherin due to the lack of the HAV cell adhesion recognition sequence specific for classic cadherins. CDH19 was previ-

ously identified and named CDH7 by Kremmidiotis et al. (1998); however, phylogenetic analysis carried out by Kools et al. (2000) led to nomenclature corrections within the cadherin gene family. CDH19 shares significant homology with chicken Cdh7, but Kools et al. (2000) identified the newly designated CDH7 gene (OMIM Ref. No. 605806) as the likely human ortholog of chicken Cdh7. Using RT-PCR analysis, Kools et al. (2000) detected CDH19 expression in all tissues tested, with the exception of uterus. By somatic cell hybrid analysis and fluorescence in situ hybridization, Kremmidiotis et al. (1998) mapped the human CDH19 gene to chromosome 18q22-q23. Using the same methods, Kools et al. (2000) mapped the CDH19 gene to the same location in a cluster with CDH7 (OMIM Ref. No. 605806) and CDH20 (OMIM Ref. No. 605807).

[74008] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74009] Kools, P.; Van Imschoot, G.; van Roy, F. : Characterization of three novel human cadherin genes (CDH7, CDH19, and CDH20) clustered on chromosome 18q22-q23 and with high homology to chicken cadherin-7. Genomics 68:

283-295, 2000. ; and

[74010] Kremmidiotis, G.; Baker, E.; Crawford, J.; Eyre, H. J.; Nahmias, J.; Callen, D. F. : Localization of human cadherin genes to chromosome regions exhibiting cancer-related loss of hetero.

[74011] Further studies establishing the function and utilities of CDH19 are found in John Hopkins OMIM database record ID 603016, and in sited publications numbered 801 and 11646 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Cytochrome B-245, Beta Polypeptide (chronic granulomatous disease) (CYBB, Accession XM_084288) is another VGAM2136 host target gene. CYBB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYBB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYBB BINDING SITE, designated SEQ ID:37537, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74012] Another function of VGAM2136 is therefore inhibition of Cytochrome B-245, Beta Polypeptide (chronic granuloma-

tous disease) (CYBB, Accession XM_084288). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYBB. Damage-specific DNA Binding Protein 1, 127kDa (DDB1, Accession NM_001923) is another VGAM2136 host target gene. DDB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DDB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDB1 BINDING SITE, designated SEQ ID:7640, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74013] Another function of VGAM2136 is therefore inhibition of Damage-specific DNA Binding Protein 1, 127kDa (DDB1, Accession NM_001923). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDB1. Glucose-6-phosphatase, Catalytic (glycogen storage disease type I, von Gierke disease) (G6PC, Accession NM_000151) is another VGAM2136 host target gene. G6PC BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by G6PC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of G6PC BINDING SITE, designated SEQ ID:5657, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74014] Another function of VGAM2136 is therefore inhibition of Glucose-6-phosphatase, Catalytic (glycogen storage disease type I, von Gierke disease) (G6PC, Accession NM_000151). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G6PC. Lysozyme (renal amyloidosis) (LYZ, Accession NM_000239) is another VGAM2136 host target gene. LYZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LYZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LYZ BINDING SITE, designated SEQ ID:5758, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74015] Another function of VGAM2136 is therefore inhibition of Lysozyme (renal amyloidosis) (LYZ, Accession NM_000239), a gene which a bacteriolytic enzyme. Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LYZ. The function of LYZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM929.Mannosidase, Alpha, Class 2A, Member 1 (MAN2A1, Accession NM_002372) is another VGAM2136 host target gene. MAN2A1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAN2A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAN2A1 BINDING SITE, designated SEQ ID:8177, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74016] Another function of VGAM2136 is therefore inhibition of Mannosidase, Alpha, Class 2A, Member 1 (MAN2A1, Accession NM_002372), a gene which catalyzes the final hydrolytic step in the asparagine-linked oligosaccharide

(N-glycan) maturation pathway. Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAN2A1. The function of MAN2A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1410.Mel Transforming Oncogene (derived from cell line NK14)- RAB8 Homolog (MEL, Accession NM_005370) is another VGAM2136 host target gene. MEL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEL BINDING SITE, designated SEQ ID:11843, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74017] Another function of VGAM2136 is therefore inhibition of Mel Transforming Oncogene (derived from cell line NK14)- RAB8 Homolog (MEL, Accession NM_005370), a gene which may be involved in vesicular trafficking and neurotransmitter release. Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MEL. The function of MEL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM40.Oxidation Resistance 1 (OXR1, Accession NM_018002) is another VGAM2136 host target gene. OXR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OXR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OXR1 BINDING SITE, designated SEQ ID:19733, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74018] Another function of VGAM2136 is therefore inhibition of Oxidation Resistance 1 (OXR1, Accession NM_018002). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OXR1. Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 3 (p55, gamma) (PIK3R3, Accession XM_027982) is another VGAM2136 host target gene. PIK3R3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

PIK3R3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIK3R3 BINDING SITE, designated SEQ ID:30608, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74019] Another function of VGAM2136 is therefore inhibition of Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 3 (p55, gamma) (PIK3R3, Accession XM_027982). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3R3. Proteasome (prosome, macropain) Activator Subunit 3 (PA28 gamma; Ki) (PSME3, Accession NM_005789) is another VGAM2136 host target gene. PSME3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSME3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSME3 BINDING SITE, designated SEQ ID:12372, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ

ID:4847.

[74020] Another function of VGAM2136 is therefore inhibition of Proteasome (prosome, macropain) Activator Subunit 3 (PA28 gamma; Ki) (PSME3, Accession NM_005789), a gene which is the activator subunit of the proteasome (prosome macropain). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSME3. The function of PSME3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1498.RNA Binding Motif Protein 8A (RBM8A, Accession NM_005105) is another VGAM2136 host target gene. RBM8A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBM8A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBM8A BINDING SITE, designated SEQ ID:11579, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74021] Another function of VGAM2136 is therefore inhibition of

RNA Binding Motif Protein 8A (RBM8A, Accession NM_005105), a gene which involves in the pathway of gene expression postsplicing nuclear preexport mRNPs, and newly exported cytoplasmic mRNPs. Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBM8A. The function of RBM8A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1864.SET Binding Factor 1 (SBF1, Accession XM_037447) is another VGAM2136 host target gene. SBF1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SBF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SBF1 BINDING SITE, designated SEQ ID:32626, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74022] Another function of VGAM2136 is therefore inhibition of SET Binding Factor 1 (SBF1, Accession XM_037447), a gene which is of unknown function, could be a tyrosine-phosphatase. Accordingly, utilities of VGAM2136 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with SBF1. The function of SBF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1452.Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 9 (SERPINB9, Accession NM_004155) is another VGAM2136 host target gene. SERPINB9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SERPINB9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERPINB9 BINDING SITE, designated SEQ ID:10359, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74023] Another function of VGAM2136 is therefore inhibition of Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 9 (SERPINB9, Accession NM_004155), a gene which may be a serpin serine protease inhibitor that interacts with granzyme B (GZMB). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with SERPINB9. The function of SERPINB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM60.TIRAP (Accession NM_052887) is another VGAM2136 host target gene. TIRAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIRAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIRAP BINDING SITE, designated SEQ ID:27478, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74024] Another function of VGAM2136 is therefore inhibition of TIRAP (Accession NM_052887), a gene which is a adapter involved in theTLR4 signaling pathway in the innate immune response. Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIRAP. The function of TIRAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM189.Thymidine Kinase 1, Soluble (TK1, Accession

NM_003258) is another VGAM2136 host target gene. TK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TK1 BINDING SITE, designated SEQ ID:9271, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74025] Another function of VGAM2136 is therefore inhibition of Thymidine Kinase 1, Soluble (TK1, Accession NM_003258). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TK1. Transient Receptor Potential Cation Channel, Subfamily V, Member 1 (TRPV1, Accession NM_080704) is another VGAM2136 host target gene. TRPV1 BINDING SITE1 through TRPV1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TRPV1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 through TRPV1 BINDING SITE4, designated SEQ

ID:27992, SEQ ID:28000, SEQ ID:28008 and SEQ ID:20812 respectively, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74026] Another function of VGAM2136 is therefore inhibition of Transient Receptor Potential Cation Channel, Subfamily V, Member 1 (TRPV1, Accession NM_080704), a gene which functions as a receptor for capsaicin. Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1. The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM146.Chromosome 1 Open Reading Frame 19 (C1orf19, Accession XM_042962) is another VGAM2136 host target gene. C1orf19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf19 BINDING SITE, designated SEQ ID:33839, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM

RNA, also designated SEQ ID:4847.

[74027] Another function of VGAM2136 is therefore inhibition of Chromosome 1 Open Reading Frame 19 (C1orf19, Accession XM_042962). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf19. CCR4-NOT Transcription Complex, Subunit 7 (CNOT7, Accession NM_013354) is another VGAM2136 host target gene. CNOT7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNOT7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNOT7 BINDING SITE, designated SEQ ID:15003, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74028] Another function of VGAM2136 is therefore inhibition of CCR4-NOT Transcription Complex, Subunit 7 (CNOT7, Accession NM_013354). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNOT7. COP9 Constitutive Photomorphogenic Homolog Subunit

7A (Arabidopsis) (COPS7A, Accession NM_016319) is another VGAM2136 host target gene. COPS7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COPS7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COPS7A BINDING SITE, designated SEQ ID:18436, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74029] Another function of VGAM2136 is therefore inhibition of COP9 Constitutive Photomorphogenic Homolog Subunit 7A (Arabidopsis) (COPS7A, Accession NM_016319). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COPS7A. DKFZp547I014 (Accession NM_020217) is another VGAM2136 host target gene. DKFZp547I014 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp547I014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547I014 BINDING SITE, des-

ignated SEQ ID:21466, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74030] Another function of VGAM2136 is therefore inhibition of DKFZp547I014 (Accession NM_020217). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547I014. DKFZP586D2223 (Accession NM_018561) is another VGAM2136 host target gene. DKFZP586D2223 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586D2223, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586D2223 BINDING SITE, designated SEQ ID:20644, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74031] Another function of VGAM2136 is therefore inhibition of DKFZP586D2223 (Accession NM_018561). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586D2223. DKFZP727C091 (Accession

XM_038689) is another VGAM2136 host target gene. DKFZP727C091 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP727C091, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP727C091 BINDING SITE, designated SEQ ID:32907, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74032] Another function of VGAM2136 is therefore inhibition of DKFZP727C091 (Accession XM_038689). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP727C091. FLJ10618 (Accession NM_018155) is another VGAM2136 host target gene. FLJ10618 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10618, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10618 BINDING SITE, designated SEQ ID:19966, to the nucleotide sequence of VGAM2136 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4847.

[74033] Another function of VGAM2136 is therefore inhibition of FLJ10618 (Accession NM_018155). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10618. FLJ10687 (Accession NM_018178) is another VGAM2136 host target gene. FLJ10687 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10687, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10687 BINDING SITE, designated SEQ ID:20008, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74034] Another function of VGAM2136 is therefore inhibition of FLJ10687 (Accession NM_018178). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10687. FLJ11184 (Accession NM_018352) is another VGAM2136 host target gene. FLJ11184 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11184, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11184 BINDING SITE, designated SEQ ID:20364, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74035] Another function of VGAM2136 is therefore inhibition of FLJ11184 (Accession NM_018352). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11184. FLJ12644 (Accession NM_023074) is another VGAM2136 host target gene. FLJ12644 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12644, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12644 BINDING SITE, designated SEQ ID:23331, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74036] Another function of VGAM2136 is therefore inhibition of FLJ12644 (Accession NM_023074). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12644. FLJ12987 (Accession NM_025170) is another VGAM2136 host target gene. FLJ12987 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12987, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12987 BINDING SITE, designated SEQ ID:24806, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74037] Another function of VGAM2136 is therefore inhibition of FLJ12987 (Accession NM_025170). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12987. FLJ20666 (Accession NM_018333) is another VGAM2136 host target gene. FLJ20666 BINDING SITE1 and FLJ20666 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ20666, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20666 BINDING SITE1 and FLJ20666

BINDING SITE2, designated SEQ ID:20335 and SEQ ID:19581 respectively, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74038] Another function of VGAM2136 is therefore inhibition of FLJ20666 (Accession NM_018333). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20666. GFR (Accession NM_012294) is another VGAM2136 host target gene. GFR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GFR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GFR BINDING SITE, designated SEQ ID:14635, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74039] Another function of VGAM2136 is therefore inhibition of GFR (Accession NM_012294). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GFR. Glutamate Receptor, Ionotropic, Delta 1 (GRID1, Accession

XM_043613) is another VGAM2136 host target gene. GRID1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRID1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRID1 BINDING SITE, designated SEQ ID:33982, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74040] Another function of VGAM2136 is therefore inhibition of Glutamate Receptor, Ionotropic, Delta 1 (GRID1, Accession XM_043613). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRID1. KIAA0258 (Accession NM_014785) is another VGAM2136 host target gene. KIAA0258 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0258, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0258 BINDING SITE, designated SEQ ID:16651, to the nucleotide sequence of VGAM2136

RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74041] Another function of VGAM2136 is therefore inhibition of KIAA0258 (Accession NM_014785). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0258. KIAA0863 (Accession NM_014913) is another VGAM2136 host target gene. KIAA0863 BINDING SITE1 and KIAA0863 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0863, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0863 BINDING SITE1 and KIAA0863 BINDING SITE2, designated SEQ ID:17152 and SEQ ID:45632 respectively, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74042] Another function of VGAM2136 is therefore inhibition of KIAA0863 (Accession NM_014913). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0863. MFN2 (Accession NM_014874) is another

VGAM2136 host target gene. MFN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MFN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MFN2 BINDING SITE, designated SEQ ID:17011, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74043] Another function of VGAM2136 is therefore inhibition of MFN2 (Accession NM_014874). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MFN2. Neurolysin (metallopeptidase M3 family) (NLN, Accession NM_020726) is another VGAM2136 host target gene. NLN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NLN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NLN BINDING SITE, designated SEQ ID:21857, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74044] Another function of VGAM2136 is therefore inhibition of Neurolysin (metallopeptidase M3 family) (NLN, Accession NM_020726). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NLN. PB1 (Accession NM_018165) is another VGAM2136 host target gene. PB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PB1 BINDING SITE, designated SEQ ID:19982, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74045] Another function of VGAM2136 is therefore inhibition of PB1 (Accession NM_018165). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PB1. Protocadherin 19 (PCDH19, Accession XM_033173) is another VGAM2136 host target gene. PCDH19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDH19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH19 BINDING SITE, designated SEQ ID:31863, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74046] Another function of VGAM2136 is therefore inhibition of Protocadherin 19 (PCDH19, Accession XM_033173). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH19. Protein Phosphatase 1, Regulatory Subunit 10 (PPP1R10, Accession NM_002714) is another VGAM2136 host target gene. PPP1R10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R10 BINDING SITE, designated SEQ ID:8579, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74047] Another function of VGAM2136 is therefore inhibition of Protein Phosphatase 1, Regulatory Subunit 10 (PPP1R10, Accession NM_002714). Accordingly, utilities of

VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R10. Proline-rich Gla (G-carboxyglutamic acid) Polypeptide 1 (PRRG1, Accession NM_000950) is another VGAM2136 host target gene. PRRG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRRG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRRG1 BINDING SITE, designated SEQ ID:6657, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74048] Another function of VGAM2136 is therefore inhibition of Proline-rich Gla (G-carboxyglutamic acid) Polypeptide 1 (PRRG1, Accession NM_000950). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRRG1. Serum Response Factor (c-fos serum response element-binding transcription factor) (SRF, Accession NM_003131) is another VGAM2136 host target gene. SRF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SRF, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SRF BINDING SITE, designated SEQ ID:9096, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74049] Another function of VGAM2136 is therefore inhibition of Serum Response Factor (c-fos serum response element-binding transcription factor) (SRF, Accession NM_003131). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRF. LOC125929 (Accession XM_064872) is another VGAM2136 host target gene. LOC125929 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC125929, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC125929 BINDING SITE, designated SEQ ID:37270, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74050] Another function of VGAM2136 is therefore inhibition of

LOC125929 (Accession XM_064872). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC125929. LOC130162 (Accession XM_059406) is another VGAM2136 host target gene. LOC130162 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130162 BINDING SITE, designated SEQ ID:36984, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74051] Another function of VGAM2136 is therefore inhibition of LOC130162 (Accession XM_059406). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130162. LOC130589 (Accession NM_138801) is another VGAM2136 host target gene. LOC130589 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130589, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC130589 BINDING SITE, designated SEQ ID:29023, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74052] Another function of VGAM2136 is therefore inhibition of LOC130589 (Accession NM_138801). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130589. LOC132228 (Accession XM_059581) is another VGAM2136 host target gene. LOC132228 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC132228, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132228 BINDING SITE, designated SEQ ID:37021, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74053] Another function of VGAM2136 is therefore inhibition of LOC132228 (Accession XM_059581). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132228. LOC146784 (Accession XM_085588) is an-

other VGAM2136 host target gene. LOC146784 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146784, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146784 BINDING SITE, designated SEQ ID:38239, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74054] Another function of VGAM2136 is therefore inhibition of LOC146784 (Accession XM_085588). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146784. LOC153077 (Accession XM_098307) is another VGAM2136 host target gene. LOC153077 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153077, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153077 BINDING SITE, designated SEQ ID:41568, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74055] Another function of VGAM2136 is therefore inhibition of LOC153077 (Accession XM_098307). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153077. LOC158581 (Accession XM_098968) is another VGAM2136 host target gene. LOC158581 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158581, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158581 BINDING SITE, designated SEQ ID:42014, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74056] Another function of VGAM2136 is therefore inhibition of LOC158581 (Accession XM_098968). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158581. LOC221143 (Accession XM_167986) is another VGAM2136 host target gene. LOC221143 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221143, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221143 BINDING SITE, designated SEQ ID:44942, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74057] Another function of VGAM2136 is therefore inhibition of LOC221143 (Accession XM_167986). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221143. LOC221296 (Accession XM_166325) is another VGAM2136 host target gene. LOC221296 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221296, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221296 BINDING SITE, designated SEQ ID:44168, to the nucleotide sequence of VGAM2136 RNA, herein designated VGAM RNA, also designated SEQ ID:4847.

[74058] Another function of VGAM2136 is therefore inhibition of LOC221296 (Accession XM_166325). Accordingly, utilities of VGAM2136 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC221296. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2137 (VGAM2137) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74059] VGAM2137 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2137 was detected is described hereinabove with reference to Figs. 1-8.

[74060] VGAM2137 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2137 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74061] VGAM2137 gene encodes a VGAM2137 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2137 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2137 precursor RNA is designated SEQ ID:2123, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2123 is located at position 174026 relative to the genome of Ectromelia Virus.

[74062] VGAM2137 precursor RNA folds onto itself, forming VGAM2137 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74063] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2137 folded precursor RNA into VGAM2137 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2137 RNA is designated SEQ ID:4848, and is provided hereinbelow with reference to the sequence listing part.

[74064] VGAM2137 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2137 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2137 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74065] VGAM2137 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2137 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2137 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2137 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2137 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74066] The complementary binding of VGAM2137 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2137 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2137 host target RNA into VGAM2137 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74067] It is appreciated that VGAM2137 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2137 host target genes. The mRNA of each one of this plurality of VGAM2137 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2137 RNA, herein designated VGAM RNA, and which when bound by VGAM2137 RNA causes

inhibition of translation of respective one or more VGAM2137 host target proteins.

[74068] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2137 gene, herein designated VGAM GENE, on one or more VGAM2137 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74069] It is yet further appreciated that a function of VGAM2137 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2137 include diagnosis, prevention and

treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2137 correlate with, and may be deduced from, the identity of the host target genes which VGAM2137 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74070] Nucleotide sequences of the VGAM2137 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2137 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2137 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2137 are further described hereinbelow with reference to Table 1.

[74071] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2137 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2137 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74072] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2137 gene, herein designated VGAM is inhibition of expression of VGAM2137 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2137 correlate with, and may be deduced from, the identity of the target genes which VGAM2137 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74073] Microtubule-associated Protein, RP/EB Family, Member 2 (MAPRE2, Accession NM_014268) is a VGAM2137 host target gene. MAPRE2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAPRE2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPRE2 BINDING SITE, designated SEQ ID:15546, to the nucleotide sequence of VGAM2137 RNA, herein designated VGAM RNA, also designated SEQ ID:4848.

[74074] A function of VGAM2137 is therefore inhibition of Microtubule-associated Protein, RP/EB Family, Member 2 (MAPRE2, Accession NM_014268), a gene which The functional inactivation of the APC gene product is a key event in colorectal tumorigenesis. Accordingly, utilities of VGAM2137 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MAPRE2. The function of MAPRE2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM178.Zinc Finger Protein 255 (ZNF255, Accession NM_005774) is another VGAM2137 host target gene. ZNF255 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF255, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF255 BINDING SITE, designated SEQ ID:12347, to the nucleotide sequence of VGAM2137 RNA, herein designated VGAM RNA, also designated SEQ ID:4848.

[74075] Another function of VGAM2137 is therefore inhibition of Zinc Finger Protein 255 (ZNF255, Accession NM_005774). Accordingly, utilities of VGAM2137 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF255. FLJ12488 (Accession NM_031218) is another VGAM2137 host target gene. FLJ12488 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12488, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12488 BINDING SITE, designated SEQ ID:25266, to the nucleotide sequence of VGAM2137 RNA, herein designated VGAM RNA, also designated SEQ ID:4848.

[74076] Another function of VGAM2137 is therefore inhibition of FLJ12488 (Accession NM_031218). Accordingly, utilities of VGAM2137 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12488. FLJ12788 (Accession NM_022492) is another VGAM2137 host target gene. FLJ12788 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12788, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12788 BINDING SITE, designated SEQ ID:22871, to the nucleotide sequence of VGAM2137 RNA, herein designated VGAM RNA, also designated SEQ ID:4848.

[74077] Another function of VGAM2137 is therefore inhibition of FLJ12788 (Accession NM_022492). Accordingly, utilities of VGAM2137 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12788. HSA250839 (Accession NM_018401) is another VGAM2137 host target gene. HSA250839 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSA250839, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSA250839 BINDING SITE, designated SEQ ID:20439, to the nucleotide sequence of VGAM2137 RNA, herein designated VGAM RNA, also designated SEQ ID:4848.

[74078] Another function of VGAM2137 is therefore inhibition of HSA250839 (Accession NM_018401). Accordingly, utilities of VGAM2137 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSA250839. KIAA1877 (Accession XM_038616) is another VGAM2137 host target gene. KIAA1877 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1877, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1877 BINDING SITE, designated SEQ ID:32886, to the

nucleotide sequence of VGAM2137 RNA, herein designated VGAM RNA, also designated SEQ ID:4848.

[74079] Another function of VGAM2137 is therefore inhibition of KIAA1877 (Accession XM_038616). Accordingly, utilities of VGAM2137 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1877. MGC3771 (Accession NM_030970) is another VGAM2137 host target gene. MGC3771 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC3771, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC3771 BINDING SITE, designated SEQ ID:25234, to the nucleotide sequence of VGAM2137 RNA, herein designated VGAM RNA, also designated SEQ ID:4848.

[74080] Another function of VGAM2137 is therefore inhibition of MGC3771 (Accession NM_030970). Accordingly, utilities of VGAM2137 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3771. LOC162333 (Accession XM_102591) is another VGAM2137 host target gene. LOC162333 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by LOC162333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162333 BINDING SITE, designated SEQ ID:42140, to the nucleotide sequence of VGAM2137 RNA, herein designated VGAM RNA, also designated SEQ ID:4848.

[74081] Another function of VGAM2137 is therefore inhibition of LOC162333 (Accession XM_102591). Accordingly, utilities of VGAM2137 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162333. LOC90410 (Accession XM_031534) is another VGAM2137 host target gene. LOC90410 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90410, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90410 BINDING SITE, designated SEQ ID:31400, to the nucleotide sequence of VGAM2137 RNA, herein designated VGAM RNA, also designated SEQ ID:4848.

[74082] Another function of VGAM2137 is therefore inhibition of LOC90410 (Accession XM_031534). Accordingly, utilities

of VGAM2137 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90410. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2138 (VGAM2138) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74083] VGAM2138 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2138 was detected is described hereinabove with reference to Figs. 1-8.

[74084] VGAM2138 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2138 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74085] VGAM2138 gene encodes a VGAM2138 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2138 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2138 precursor RNA is designated SEQ ID:2124, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2124 is located at position 168635 relative to the genome of Ectromelia Virus.

[74086] VGAM2138 precursor RNA folds onto itself, forming VGAM2138 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74087] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2138 folded precursor RNA into VGAM2138 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2138 RNA is designated SEQ ID:4849, and

is provided hereinbelow with reference to the sequence listing part.

[74088] VGAM2138 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2138 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2138 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74089] VGAM2138 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2138 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2138 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2138 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2138 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74090] The complementary binding of VGAM2138 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2138 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2138 host target RNA into VGAM2138 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74091] It is appreciated that VGAM2138 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2138 host target genes. The mRNA of each one of this plurality of VGAM2138 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2138 RNA, herein designated VGAM RNA, and which when bound by VGAM2138 RNA causes inhibition of translation of respective one or more VGAM2138 host target proteins.

[74092] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2138 gene, herein designated VGAM GENE, on one or more VGAM2138 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74093] It is yet further appreciated that a function of VGAM2138 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2138 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2138 correlate with, and may be deduced from, the identity of the host target genes which VGAM2138 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74094] Nucleotide sequences of the VGAM2138 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2138 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2138 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2138 are further described hereinbelow with reference to Table 1.

[74095] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2138 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2138 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74096] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2138 gene, herein designated VGAM is inhibition of expression of VGAM2138 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2138 correlate with, and may be deduced from, the identity of the target genes which VGAM2138 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74097] Cytochrome P450, Subfamily XXVIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), Polypeptide 1 (CYP27B1, Accession NM_000785) is a VGAM2138 host target gene. CYP27B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP27B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP27B1 BINDING SITE, designated SEQ ID:6434, to the nucleotide sequence of VGAM2138 RNA, herein designated VGAM RNA, also designated SEQ ID:4849.

[74098] A function of VGAM2138 is therefore inhibition of Cytochrome P450, Subfamily XXVIIB (25-hydroxyvitamin D-1-alpha-hydroxylase), Polypeptide 1 (CYP27B1, Accession NM_000785). Accordingly, utilities of VGAM2138 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP27B1. Glucose-6-phosphatase, Catalytic (glycogen storage disease type I, von Gierke disease) (G6PC, Accession NM_000151) is another VGAM2138 host target gene. G6PC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by G6PC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of G6PC BINDING SITE, designated SEQ ID:5654, to the nucleotide sequence of VGAM2138 RNA, herein designated VGAM RNA, also designated SEQ ID:4849.

[74099] Another function of VGAM2138 is therefore inhibition of Glucose-6-phosphatase, Catalytic (glycogen storage disease type I, von Gierke disease) (G6PC, Accession NM_000151). Accordingly, utilities of VGAM2138 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G6PC. KIAA0349 (Accession XM_166449) is another VGAM2138 host target gene. KIAA0349 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0349, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0349 BINDING SITE, designated SEQ ID:44340, to the nucleotide sequence of VGAM2138 RNA, herein designated VGAM RNA, also designated SEQ ID:4849.

[74100] Another function of VGAM2138 is therefore inhibition of KIAA0349 (Accession XM_166449). Accordingly, utilities of VGAM2138 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0349. MIG (Accession NM_002416) is another VGAM2138 host target gene. MIG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MIG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MIG BINDING SITE, designated SEQ ID:8249, to the nucleotide sequence of VGAM2138 RNA, herein designated VGAM RNA, also designated SEQ ID:4849.

[74101] Another function of VGAM2138 is therefore inhibition of MIG (Accession NM_002416). Accordingly, utilities of VGAM2138 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MIG. LOC152925 (Accession XM_087559) is another VGAM2138 host target gene. LOC152925 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152925, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152925 BINDING SITE, designated SEQ ID:39338, to the nucleotide sequence of VGAM2138 RNA, herein designated VGAM RNA, also designated SEQ ID:4849.

[74102] Another function of VGAM2138 is therefore inhibition of LOC152925 (Accession XM_087559). Accordingly, utilities of VGAM2138 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152925. LOC158295 (Accession XM_098915) is another VGAM2138 host target gene. LOC158295 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158295, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158295 BINDING SITE, designated SEQ ID:41937, to

the nucleotide sequence of VGAM2138 RNA, herein designated VGAM RNA, also designated SEQ ID:4849.

[74103] Another function of VGAM2138 is therefore inhibition of LOC158295 (Accession XM_098915). Accordingly, utilities of VGAM2138 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158295. LOC55885 (Accession NM_018640) is another VGAM2138 host target gene. LOC55885 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC55885, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC55885 BINDING SITE, designated SEQ ID:20710, to the nucleotide sequence of VGAM2138 RNA, herein designated VGAM RNA, also designated SEQ ID:4849.

[74104] Another function of VGAM2138 is therefore inhibition of LOC55885 (Accession NM_018640). Accordingly, utilities of VGAM2138 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC55885. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2139 (VGAM2139) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74105] VGAM2139 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2139 was detected is described hereinabove with reference to Figs. 1-8.

[74106] VGAM2139 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2139 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74107] VGAM2139 gene encodes a VGAM2139 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2139 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2139 precursor RNA is designated SEQ ID:2125, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2125 is located at position 179020 relative to the genome of Ectromelia Virus.

[74108] VGAM2139 precursor RNA folds onto itself, forming VGAM2139 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74109] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2139 folded precursor RNA into VGAM2139 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2139 RNA is designated SEQ ID:4850, and is provided hereinbelow with reference to the sequence listing part.

[74110] VGAM2139 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2139 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2139 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74111] VGAM2139 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2139 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2139 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2139 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2139 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74112] The complementary binding of VGAM2139 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2139 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2139 host target RNA into VGAM2139 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74113] It is appreciated that VGAM2139 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2139 host target genes. The mRNA of each one of this plurality of VGAM2139 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2139 RNA, herein designated VGAM RNA, and which when bound by VGAM2139 RNA causes inhibition of translation of respective one or more VGAM2139 host target proteins.

[74114] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2139 gene, herein designated VGAM GENE, on one or more VGAM2139 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74115] It is yet further appreciated that a function of VGAM2139 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2139 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2139 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2139 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74116] Nucleotide sequences of the VGAM2139 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2139 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2139 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2139 are further described hereinbelow with reference to Table 1.

[74117] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2139 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2139 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74118] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2139 gene, herein designated VGAM is inhibition of expression of VGAM2139 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2139 correlate with, and may be deduced from, the identity of the target genes which VGAM2139

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74119] Notch Homolog 2 (Drosophila) (NOTCH2, Accession NM_024408) is a VGAM2139 host target gene. NOTCH2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NOTCH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NOTCH2 BINDING SITE, designated SEQ ID:23649, to the nucleotide sequence of VGAM2139 RNA, herein designated VGAM RNA, also designated SEQ ID:4850.

[74120] A function of VGAM2139 is therefore inhibition of Notch Homolog 2 (Drosophila) (NOTCH2, Accession NM_024408), a gene which is moderately similar to a region of murine Notch1 and contains an ankyrin repeat. Accordingly, utilities of VGAM2139 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOTCH2. The function of NOTCH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM93.Guanine

Nucleotide Binding Protein (G protein), Gamma 4 (GNG4, Accession NM_004485) is another VGAM2139 host target gene. GNG4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNG4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNG4 BINDING SITE, designated SEQ ID:10807, to the nucleotide sequence of VGAM2139 RNA, herein designated VGAM RNA, also designated SEQ ID:4850.

[74121] Another function of VGAM2139 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Gamma 4 (GNG4, Accession NM_004485). Accordingly, utilities of VGAM2139 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNG4. KIAA1495 (Accession XM_055080) is another VGAM2139 host target gene. KIAA1495 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1495, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1495 BINDING SITE, designated SEQ ID:36223, to the nucleotide sequence of

VGAM2139 RNA, herein designated VGAM RNA, also designated SEQ ID:4850.

[74122] Another function of VGAM2139 is therefore inhibition of KIAA1495 (Accession XM_055080). Accordingly, utilities of VGAM2139 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1495. KIAA1582 (Accession XM_037262) is another VGAM2139 host target gene. KIAA1582 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1582, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1582 BINDING SITE, designated SEQ ID:32582, to the nucleotide sequence of VGAM2139 RNA, herein designated VGAM RNA, also designated SEQ ID:4850.

[74123] Another function of VGAM2139 is therefore inhibition of KIAA1582 (Accession XM_037262). Accordingly, utilities of VGAM2139 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1582. LOC254826 (Accession XM_173188) is another VGAM2139 host target gene. LOC254826 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC254826, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254826 BINDING SITE, designated SEQ ID:46435, to the nucleotide sequence of VGAM2139 RNA, herein designated VGAM RNA, also designated SEQ ID:4850.

[74124] Another function of VGAM2139 is therefore inhibition of LOC254826 (Accession XM_173188). Accordingly, utilities of VGAM2139 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254826. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2140 (VGAM2140) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74125] VGAM2140 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2140 was detected is described hereinabove with reference to Figs. 1-8.

[74126] VGAM2140 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Ectromelia Virus. VGAM2140 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74127] VGAM2140 gene encodes a VGAM2140 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2140 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2140 precursor RNA is designated SEQ ID:2126, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2126 is located at position 172080 relative to the genome of Ectromelia Virus.

[74128] VGAM2140 precursor RNA folds onto itself, forming VGAM2140 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74129] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2140 folded precursor RNA into VGAM2140 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2140 RNA is designated SEQ ID:4851, and is provided hereinbelow with reference to the sequence listing part.

[74130] VGAM2140 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2140 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2140 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74131] VGAM2140 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2140 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2140 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2140 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2140 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74132] The complementary binding of VGAM2140 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2140 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2140

host target RNA into VGAM2140 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74133] It is appreciated that VGAM2140 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2140 host target genes. The mRNA of each one of this plurality of VGAM2140 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2140 RNA, herein designated VGAM RNA, and which when bound by VGAM2140 RNA causes inhibition of translation of respective one or more VGAM2140 host target proteins.

[74134] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2140 gene, herein designated VGAM GENE, on one or more VGAM2140 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74135] It is yet further appreciated that a function of VGAM2140 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2140 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2140 correlate with, and may be deduced from, the identity of the host target genes which VGAM2140 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74136] Nucleotide sequences of the VGAM2140 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2140 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2140 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2140 are further

described hereinbelow with reference to Table 1.

[74137] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2140 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2140 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74138] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2140 gene, herein designated VGAM is inhibition of expression of VGAM2140 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2140 correlate with, and may be deduced from, the identity of the target genes which VGAM2140 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74139] Bromodomain Adjacent to Zinc Finger Domain, 1A (BAZ1A, Accession NM_013448) is a VGAM2140 host target gene. BAZ1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAZ1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of BAZ1A BINDING SITE, designated SEQ ID:15115, to the nucleotide sequence of VGAM2140 RNA, herein designated VGAM RNA, also designated SEQ ID:4851.

[74140] A function of VGAM2140 is therefore inhibition of Bromodomain Adjacent to Zinc Finger Domain, 1A (BAZ1A, Accession NM_013448), a gene which acts as a chromatin-mediated transcriptional regulator. Accordingly, utilities of VGAM2140 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAZ1A. The function of BAZ1A has been established by previous studies. Bochar et al. (2000) purified a chromatin-remodeling complex, which they called WCRF, from HeLa nuclear extracts. The purified complex contains 2 proteins, BAZ1A at 180 kD, which they designated WCRF180, and SMARCA5 (OMIM Ref. No. 603375), which they designated WCRF135. Using in vitro ATP-dependent DNase I cleavage of mononucleosomes, they confirmed an ATP-dependent chromatin remodeling activity in the complex. Poot et al. (2000) identified BAZ1A, which they designated ACF1, within a chromatin remodeling complex, CHRAC, purified from HeLa cell nuclear extracts. They confirmed an interaction between BAZ1A and SNF2H

(SMARCA5). Two small histone-fold proteins, CHRAC17 (POLE3; 607267) and CHRAC15 (CHRAC1; 607268), copurified with the complex, and the authors showed that these proteins form a DNA-binding heterodimer. Poot et al. (2000) determined that the purified complex could mobilize nucleosomes into a regularly spaced nucleosomal array and that the spacing activity was strictly ATP-dependent.

[74141] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74142] Bochar, D. A.; Savard, J.; Wang, W.; Lafleur, D. W.; Moore, P.; Cote, J.; Shiekhattar, R. : A family of chromatin remodeling factors related to Williams syndrome transcription factor. Proc. Nat. Acad. Sci. 97: 1038-1043, 2000. ; and

[74143] Poot, R. A.; Dellaire, G.; Hulsmann, B. B.; Grimaldi, M. A.; Corona, D. F. V.; Becker, P. B.; Bickmore, W. A.; Varga-Weisz, P. D. : HuCHRAC, a human ISWI chromatin remodelling complex.

[74144] Further studies establishing the function and utilities of BAZ1A are found in John Hopkins OMIM database record ID 605680, and in sited publications numbered 507 and 5074 listed in the bibliography section hereinbelow, which

are also hereby incorporated by reference.APCL (Accession NM_005883) is another VGAM2140 host target gene. APCL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APCL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APCL BINDING SITE, designated SEQ ID:12503, to the nucleotide sequence of VGAM2140 RNA, herein designated VGAM RNA, also designated SEQ ID:4851.

[74145] Another function of VGAM2140 is therefore inhibition of APCL (Accession NM_005883). Accordingly, utilities of VGAM2140 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APCL. P5-1 (Accession NM_006674) is another VGAM2140 host target gene. P5-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P5-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P5-1 BINDING SITE, designated SEQ ID:13497, to the nucleotide sequence of VGAM2140 RNA, herein designated VGAM RNA, also designated SEQ

ID:4851.

[74146] Another function of VGAM2140 is therefore inhibition of P5-1 (Accession NM_006674). Accordingly, utilities of VGAM2140 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P5-1. LOC91286 (Accession XM_037444) is another VGAM2140 host target gene. LOC91286 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91286, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91286 BINDING SITE, designated SEQ ID:32623, to the nucleotide sequence of VGAM2140 RNA, herein designated VGAM RNA, also designated SEQ ID:4851.

[74147] Another function of VGAM2140 is therefore inhibition of LOC91286 (Accession XM_037444). Accordingly, utilities of VGAM2140 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91286. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2141 (VGAM2141) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74148] VGAM2141 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2141 was detected is described hereinabove with reference to Figs. 1-8.

[74149] VGAM2141 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2141 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74150] VGAM2141 gene encodes a VGAM2141 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2141 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2141 precursor RNA is designated SEQ ID:2127, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2127 is located at position 169712 relative to the genome of Ectromelia Virus.

[74151] VGAM2141 precursor RNA folds onto itself, forming

VGAM2141 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74152] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2141 folded precursor RNA into VGAM2141 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2141 RNA is designated SEQ ID:4852, and is provided hereinbelow with reference to the sequence listing part.

[74153] VGAM2141 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2141 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2141 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74154] VGAM2141 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2141 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2141 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2141 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2141 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74155] The complementary binding of VGAM2141 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2141 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2141 host target RNA into VGAM2141 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74156] It is appreciated that VGAM2141 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2141 host target genes. The mRNA of each one of this plurality of VGAM2141 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2141 RNA, herein designated VGAM RNA, and which when bound by VGAM2141 RNA causes inhibition of translation of respective one or more VGAM2141 host target proteins.

[74157] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2141 gene, herein designated VGAM GENE, on one or more VGAM2141 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74158] It is yet further appreciated that a function of VGAM2141 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2141 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2141 correlate with, and may be deduced from, the identity of the host target genes which VGAM2141 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[74159] Nucleotide sequences of the VGAM2141 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2141 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2141 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2141 are further described hereinbelow with reference to Table 1.

[74160] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2141 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2141 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74161] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2141 gene, herein designated VGAM is inhibition of expression of VGAM2141 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2141 correlate with, and may be deduced from, the identity of the target genes which VGAM2141 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[74162] ESDN (Accession NM_080927) is a VGAM2141 host target gene. ESDN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ESDN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESDN BINDING SITE, designated SEQ ID:28151, to the nucleotide sequence of VGAM2141 RNA, herein designated VGAM RNA, also designated SEQ ID:4852.

[74163] A function of VGAM2141 is therefore inhibition of ESDN (Accession NM_080927). Accordingly, utilities of VGAM2141 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESDN. KIAA1317 (Accession XM_098368) is another VGAM2141 host target gene. KIAA1317 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1317, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1317 BINDING SITE, designated SEQ ID:41631, to the nucleotide sequence of VGAM2141 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4852.

[74164] Another function of VGAM2141 is therefore inhibition of KIAA1317 (Accession XM_098368). Accordingly, utilities of VGAM2141 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1317. LOC158295 (Accession XM_098915) is another VGAM2141 host target gene. LOC158295 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158295, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158295 BINDING SITE, designated SEQ ID:41939, to the nucleotide sequence of VGAM2141 RNA, herein designated VGAM RNA, also designated SEQ ID:4852.

[74165] Another function of VGAM2141 is therefore inhibition of LOC158295 (Accession XM_098915). Accordingly, utilities of VGAM2141 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158295. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2142 (VGAM2142) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74166] VGAM2142 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2142 was detected is described hereinabove with reference to Figs. 1-8.

[74167] VGAM2142 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2142 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74168] VGAM2142 gene encodes a VGAM2142 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2142 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2142 precursor RNA is designated SEQ ID:2128, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2128 is located at position 168447 relative to the genome of Ectromelia Virus.

[74169] VGAM2142 precursor RNA folds onto itself, forming

VGAM2142 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74170] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2142 folded precursor RNA into VGAM2142 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2142 RNA is designated SEQ ID:4853, and is provided hereinbelow with reference to the sequence listing part.

[74171] VGAM2142 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2142 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2142 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74172] VGAM2142 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2142 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2142 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2142 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2142 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74173] The complementary binding of VGAM2142 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2142 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2142 host target RNA into VGAM2142 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74174] It is appreciated that VGAM2142 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2142 host target genes. The mRNA of each one of this plurality of VGAM2142 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2142 RNA, herein designated VGAM RNA, and which when bound by VGAM2142 RNA causes inhibition of translation of respective one or more VGAM2142 host target proteins.

[74175] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2142 gene, herein designated VGAM GENE, on one or more VGAM2142 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74176] It is yet further appreciated that a function of VGAM2142 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2142 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2142 correlate with, and may be deduced from, the identity of the host target genes which VGAM2142 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[74177] Nucleotide sequences of the VGAM2142 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2142 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2142 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2142 are further described hereinbelow with reference to Table 1.

[74178] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2142 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2142 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74179] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2142 gene, herein designated VGAM is inhibition of expression of VGAM2142 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2142 correlate with, and may be deduced from, the identity of the target genes which VGAM2142 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[74180] Dihydrolipoamide Branched Chain Transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) (DBT, Accession NM_001918) is a VGAM2142 host target gene. DBT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DBT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DBT BINDING SITE, designated SEQ ID:7634, to the nucleotide sequence of VGAM2142 RNA, herein designated VGAM RNA, also designated SEQ ID:4853.

[74181] A function of VGAM2142 is therefore inhibition of Dihydrolipoamide Branched Chain Transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) (DBT, Accession NM_001918). Accordingly, utilities of VGAM2142 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DBT. Replication Factor C (activator 1) 1, 145kDa (RFC1, Accession NM_002913) is another VGAM2142 host target gene. RFC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by RFC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RFC1 BINDING SITE, designated SEQ ID:8817, to the nucleotide sequence of VGAM2142 RNA, herein designated VGAM RNA, also designated SEQ ID:4853.

[74182] Another function of VGAM2142 is therefore inhibition of Replication Factor C (activator 1) 1, 145kDa (RFC1, Accession NM_002913), a gene which plays a role in dna transcription, replication and/or repair. Accordingly, utilities of VGAM2142 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFC1. The function of RFC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM217.Suppressor of Cytokine Signaling 5 (SOCS5, Accession NM_014011) is another VGAM2142 host target gene. SOCS5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOCS5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of SOCS5 BINDING SITE, designated SEQ ID:15232, to the nucleotide sequence of VGAM2142 RNA, herein designated VGAM RNA, also designated SEQ ID:4853.

[74183] Another function of VGAM2142 is therefore inhibition of Suppressor of Cytokine Signaling 5 (SOCS5, Accession NM_014011). Accordingly, utilities of VGAM2142 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOCS5. KIAA1376 (Accession XM_033042) is another VGAM2142 host target gene. KIAA1376 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1376, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1376 BINDING SITE, designated SEQ ID:31822, to the nucleotide sequence of VGAM2142 RNA, herein designated VGAM RNA, also designated SEQ ID:4853.

[74184] Another function of VGAM2142 is therefore inhibition of KIAA1376 (Accession XM_033042). Accordingly, utilities of VGAM2142 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1376. KIAA1617 (Accession XM_166140) is another VGAM2142 host target gene. KIAA1617 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1617, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1617 BINDING SITE, designated SEQ ID:43945, to the nucleotide sequence of VGAM2142 RNA, herein designated VGAM RNA, also designated SEQ ID:4853.

[74185] Another function of VGAM2142 is therefore inhibition of KIAA1617 (Accession XM_166140). Accordingly, utilities of VGAM2142 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1617. NYD-SP20 (Accession NM_032598) is another VGAM2142 host target gene. NYD-SP20 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NYD-SP20, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NYD-SP20 BINDING SITE, designated SEQ ID:26328, to the nucleotide sequence of VGAM2142 RNA, herein designated

VGAM RNA, also designated SEQ ID:4853.

[74186] Another function of VGAM2142 is therefore inhibition of NYD-SP20 (Accession NM_032598). Accordingly, utilities of VGAM2142 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NYD-SP20. TGFB Inducible Early Growth Response (TIEG, Accession NM_005655) is another VGAM2142 host target gene. TIEG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIEG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIEG BINDING SITE, designated SEQ ID:12193, to the nucleotide sequence of VGAM2142 RNA, herein designated VGAM RNA, also designated SEQ ID:4853.

[74187] Another function of VGAM2142 is therefore inhibition of TGFB Inducible Early Growth Response (TIEG, Accession NM_005655). Accordingly, utilities of VGAM2142 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIEG. LOC51339 (Accession NM_016651) is another VGAM2142 host target gene. LOC51339 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

LOC51339, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51339 BINDING SITE, designated SEQ ID:18768, to the nucleotide sequence of VGAM2142 RNA, herein designated VGAM RNA, also designated SEQ ID:4853.

[74188] Another function of VGAM2142 is therefore inhibition of LOC51339 (Accession NM_016651). Accordingly, utilities of VGAM2142 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51339. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2143 (VGAM2143) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74189] VGAM2143 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2143 was detected is described hereinabove with reference to Figs. 1-8.

[74190] VGAM2143 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Ectromelia Virus. VGAM2143 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74191] VGAM2143 gene encodes a VGAM2143 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2143 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2143 precursor RNA is designated SEQ ID:2129, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2129 is located at position 165143 relative to the genome of Ectromelia Virus.

[74192] VGAM2143 precursor RNA folds onto itself, forming VGAM2143 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74193] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2143 folded precursor RNA into VGAM2143 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2143 RNA is designated SEQ ID:4854, and is provided hereinbelow with reference to the sequence listing part.

[74194] VGAM2143 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2143 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2143 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74195] VGAM2143 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2143 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2143 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2143 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2143 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74196] The complementary binding of VGAM2143 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2143 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2143

host target RNA into VGAM2143 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74197] It is appreciated that VGAM2143 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2143 host target genes. The mRNA of each one of this plurality of VGAM2143 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2143 RNA, herein designated VGAM RNA, and which when bound by VGAM2143 RNA causes inhibition of translation of respective one or more VGAM2143 host target proteins.

[74198] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2143 gene, herein designated VGAM GENE, on one or more VGAM2143 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74199] It is yet further appreciated that a function of VGAM2143 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2143 correlate with, and may be deduced from, the identity of the host target genes which VGAM2143 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74200] Nucleotide sequences of the VGAM2143 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2143 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2143 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2143 are further

described hereinbelow with reference to Table 1.

[74201] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2143 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2143 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74202] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2143 gene, herein designated VGAM is inhibition of expression of VGAM2143 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2143 correlate with, and may be deduced from, the identity of the target genes which VGAM2143 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74203] Espin (ESPN, Accession NM_031475) is a VGAM2143 host target gene. ESPN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ESPN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESPN BINDING SITE, designated SEQ

ID:25548, to the nucleotide sequence of VGAM2143 RNA, herein designated VGAM RNA, also designated SEQ ID:4854.

[74204] A function of VGAM2143 is therefore inhibition of Espin (ESPN, Accession NM_031475), a gene which a membrane-cytoskeletal assemblages . Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESPN. The function of ESPN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1006.Glucocorticoid Receptor DNA Binding Factor 1 (GRLF1, Accession XM_085943) is another VGAM2143 host target gene. GRLF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRLF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRLF1 BINDING SITE, designated SEQ ID:38407, to the nucleotide sequence of VGAM2143 RNA, herein designated VGAM RNA, also designated SEQ ID:4854.

[74205] Another function of VGAM2143 is therefore inhibition of

Glucocorticoid Receptor DNA Binding Factor 1 (GRLF1, Accession XM_085943), a gene which inhibits transcription of the glucocorticoid receptor gene. Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRLF1. The function of GRLF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Integrin, Alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) (ITGA2, Accession NM_002203) is another VGAM2143 host target gene. ITGA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA2 BINDING SITE, designated SEQ ID:7962, to the nucleotide sequence of VGAM2143 RNA, herein designated VGAM RNA, also designated SEQ ID:4854.

[74206] Another function of VGAM2143 is therefore inhibition of Integrin, Alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) (ITGA2, Accession NM_002203), a gene which has roles in blood clotting and angiogenesis, acts as a colla-

gen and laminin receptor. Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA2. The function of ITGA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM827.Wilms Tumor 1 (WT1, Accession NM_024424) is another VGAM2143 host target gene. WT1 BINDING SITE1 through WT1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WT1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WT1 BINDING SITE1 through WT1 BINDING SITE4, designated SEQ ID:23667, SEQ ID:23671, SEQ ID:23675 and SEQ ID:5951 respectively, to the nucleotide sequence of VGAM2143 RNA, herein designated VGAM RNA, also designated SEQ ID:4854.

[74207] Another function of VGAM2143 is therefore inhibition of Wilms Tumor 1 (WT1, Accession NM_024424). Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WT1. KIAA0993 (Accession XM_034413) is an-

other VGAM2143 host target gene. KIAA0993 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0993, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0993 BINDING SITE, designated SEQ ID:32083, to the nucleotide sequence of VGAM2143 RNA, herein designated VGAM RNA, also designated SEQ ID:4854.

[74208] Another function of VGAM2143 is therefore inhibition of KIAA0993 (Accession XM_034413). Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0993. KIAA1416 (Accession XM_098762) is another VGAM2143 host target gene. KIAA1416 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1416 BINDING SITE, designated SEQ ID:41797, to the nucleotide sequence of VGAM2143 RNA, herein designated VGAM RNA, also designated SEQ ID:4854.

[74209] Another function of VGAM2143 is therefore inhibition of KIAA1416 (Accession XM_098762). Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1416. My015 (Accession XM_039512) is another VGAM2143 host target gene. My015 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by My015, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of My015 BINDING SITE, designated SEQ ID:33103, to the nucleotide sequence of VGAM2143 RNA, herein designated VGAM RNA, also designated SEQ ID:4854.

[74210] Another function of VGAM2143 is therefore inhibition of My015 (Accession XM_039512). Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of diseases and clinical conditions associated with My015. Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2, Accession NM_014737) is another VGAM2143 host target gene. RASSF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RASSF2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:16388, to the nucleotide sequence of VGAM2143 RNA, herein designated VGAM RNA, also designated SEQ ID:4854.

[74211] Another function of VGAM2143 is therefore inhibition of Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2, Accession NM_014737). Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2. Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession NM_033285) is another VGAM2143 host target gene. TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TP53INP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2, designated SEQ ID:27101 and SEQ ID:36112 respectively, to the nucleotide sequence of VGAM2143 RNA, herein designated VGAM RNA, also designated SEQ ID:4854.

[74212] Another function of VGAM2143 is therefore inhibition of Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession NM_033285). Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53INP1. LOC157503 (Accession XM_098767) is another VGAM2143 host target gene. LOC157503 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157503, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157503 BINDING SITE, designated SEQ ID:41815, to the nucleotide sequence of VGAM2143 RNA, herein designated VGAM RNA, also designated SEQ ID:4854.

[74213] Another function of VGAM2143 is therefore inhibition of LOC157503 (Accession XM_098767). Accordingly, utilities of VGAM2143 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157503. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2144 (VGAM2144) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74214] VGAM2144 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2144 was detected is described hereinabove with reference to Figs. 1-8.

[74215] VGAM2144 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2144 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74216] VGAM2144 gene encodes a VGAM2144 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2144 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2144 precursor RNA is designated SEQ ID:2130, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2130 is located at position 168263 relative to the genome of Ectromelia Virus.

[74217] VGAM2144 precursor RNA folds onto itself, forming

VGAM2144 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74218] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2144 folded precursor RNA into VGAM2144 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2144 RNA is designated SEQ ID:4855, and is provided hereinbelow with reference to the sequence listing part.

[74219] VGAM2144 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2144 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2144 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74220] VGAM2144 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2144 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2144 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2144 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2144 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74221] The complementary binding of VGAM2144 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2144 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2144 host target RNA into VGAM2144 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74222] It is appreciated that VGAM2144 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2144 host target genes. The mRNA of each one of this plurality of VGAM2144 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2144 RNA, herein designated VGAM RNA, and which when bound by VGAM2144 RNA causes inhibition of translation of respective one or more VGAM2144 host target proteins.

[74223] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2144 gene, herein designated VGAM GENE, on one or more VGAM2144 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74224] It is yet further appreciated that a function of VGAM2144 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2144 correlate with, and may be deduced from, the identity of the host target genes which VGAM2144 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[74225] Nucleotide sequences of the VGAM2144 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2144 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2144 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2144 are further described hereinbelow with reference to Table 1.

[74226] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2144 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2144 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74227] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2144 gene, herein designated VGAM is inhibition of expression of VGAM2144 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2144 correlate with, and may be deduced from, the identity of the target genes which VGAM2144 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[74228] ATPase, Class VI, Type 11A (ATP11A, Accession XM_085028) is a VGAM2144 host target gene. ATP11A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP11A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP11A BINDING SITE, designated SEQ ID:37808, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74229] A function of VGAM2144 is therefore inhibition of ATPase, Class VI, Type 11A (ATP11A, Accession XM_085028). Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP11A. Chemokine (C-X-C motif) Receptor 6 (CXCR6, Accession NM_006564) is another VGAM2144 host target gene. CXCR6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CXCR6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CXCR6 BINDING SITE,

designated SEQ ID:13333, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74230] Another function of VGAM2144 is therefore inhibition of Chemokine (C-X-C motif) Receptor 6 (CXCR6, Accession NM_006564), a gene which probably interacts between dendritic cells and T cells and regulates T-cell migration. Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCR6. The function of CXCR6 has been established by previous studies. By RT-PCR on tumor-infiltrating lymphocyte lines with degenerate primers based on sequences of known chemokine receptors, Liao et al. (1997) isolated a cDNA encoding a GPCR, which they designated STRL33. Using an expression cloning strategy with a T-cell cDNA library, Deng et al. (1997) isolated an identical cDNA that they named BONZO. The predicted 342-amino acid STRL33/BONZO protein shares 25 to 30% amino acid identity with other chemokine receptors and is most similar to other GPCRs in the transmembrane domains. Northern blot analysis detected a 2.1-kb transcript in spleen, thymus, small intestine, and to a lesser extent in peripheral blood leukocytes, prostate, and colon; a

2.6-kb transcript was detected in placenta (Deng et al., 1997). By fluorometric calcium flux analysis, Liao et al. (1997) were unable to detect responses in STRL33-expressing cells to a variety of chemokines. However, coexpression of CD4 and STRL33/BONZO rendered cells able to fuse with macrophage-tropic HIV-1 (transmission-type) strains as well as with simian immunodeficiency virus. Liao et al. (1997) but not Deng et al. (1997) also detected fusion with T-cell-tropic HIV-1 strains. Liao et al. (1997) and Deng et al. (1997) speculated that expression of STRL33/BONZO may substitute for other HIV coreceptors, for example in CCR5 -/- individuals who become infected with HIV. By expression cloning of mouse Cxcl16 (OMIM Ref. No. 605398), Matloubian et al. (2000) identified a protein with 71% amino acid identity to human BONZO, which they renamed CXCR6. Human and mouse cells expressing CXCR6 showed a strong chemotactic response to CXCL16 but not to other chemokines. The authors concluded that CXCL16 and CXCR6 probably function in interactions between dendritic cells and T cells and in regulating T-cell migration in the splenic red pulp.

[74231] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[74232] Liao, F.; Alkhatib, G.; Peden, K. W. C.; Sharma, G.; Berger, E. A.; Farber, J. M. : STRL33, a novel chemokine receptor-like protein, functions as a fusion cofactor for both macrophage-tropic and T cell line-tropic HIV-1. J. Exp. Med. 185: 2015-2023, 1997. ; and

[74233] Matloubian, M.; David, A.; Engel, S.; Ryan, J. E.; Cyster, J. G. : A transmembrane CXC chemokine is a ligand for HIV-coreceptor Bonzo. Nature Immun. 1: 298-304, 2000.

[74234] Further studies establishing the function and utilities of CXCR6 are found in John Hopkins OMIM database record ID 605163, and in sited publications numbered 4392-4394 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.DNA-damage-inducible Transcript 3 (DDIT3, Accession NM_004083) is another VGAM2144 host target gene. DDIT3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DDIT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDIT3 BINDING SITE, designated SEQ

ID:10287, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74235] Another function of VGAM2144 is therefore inhibition of DNA-damage-inducible Transcript 3 (DDIT3, Accession NM_004083), a gene which May be a transcription factor and inhibits the DNA-binding activity of C/EBP and LAP. Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDIT3. The function of DDIT3 has been established by previous studies. CHOP is consistently rearranged in myxoid liposarcomas (Aman et al., 1992). In the characteristic chromosomal translocation t(12;16)(q13;p11), Crozat et al. (1993) showed that the CHOP gene is fused with a gene on chromosome 16 provisionally designated TLS (for 'translocated in liposarcoma'). The same gene was called FUS by Rabbitts et al. (1993); see 137070. The TLS gene was found to be a novel nuclear RNA-binding protein with extensive sequence similarity to EWS (OMIM Ref. No. 133450), the product of a gene commonly translocated in Ewing sarcoma. In TLS-CHOP, the RNA-binding domain of TLS is replaced by the DNA-binding and leucine zipper dimer-

ization domain of CHOP. Targeting of a conserved effector domain of RNA-binding proteins to DNA may play a role in tumor formation. In an analysis of peripheral blood samples from 19 patients with myxoid liposarcoma due to t(12;16) and in 1 patient with myxoid liposarcoma due to t(12;22;20), resulting in the fusion of the CHOP and EWS genes, Panagopoulos et al. (1996) found FUS/CHOP hybrid fragments in 3 patients with t(12;16) and a EWS/CHOP hybrid in the patient with the latter translocation.

[74236] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74237] Crozat, A.; Aman, P.; Mandahl, N.; Ron, D. : Fusion of CHOP to a novel RNA-binding protein in human myxoid liposarcoma. Nature 363: 640-644, 1993. ; and

[74238] Panagopoulos, I.; Aman, P.; Mertens, F.; Mandahl, N.; Rydholm, A.; Bauer, H. F. C.; Mitelman, F. : Genomic PCR detects tumor cells in peripheral blood from patients with myxoid liposarco.

[74239] Further studies establishing the function and utilities of DDIT3 are found in John Hopkins OMIM database record ID 126337, and in sited publications numbered 87 and 3095-3100 listed in the bibliography section hereinbelow,

which are also hereby incorporated by reference.Fibroblast Growth Factor Receptor-like 1 (FGFRL1, Accession NM_021923) is another VGAM2144 host target gene. FGFRL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGFRL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGFRL1 BINDING SITE, designated SEQ ID:22451, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74240] Another function of VGAM2144 is therefore inhibition of Fibroblast Growth Factor Receptor-like 1 (FGFRL1, Accession NM_021923). Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFRL1. Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 4 (SLC4A4, Accession NM_003759) is another VGAM2144 host target gene. SLC4A4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC4A4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC4A4 BINDING SITE, designated SEQ ID:9838, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74241] Another function of VGAM2144 is therefore inhibition of Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 4 (SLC4A4, Accession NM_003759), a gene which is a sodium bicarbonate cotransporter. Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC4A4. The function of SLC4A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM222.Tropomodulin (TMOD, Accession NM_003275) is another VGAM2144 host target gene. TMOD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TMOD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMOD BINDING SITE, designated SEQ ID:9294, to the nucleotide sequence of

VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74242] Another function of VGAM2144 is therefore inhibition of Tropomodulin (TMOD, Accession NM_003275), a gene which blocks the elongation and depolymerization of the actin filaments at the pointed end. Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMOD. The function of TMOD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM716.FGD1 Family, Member 3 (FGD3, Accession XM_053487) is another VGAM2144 host target gene. FGD3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGD3 BINDING SITE, designated SEQ ID:36091, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74243] Another function of VGAM2144 is therefore inhibition of FGD1 Family, Member 3 (FGD3, Accession XM_053487).

Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGD3. FLJ12838 (Accession NM_024641) is another VGAM2144 host target gene. FLJ12838 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12838, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12838 BINDING SITE, designated SEQ ID:23924, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74244] Another function of VGAM2144 is therefore inhibition of FLJ12838 (Accession NM_024641). Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12838. HIC (Accession XM_041273) is another VGAM2144 host target gene. HIC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HIC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of HIC BINDING SITE, designated SEQ ID:33494, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74245] Another function of VGAM2144 is therefore inhibition of HIC (Accession XM_041273). Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIC. KIAA1309 (Accession NM_033495) is another VGAM2144 host target gene. KIAA1309 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1309, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1309 BINDING SITE, designated SEQ ID:27264, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74246] Another function of VGAM2144 is therefore inhibition of KIAA1309 (Accession NM_033495). Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1309. Sodium Channel, Voltage-gated, Type XII, Al-

pha Polypeptide (SCN12A, Accession NM_014139) is another VGAM2144 host target gene. SCN12A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCN12A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCN12A BINDING SITE, designated SEQ ID:15410, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74247] Another function of VGAM2144 is therefore inhibition of Sodium Channel, Voltage-gated, Type XII, Alpha Polypeptide (SCN12A, Accession NM_014139). Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN12A. LOC145333 (Accession XM_096766) is another VGAM2144 host target gene. LOC145333 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145333 BINDING SITE, designated SEQ ID:40533, to

the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74248] Another function of VGAM2144 is therefore inhibition of LOC145333 (Accession XM_096766). Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145333. LOC162333 (Accession XM_102591) is another VGAM2144 host target gene. LOC162333 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC162333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162333 BINDING SITE, designated SEQ ID:42137, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74249] Another function of VGAM2144 is therefore inhibition of LOC162333 (Accession XM_102591). Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162333. LOC222662 (Accession XM_167086) is another VGAM2144 host target gene. LOC222662 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC222662, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222662 BINDING SITE, designated SEQ ID:44600, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74250] Another function of VGAM2144 is therefore inhibition of LOC222662 (Accession XM_167086). Accordingly, utilities of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222662. LOC255082 (Accession XM_172843) is another VGAM2144 host target gene. LOC255082 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255082, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255082 BINDING SITE, designated SEQ ID:46115, to the nucleotide sequence of VGAM2144 RNA, herein designated VGAM RNA, also designated SEQ ID:4855.

[74251] Another function of VGAM2144 is therefore inhibition of LOC255082 (Accession XM_172843). Accordingly, utilities

of VGAM2144 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255082. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2145 (VGAM2145) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74252] VGAM2145 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2145 was detected is described hereinabove with reference to Figs. 1-8.

[74253] VGAM2145 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2145 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74254] VGAM2145 gene encodes a VGAM2145 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2145 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2145 precursor RNA is designated SEQ ID:2131, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2131 is located at position 182220 relative to the genome of Ectromelia Virus.

[74255] VGAM2145 precursor RNA folds onto itself, forming VGAM2145 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74256] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2145 folded precursor RNA into VGAM2145 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2145 RNA is designated SEQ ID:4856, and

is provided hereinbelow with reference to the sequence listing part.

[74257] VGAM2145 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2145 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2145 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74258] VGAM2145 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2145 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2145 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2145 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2145 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74259] The complementary binding of VGAM2145 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2145 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2145 host target RNA into VGAM2145 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74260] It is appreciated that VGAM2145 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2145 host target genes. The mRNA of each one of this plurality of VGAM2145 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2145 RNA, herein designated VGAM RNA, and which when bound by VGAM2145 RNA causes inhibition of translation of respective one or more VGAM2145 host target proteins.

[74261] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2145 gene, herein designated VGAM GENE, on one or more VGAM2145 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74262] It is yet further appreciated that a function of VGAM2145 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2145 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2145 correlate with, and may be deduced from, the identity of the host target genes which VGAM2145 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74263] Nucleotide sequences of the VGAM2145 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2145 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2145 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2145 are further described hereinbelow with reference to Table 1.

[74264] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2145 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2145 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74265] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2145 gene, herein designated VGAM is inhibition of expression of VGAM2145 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2145 correlate with, and may be deduced from, the identity of the target genes which VGAM2145 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74266] Early Growth Response 2 (Krox-20 homolog, Drosophila) (EGR2, Accession NM_000399) is a VGAM2145 host target gene. EGR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EGR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGR2 BINDING SITE, designated SEQ ID:5971, to the nucleotide sequence of VGAM2145 RNA, herein designated VGAM RNA, also designated SEQ ID:4856.

[74267] A function of VGAM2145 is therefore inhibition of Early Growth Response 2 (Krox-20 homolog, Drosophila) (EGR2, Accession NM_000399), a gene which binds to two specific dna sites located in the promoter region of hox-1.4. Accordingly, utilities of VGAM2145 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with EGR2. The function of EGR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM234.LOC147184 (Accession NM_145274) is another VGAM2145 host target gene. LOC147184 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147184, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147184 BINDING SITE, designated SEQ ID:29787, to the nucleotide sequence of VGAM2145 RNA, herein designated VGAM RNA, also designated SEQ ID:4856.

[74268] Another function of VGAM2145 is therefore inhibition of LOC147184 (Accession NM_145274). Accordingly, utilities of VGAM2145 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147184. LOC90499 (Accession XM_032170) is another VGAM2145 host target gene. LOC90499 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90499, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90499 BINDING SITE, designated SEQ ID:31583, to the nucleotide sequence of VGAM2145 RNA, herein designated VGAM RNA, also designated SEQ ID:4856.

[74269] Another function of VGAM2145 is therefore inhibition of LOC90499 (Accession XM_032170). Accordingly, utilities of VGAM2145 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90499. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2146 (VGAM2146) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74270] VGAM2146 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2146 was detected is described hereinabove with reference to Figs. 1-8.

[74271] VGAM2146 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2146 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[74272] VGAM2146 gene encodes a VGAM2146 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2146 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2146 precursor RNA is designated SEQ ID:2132, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2132 is located at position 55138 relative to the genome of Rana Tigrina Ranavirus.

[74273] VGAM2146 precursor RNA folds onto itself, forming VGAM2146 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74274] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2146 folded precursor RNA into VGAM2146

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2146 RNA is designated SEQ ID:4857, and is provided hereinbelow with reference to the sequence listing part.

[74275] VGAM2146 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2146 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2146 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74276] VGAM2146 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2146 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2146 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2146 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2146 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74277] The complementary binding of VGAM2146 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2146 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2146 host target RNA into VGAM2146 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[74278] It is appreciated that VGAM2146 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2146 host target genes. The mRNA of each one of this plurality of VGAM2146 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2146 RNA, herein designated VGAM RNA, and which when bound by VGAM2146 RNA causes inhibition of translation of respective one or more VGAM2146 host target proteins.

[74279] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2146 gene, herein designated VGAM GENE, on one or more VGAM2146 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74280] It is yet further appreciated that a function of VGAM2146 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2146 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2146 correlate with, and may be deduced from, the identity of the host target genes which VGAM2146 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74281] Nucleotide sequences of the VGAM2146 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2146 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2146 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2146 are further described hereinbelow with reference to Table 1.

[74282] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2146 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2146 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74283] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2146 gene, herein designated VGAM is inhibition of expression of VGAM2146 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2146 correlate with, and may be deduced from, the identity of the target genes which VGAM2146 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74284] Lipin 2 (LPIN2, Accession NM_014646) is a VGAM2146 host target gene. LPIN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LPIN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LPIN2 BINDING SITE, designated SEQ ID:16059, to the nucleotide sequence of VGAM2146 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4857.

[74285] A function of VGAM2146 is therefore inhibition of Lipin 2 (LPIN2, Accession NM_014646). Accordingly, utilities of VGAM2146 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPIN2. Aminocarboxymuconate Semialdehyde Decarboxylase (acmsd, Accession NM_138326) is another VGAM2146 host target gene. acmsd BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by acmsd, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of acmsd BINDING SITE, designated SEQ ID:28728, to the nucleotide sequence of VGAM2146 RNA, herein designated VGAM RNA, also designated SEQ ID:4857.

[74286] Another function of VGAM2146 is therefore inhibition of Aminocarboxymuconate Semialdehyde Decarboxylase (acmsd, Accession NM_138326). Accordingly, utilities of VGAM2146 include diagnosis, prevention and treatment of diseases and clinical conditions associated with acmsd. Chromosome 1 Open Reading Frame 34 (C1orf34, Accession XM_027172) is another VGAM2146 host target gene.

C1orf34 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf34, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf34 BINDING SITE, designated SEQ ID:30431, to the nucleotide sequence of VGAM2146 RNA, herein designated VGAM RNA, also designated SEQ ID:4857.

[74287] Another function of VGAM2146 is therefore inhibition of Chromosome 1 Open Reading Frame 34 (C1orf34, Accession XM_027172). Accordingly, utilities of VGAM2146 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf34. KIAA1110 (Accession XM_029973) is another VGAM2146 host target gene. KIAA1110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1110 BINDING SITE, designated SEQ ID:30980, to the nucleotide sequence of VGAM2146 RNA, herein designated VGAM RNA, also designated SEQ

ID:4857.

[74288] Another function of VGAM2146 is therefore inhibition of KIAA1110 (Accession XM_029973). Accordingly, utilities of VGAM2146 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1110. MGC14258 (Accession NM_032900) is another VGAM2146 host target gene. MGC14258 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC14258, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC14258 BINDING SITE, designated SEQ ID:26724, to the nucleotide sequence of VGAM2146 RNA, herein designated VGAM RNA, also designated SEQ ID:4857.

[74289] Another function of VGAM2146 is therefore inhibition of MGC14258 (Accession NM_032900). Accordingly, utilities of VGAM2146 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14258. LOC150372 (Accession XM_086893) is another VGAM2146 host target gene. LOC150372 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150372, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150372 BINDING SITE, designated SEQ ID:38942, to the nucleotide sequence of VGAM2146 RNA, herein designated VGAM RNA, also designated SEQ ID:4857.

[74290] Another function of VGAM2146 is therefore inhibition of LOC150372 (Accession XM_086893). Accordingly, utilities of VGAM2146 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150372. LOC153516 (Accession NM_138491) is another VGAM2146 host target gene. LOC153516 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153516 BINDING SITE, designated SEQ ID:28840, to the nucleotide sequence of VGAM2146 RNA, herein designated VGAM RNA, also designated SEQ ID:4857.

[74291] Another function of VGAM2146 is therefore inhibition of LOC153516 (Accession NM_138491). Accordingly, utilities of VGAM2146 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC153516. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2147 (VGAM2147) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74292] VGAM2147 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2147 was detected is described hereinabove with reference to Figs. 1-8.

[74293] VGAM2147 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2147 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74294] VGAM2147 gene encodes a VGAM2147 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2147 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2147 precursor RNA is desig-

nated SEQ ID:2133, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2133 is located at position 47097 relative to the genome of Rana Tigrina Ranavirus.

[74295] VGAM2147 precursor RNA folds onto itself, forming VGAM2147 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74296] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2147 folded precursor RNA into VGAM2147 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2147 RNA is designated SEQ ID:4858, and is provided hereinbelow with reference to the sequence

listing part.

[74297] VGAM2147 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2147 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2147 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74298] VGAM2147 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2147 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2147 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2147 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2147 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74299] The complementary binding of VGAM2147 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2147 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2147 host target RNA into VGAM2147 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74300] It is appreciated that VGAM2147 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2147 host target genes. The mRNA of each one of this plurality of VGAM2147 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2147 RNA, herein designated VGAM

RNA, and which when bound by VGAM2147 RNA causes inhibition of translation of respective one or more VGAM2147 host target proteins.

[74301] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2147 gene, herein designated VGAM GENE, on one or more VGAM2147 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74302] It is yet further appreciated that a function of VGAM2147 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2147 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2147 correlate with, and may be deduced from, the identity of the host target genes which VGAM2147 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74303] Nucleotide sequences of the VGAM2147 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2147 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2147 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2147 are further described hereinbelow with reference to Table 1.

[74304] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2147 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2147 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74305] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2147 gene, herein designated VGAM is

inhibition of expression of VGAM2147 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2147 correlate with, and may be deduced from, the identity of the target genes which VGAM2147 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74306] GAC1 (Accession NM_006338) is a VGAM2147 host target gene. GAC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GAC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAC1 BINDING SITE, designated SEQ ID:13038, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74307] A function of VGAM2147 is therefore inhibition of GAC1 (Accession NM_006338). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAC1. LAPTM5 (Accession NM_006762) is another VGAM2147 host target gene. LAPTM5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LAPTM5, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAPTM5 BINDING SITE, designated SEQ ID:13617, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74308] Another function of VGAM2147 is therefore inhibition of LAPTM5 (Accession NM_006762). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAPTM5. Sodium Channel, Voltage-gated, Type IV, Alpha Polypeptide (SCN4A, Accession NM_000334) is another VGAM2147 host target gene. SCN4A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCN4A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCN4A BINDING SITE, designated SEQ ID:5889, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74309] Another function of VGAM2147 is therefore inhibition of Sodium Channel, Voltage-gated, Type IV, Alpha Polypep-

tide (SCN4A, Accession NM_000334). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN4A. Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977) is another VGAM2147 host target gene. SLC22A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC22A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC22A3 BINDING SITE, designated SEQ ID:22506, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74310] Another function of VGAM2147 is therefore inhibition of Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977), a gene which is a sodium-ion dependent, high affinity carnitine transporter. also transports organic cations without the involvement of sodium. involved in the active cellular uptake of carnitine. Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with SLC22A3. The function of SLC22A3 has been established by previous studies. By PCR using degenerate oligonucleotides corresponding to common sequence motifs of amphiphilic solute facilitators (e.g., SLC22A1; 602607) on cDNA from a human kidney carcinoma cell line, Grundemann et al. (1998) isolated a cDNA encoding SLC22A3, which they termed 'extraneuronal transporter for monoamine transmitters,' or EMT. The SLC22A3 gene encodes a deduced 556-amino acid protein containing 12 transmembrane segments. Expression analysis showed uptake of known catecholamine substrates by SLC22A3. RT-PCR analysis detected SLC22A3 expression in brain cortex, heart, and liver. Wu et al. (1998) showed that recombinant rat Oct3 can transport a wide variety of cationic neurotoxins and neurotransmitters, including 1-methyl-4-phenylpyridinium ion (MPP+) and dopamine. Oct3 was inhibited by several steroids, with beta-estradiol the most potent inhibitor. The authors stated that the transport characteristics and steroid sensitivity of Oct3 provide strong evidence for its molecular identity as the extraneuronal monoamine transporter (uptake-2). Northern blot analysis detected Oct3 expression in a number of

rat tissues, including brain. In situ hybridization of rat brain showed that Oct3 is widely expressed in the brain, including in the hippocampus, cerebellum, and cerebral cortex. Wu et al. (1998) suggested that OCT3 plays a significant role in the disposition of cationic neurotoxins and neurotransmitters in the brain.

[74311] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74312] Grundemann, D.; Schechinger, B.; Rappold, G. A.; Schomig, E. : Molecular identification of the corticosterone-sensitive extraneuronal catecholamine transporter. Nature Neurosci. 1: 349-351, 1998. ; and

[74313] Wu, X.; Kekuda, R.; Huang, W.; Fei, Y.-J.; Leibach, F. H.; Chen, J.; Conway, S. J.; Ganapathy, V. : Identity of the organic cation transporter OCT3 as the extraneuronal monoamine transport.

[74314] Further studies establishing the function and utilities of SLC22A3 are found in John Hopkins OMIM database record ID 604842, and in sited publications numbered 694 and 5233 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.T-cell Leukemia Translocation Altered Gene (TCTA,

Accession NM_022171) is another VGAM2147 host target gene. TCTA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCTA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCTA BINDING SITE, designated SEQ ID:22731, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74315] Another function of VGAM2147 is therefore inhibition of T-cell Leukemia Translocation Altered Gene (TCTA, Accession NM_022171). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCTA. Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_007331) is another VGAM2147 host target gene. WHSC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WHSC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE, designated SEQ ID:14251, to the nucleotide sequence of VGAM2147 RNA,

herein designated VGAM RNA, also designated SEQ ID:4858.

[74316] Another function of VGAM2147 is therefore inhibition of Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_007331), a gene which binds covalently to and repairs g/t mismatches. Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WHSC1. The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.WWP2 (Accession XM_028151) is another VGAM2147 host target gene. WWP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WWP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WWP2 BINDING SITE, designated SEQ ID:30622, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74317] Another function of VGAM2147 is therefore inhibition of WWP2 (Accession XM_028151), a gene which exhibits

ubiquitin-protein ligase activity and contains WW and HECT domains. Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WWP2. The function of WWP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.Complement Component 1, Q Subcomponent, Receptor 1 (C1QR1, Accession NM_012072) is another VGAM2147 host target gene. C1QR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1QR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1QR1 BINDING SITE, designated SEQ ID:14332, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74318] Another function of VGAM2147 is therefore inhibition of Complement Component 1, Q Subcomponent, Receptor 1 (C1QR1, Accession NM_012072). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QR1.

CPR2 (Accession NM_030900) is another VGAM2147 host target gene. CPR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CPR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPR2 BINDING SITE, designated SEQ ID:25174, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74319] Another function of VGAM2147 is therefore inhibition of CPR2 (Accession NM_030900). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPR2. FLJ21195 (Accession NM_022469) is another VGAM2147 host target gene. FLJ21195 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21195 BINDING SITE, designated SEQ ID:22827, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4858.

[74320] Another function of VGAM2147 is therefore inhibition of FLJ21195 (Accession NM_022469). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21195. FLJ22795 (Accession NM_025084) is another VGAM2147 host target gene. FLJ22795 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22795, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22795 BINDING SITE, designated SEQ ID:24690, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74321] Another function of VGAM2147 is therefore inhibition of FLJ22795 (Accession NM_025084). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22795. Glutamate Receptor Interacting Protein 1 (GRIP1, Accession XM_047362) is another VGAM2147 host target gene. GRIP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded

by GRIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRIP1 BINDING SITE, designated SEQ ID:34962, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74322] Another function of VGAM2147 is therefore inhibition of Glutamate Receptor Interacting Protein 1 (GRIP1, Accession XM_047362). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIP1. KIAA0014 (Accession NM_014665) is another VGAM2147 host target gene. KIAA0014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0014 BINDING SITE, designated SEQ ID:16116, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74323] Another function of VGAM2147 is therefore inhibition of

KIAA0014 (Accession NM_014665). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0014. KIAA1157 (Accession XM_051093) is another VGAM2147 host target gene. KIAA1157 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1157, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1157 BINDING SITE, designated SEQ ID:35752, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74324] Another function of VGAM2147 is therefore inhibition of KIAA1157 (Accession XM_051093). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1157. KIAA1274 (Accession XM_166125) is another VGAM2147 host target gene. KIAA1274 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1274, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1274 BINDING SITE, designated SEQ ID:43912, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74325] Another function of VGAM2147 is therefore inhibition of KIAA1274 (Accession XM_166125). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1274. KIAA1393 (Accession XM_050793) is another VGAM2147 host target gene. KIAA1393 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1393, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1393 BINDING SITE, designated SEQ ID:35687, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74326] Another function of VGAM2147 is therefore inhibition of KIAA1393 (Accession XM_050793). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1393. KIAA1909 (Accession XM_057996) is another

VGAM2147 host target gene. KIAA1909 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1909, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1909 BINDING SITE, designated SEQ ID:36558, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74327] Another function of VGAM2147 is therefore inhibition of KIAA1909 (Accession XM_057996). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1909. Kallikrein 6 (neurosin, zyme) (KLK6, Accession NM_002774) is another VGAM2147 host target gene. KLK6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KLK6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLK6 BINDING SITE, designated SEQ ID:8665, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74328] Another function of VGAM2147 is therefore inhibition of Kallikrein 6 (neurosin, zyme) (KLK6, Accession NM_002774). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLK6. l(3)mbt-like 2 (Drosophila) (L3MBTL2, Accession XM_114201) is another VGAM2147 host target gene. L3MBTL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by L3MBTL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of L3MBTL2 BINDING SITE, designated SEQ ID:42792, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74329] Another function of VGAM2147 is therefore inhibition of l(3)mbt-like 2 (Drosophila) (L3MBTL2, Accession XM_114201). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with L3MBTL2. LIM Domain Kinase 2 (LIMK2, Accession NM_016733) is another VGAM2147 host target gene. LIMK2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region

of mRNA encoded by LIMK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIMK2 BINDING SITE, designated SEQ ID:18786, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74330] Another function of VGAM2147 is therefore inhibition of LIM Domain Kinase 2 (LIMK2, Accession NM_016733). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIMK2. MGC15476 (Accession NM_145056) is another VGAM2147 host target gene. MGC15476 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC15476, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15476 BINDING SITE, designated SEQ ID:29689, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74331] Another function of VGAM2147 is therefore inhibition of

MGC15476 (Accession NM_145056). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15476. Matrix Metalloproteinase 24 (membrane-inserted) (MMP24, Accession NM_006690) is another VGAM2147 host target gene. MMP24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MMP24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MMP24 BINDING SITE, designated SEQ ID:13505, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74332] Another function of VGAM2147 is therefore inhibition of Matrix Metalloproteinase 24 (membrane-inserted) (MMP24, Accession NM_006690). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMP24. Oxysterol Binding Protein-like 5 (OSBPL5, Accession XM_052567) is another VGAM2147 host target gene. OSBPL5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OS-

BPL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL5 BINDING SITE, designated SEQ ID:35989, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74333] Another function of VGAM2147 is therefore inhibition of Oxysterol Binding Protein-like 5 (OSBPL5, Accession XM_052567). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL5. SH3 and Multiple Ankyrin Repeat Domains 3 (SHANK3, Accession XM_037493) is another VGAM2147 host target gene. SHANK3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SHANK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SHANK3 BINDING SITE, designated SEQ ID:32633, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74334] Another function of VGAM2147 is therefore inhibition of SH3 and Multiple Ankyrin Repeat Domains 3 (SHANK3, Accession XM_037493). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHANK3. Ubiquitin Specific Protease 20 (USP20, Accession NM_006676) is another VGAM2147 host target gene. USP20 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP20, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP20 BINDING SITE, designated SEQ ID:13503, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74335] Another function of VGAM2147 is therefore inhibition of Ubiquitin Specific Protease 20 (USP20, Accession NM_006676). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP20. LOC145717 (Accession XM_039771) is another VGAM2147 host target gene. LOC145717 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by LOC145717, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145717 BINDING SITE, designated SEQ ID:33194, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74336] Another function of VGAM2147 is therefore inhibition of LOC145717 (Accession XM_039771). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145717. LOC157503 (Accession XM_098767) is another VGAM2147 host target gene. LOC157503 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157503, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157503 BINDING SITE, designated SEQ ID:41814, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74337] Another function of VGAM2147 is therefore inhibition of LOC157503 (Accession XM_098767). Accordingly, utilities

of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157503. LOC159199 (Accession XM_089441) is another VGAM2147 host target gene. LOC159199 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC159199, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159199 BINDING SITE, designated SEQ ID:39981, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74338] Another function of VGAM2147 is therefore inhibition of LOC159199 (Accession XM_089441). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159199. LOC205143 (Accession XM_119394) is another VGAM2147 host target gene. LOC205143 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC205143, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC205143 BINDING SITE, designated SEQ ID:43585, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74339] Another function of VGAM2147 is therefore inhibition of LOC205143 (Accession XM_119394). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC205143. LOC220537 (Accession XM_165406) is another VGAM2147 host target gene. LOC220537 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220537, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220537 BINDING SITE, designated SEQ ID:43623, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74340] Another function of VGAM2147 is therefore inhibition of LOC220537 (Accession XM_165406). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220537. LOC256230 (Accession XM_173371) is another VGAM2147 host target gene. LOC256230 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256230, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256230 BINDING SITE, designated SEQ ID:46541, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74341] Another function of VGAM2147 is therefore inhibition of LOC256230 (Accession XM_173371). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256230. LOC256231 (Accession XM_173372) is another VGAM2147 host target gene. LOC256231 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256231 BINDING SITE, designated SEQ ID:46543, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74342] Another function of VGAM2147 is therefore inhibition of

LOC256231 (Accession XM_173372). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256231. LOC256789 (Accession XM_173369) is another VGAM2147 host target gene. LOC256789 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256789, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256789 BINDING SITE, designated SEQ ID:46537, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74343] Another function of VGAM2147 is therefore inhibition of LOC256789 (Accession XM_173369). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256789. LOC93538 (Accession XM_051927) is another VGAM2147 host target gene. LOC93538 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93538, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of LOC93538 BINDING SITE, designated SEQ ID:35924, to the nucleotide sequence of VGAM2147 RNA, herein designated VGAM RNA, also designated SEQ ID:4858.

[74344] Another function of VGAM2147 is therefore inhibition of LOC93538 (Accession XM_051927). Accordingly, utilities of VGAM2147 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93538. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2148 (VGAM2148) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74345] VGAM2148 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2148 was detected is described hereinabove with reference to Figs. 1-8.

[74346] VGAM2148 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2148 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[74347] VGAM2148 gene encodes a VGAM2148 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2148 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2148 precursor RNA is designated SEQ ID:2134, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2134 is located at position 62911 relative to the genome of Rana Tigrina Ranavirus.

[74348] VGAM2148 precursor RNA folds onto itself, forming VGAM2148 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74349] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2148 folded precursor RNA into VGAM2148 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 73%) nucleotide sequence of VGAM2148 RNA is designated SEQ ID:4859, and is provided hereinbelow with reference to the sequence listing part.

[74350] VGAM2148 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2148 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2148 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74351] VGAM2148 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2148 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2148 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2148 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2148 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74352] The complementary binding of VGAM2148 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2148 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2148 host target RNA into VGAM2148 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74353] It is appreciated that VGAM2148 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2148 host target genes. The mRNA of each one of this plurality of VGAM2148 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2148 RNA, herein designated VGAM RNA, and which when bound by VGAM2148 RNA causes inhibition of translation of respective one or more VGAM2148 host target proteins.

[74354] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2148 gene, herein designated VGAM GENE, on one or more VGAM2148 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74355] It is yet further appreciated that a function of VGAM2148 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2148 correlate with, and may be deduced from, the identity of the host target genes which VGAM2148 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74356] Nucleotide sequences of the VGAM2148 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2148 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2148 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2148 are further described hereinbelow with reference to Table 1.

[74357] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2148 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2148 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74358] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2148 gene, herein designated VGAM is inhibition of expression of VGAM2148 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2148 correlate with, and may be deduced from, the identity of the target genes which VGAM2148 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74359] Low Density Lipoprotein Receptor (familial hypercholesterolemia) (LDLR, Accession NM_000527) is a VGAM2148 host target gene. LDLR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LDLR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LDLR BINDING SITE, designated SEQ ID:6126, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ

ID:4859.

[74360] A function of VGAM2148 is therefore inhibition of Low Density Lipoprotein Receptor (familial hypercholesterolemia) (LDLR, Accession NM_000527), a gene which also acts as a tumor suppressor. Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LDLR. The function of LDLR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1030.Platelet-activating Factor Acetylhydrolase, Isoform Ib, Alpha Subunit 45kDa (PAFAH1B1, Accession NM_000430) is another VGAM2148 host target gene. PAFAH1B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAFAH1B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAFAH1B1 BINDING SITE, designated SEQ ID:6007, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74361] Another function of VGAM2148 is therefore inhibition of

Platelet-activating Factor Acetylhydrolase, Isoform Ib, Alpha Subunit 45kDa (PAFAH1B1, Accession NM_000430). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAFAH1B1. RAD50 Homolog (S. cerevisiae) (RAD50, Accession NM_005732) is another VGAM2148 host target gene. RAD50 BINDING SITE1 and RAD50 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RAD50, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD50 BINDING SITE1 and RAD50 BINDING SITE2, designated SEQ ID:12296 and SEQ ID:28554 respectively, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74362] Another function of VGAM2148 is therefore inhibition of RAD50 Homolog (S. cerevisiae) (RAD50, Accession NM_005732), a gene which is involved in dna double-strand break repair (dsbr). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD50.

The function of RAD50 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM132.FLJ10618 (Accession NM_018155) is another VGAM2148 host target gene. FLJ10618 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10618, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10618 BINDING SITE, designated SEQ ID:19965, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74363] Another function of VGAM2148 is therefore inhibition of FLJ10618 (Accession NM_018155). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10618. KIAA0560 (Accession XM_029045) is another VGAM2148 host target gene. KIAA0560 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0560, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0560 BINDING SITE, designated SEQ ID:30836, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74364] Another function of VGAM2148 is therefore inhibition of KIAA0560 (Accession XM_029045). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0560. KIAA0748 (Accession NM_014796) is another VGAM2148 host target gene. KIAA0748 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0748, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0748 BINDING SITE, designated SEQ ID:16700, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74365] Another function of VGAM2148 is therefore inhibition of KIAA0748 (Accession NM_014796). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0748. KIAA0930 (Accession XM_047214) is another

VGAM2148 host target gene. KIAA0930 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0930, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0930 BINDING SITE, designated SEQ ID:34910, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74366] Another function of VGAM2148 is therefore inhibition of KIAA0930 (Accession XM_047214). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0930. KIAA1238 (Accession XM_048675) is another VGAM2148 host target gene. KIAA1238 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1238, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1238 BINDING SITE, designated SEQ ID:35214, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74367] Another function of VGAM2148 is therefore inhibition of KIAA1238 (Accession XM_048675). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1238. SEF (Accession XM_045300) is another VGAM2148 host target gene. SEF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEF BINDING SITE, designated SEQ ID:34425, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74368] Another function of VGAM2148 is therefore inhibition of SEF (Accession XM_045300). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEF. Ubiquitin-like, Containing PHD and RING Finger Domains, 2 (UHRF2, Accession XM_055929) is another VGAM2148 host target gene. UHRF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UHRF2, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UHRF2 BINDING SITE, designated SEQ ID:36355, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74369] Another function of VGAM2148 is therefore inhibition of Ubiquitin-like, Containing PHD and RING Finger Domains, 2 (UHRF2, Accession XM_055929). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UHRF2. LOC133258 (Accession XM_068260) is another VGAM2148 host target gene. LOC133258 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC133258, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133258 BINDING SITE, designated SEQ ID:37377, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74370] Another function of VGAM2148 is therefore inhibition of LOC133258 (Accession XM_068260). Accordingly, utilities

of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133258. LOC146229 (Accession XM_085387) is another VGAM2148 host target gene. LOC146229 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146229 BINDING SITE, designated SEQ ID:38106, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74371] Another function of VGAM2148 is therefore inhibition of LOC146229 (Accession XM_085387). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146229. LOC148824 (Accession XM_097527) is another VGAM2148 host target gene. LOC148824 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148824, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC148824 BINDING SITE, designated SEQ ID:40907, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74372] Another function of VGAM2148 is therefore inhibition of LOC148824 (Accession XM_097527). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148824. LOC221042 (Accession XM_167669) is another VGAM2148 host target gene. LOC221042 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221042, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221042 BINDING SITE, designated SEQ ID:44749, to the nucleotide sequence of VGAM2148 RNA, herein designated VGAM RNA, also designated SEQ ID:4859.

[74373] Another function of VGAM2148 is therefore inhibition of LOC221042 (Accession XM_167669). Accordingly, utilities of VGAM2148 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221042. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2149 (VGAM2149) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74374] VGAM2149 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2149 was detected is described hereinabove with reference to Figs. 1-8.

[74375] VGAM2149 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2149 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74376] VGAM2149 gene encodes a VGAM2149 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2149 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2149 precursor RNA is designated SEQ ID:2135, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2135 is located at position 50593 relative to the

genome of Rana Tigrina Ranavirus.

[74377] VGAM2149 precursor RNA folds onto itself, forming VGAM2149 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74378] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2149 folded precursor RNA into VGAM2149 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2149 RNA is designated SEQ ID:4860, and is provided hereinbelow with reference to the sequence listing part.

[74379] VGAM2149 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2149 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2149 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74380] VGAM2149 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2149 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2149 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2149 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2149 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74381] The complementary binding of VGAM2149 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2149 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2149 host target RNA into VGAM2149 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74382] It is appreciated that VGAM2149 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2149 host target genes. The mRNA of each one of this plurality of VGAM2149 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2149 RNA, herein designated VGAM RNA, and which when bound by VGAM2149 RNA causes inhibition of translation of respective one or more VGAM2149 host target proteins.

[74383] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2149 gene, herein designated VGAM GENE, on one or more VGAM2149 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74384] It is yet further appreciated that a function of VGAM2149 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2149 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2149

correlate with, and may be deduced from, the identity of the host target genes which VGAM2149 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74385] Nucleotide sequences of the VGAM2149 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2149 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2149 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2149 are further described hereinbelow with reference to Table 1.

[74386] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2149 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2149 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74387] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2149 gene, herein designated VGAM is inhibition of expression of VGAM2149 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2149 correlate with, and may be deduced

from, the identity of the target genes which VGAM2149 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74388] ATP-binding Cassette, Sub-family A (ABC1), Member 1 (ABCA1, Accession NM_005502) is a VGAM2149 host target gene. ABCA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCA1 BINDING SITE, designated SEQ ID:12014, to the nucleotide sequence of VGAM2149 RNA, herein designated VGAM RNA, also designated SEQ ID:4860.

[74389] A function of VGAM2149 is therefore inhibition of ATP-binding Cassette, Sub-family A (ABC1), Member 1 (ABCA1, Accession NM_005502), a gene which camp-dependent and sulfonylurea-sensitive anion transporter. Accordingly, utilities of VGAM2149 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCA1. The function of ABCA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to VGAM1956.General Transcription Factor II, I (GTF2I, Accession NM_032999) is another VGAM2149 host target gene. GTF2I BINDING SITE1 and GTF2I BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GTF2I, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTF2I BINDING SITE1 and GTF2I BINDING SITE2, designated SEQ ID:26884 and SEQ ID:26888 respectively, to the nucleotide sequence of VGAM2149 RNA, herein designated VGAM RNA, also designated SEQ ID:4860.

[74390] Another function of VGAM2149 is therefore inhibition of General Transcription Factor II, I (GTF2I, Accession NM_032999), a gene which interacts with the basal transcription machinery by coordinating the formation of a multiprotein complex at the c-fos promoter, and linking specific signal responsive activator complexes. Accordingly, utilities of VGAM2149 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2I. The function of GTF2I and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to VGAM115.FLJ21736 (Accession NM_024922) is another VGAM2149 host target gene. FLJ21736 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ21736, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21736 BINDING SITE, designated SEQ ID:24457, to the nucleotide sequence of VGAM2149 RNA, herein designated VGAM RNA, also designated SEQ ID:4860.

[74391] Another function of VGAM2149 is therefore inhibition of FLJ21736 (Accession NM_024922). Accordingly, utilities of VGAM2149 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21736. KIAA1582 (Accession XM_037262) is another VGAM2149 host target gene. KIAA1582 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1582, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1582 BINDING SITE, designated SEQ ID:32588, to the

nucleotide sequence of VGAM2149 RNA, herein designated VGAM RNA, also designated SEQ ID:4860.

[74392] Another function of VGAM2149 is therefore inhibition of KIAA1582 (Accession XM_037262). Accordingly, utilities of VGAM2149 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1582. KIAA1775 (Accession NM_033100) is another VGAM2149 host target gene. KIAA1775 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1775, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1775 BINDING SITE, designated SEQ ID:26940, to the nucleotide sequence of VGAM2149 RNA, herein designated VGAM RNA, also designated SEQ ID:4860.

[74393] Another function of VGAM2149 is therefore inhibition of KIAA1775 (Accession NM_033100). Accordingly, utilities of VGAM2149 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1775. Lysosomal-associated Membrane Protein 3 (LAMP3, Accession XM_003022) is another VGAM2149 host target gene. LAMP3 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by LAMP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAMP3 BINDING SITE, designated SEQ ID:29918, to the nucleotide sequence of VGAM2149 RNA, herein designated VGAM RNA, also designated SEQ ID:4860.

[74394] Another function of VGAM2149 is therefore inhibition of Lysosomal-associated Membrane Protein 3 (LAMP3, Accession XM_003022). Accordingly, utilities of VGAM2149 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMP3. LW-1 (Accession XM_013128) is another VGAM2149 host target gene. LW-1 BINDING SITE1 and LW-1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LW-1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LW-1 BINDING SITE1 and LW-1 BINDING SITE2, designated SEQ ID:30232 and SEQ ID:18241 respectively, to the nucleotide sequence of VGAM2149 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4860.

[74395] Another function of VGAM2149 is therefore inhibition of LW-1 (Accession XM_013128). Accordingly, utilities of VGAM2149 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LW-1. LOC145781 (Accession XM_085235) is another VGAM2149 host target gene. LOC145781 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145781, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145781 BINDING SITE, designated SEQ ID:37981, to the nucleotide sequence of VGAM2149 RNA, herein designated VGAM RNA, also designated SEQ ID:4860.

[74396] Another function of VGAM2149 is therefore inhibition of LOC145781 (Accession XM_085235). Accordingly, utilities of VGAM2149 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145781. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2150 (VGAM2150) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74397] VGAM2150 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2150 was detected is described hereinabove with reference to Figs. 1-8.

[74398] VGAM2150 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2150 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74399] VGAM2150 gene encodes a VGAM2150 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2150 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2150 precursor RNA is designated SEQ ID:2136, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2136 is located at position 52091 relative to the genome of Rana Tigrina Ranavirus.

[74400] VGAM2150 precursor RNA folds onto itself, forming

VGAM2150 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74401] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2150 folded precursor RNA into VGAM2150 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2150 RNA is designated SEQ ID:4861, and is provided hereinbelow with reference to the sequence listing part.

[74402] VGAM2150 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2150 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2150 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74403] VGAM2150 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2150 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2150 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2150 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2150 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74404] The complementary binding of VGAM2150 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2150 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2150 host target RNA into VGAM2150 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74405] It is appreciated that VGAM2150 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2150 host target genes. The mRNA of each one of this plurality of VGAM2150 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2150 RNA, herein designated VGAM RNA, and which when bound by VGAM2150 RNA causes inhibition of translation of respective one or more VGAM2150 host target proteins.

[74406] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2150 gene, herein designated VGAM GENE, on one or more VGAM2150 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74407] It is yet further appreciated that a function of VGAM2150 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2150 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2150 correlate with, and may be deduced from, the identity of the host target genes which VGAM2150 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74408] Nucleotide sequences of the VGAM2150 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2150 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2150 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2150 are further described hereinbelow with reference to Table 1.

[74409] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2150 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2150 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74410] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2150 gene, herein designated VGAM is inhibition of expression of VGAM2150 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2150 correlate with, and may be deduced from, the identity of the target genes which VGAM2150 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74411] Membrane-spanning 4-domains, Subfamily A, Member 1 (MS4A1, Accession NM_000139) is a VGAM2150 host target gene. MS4A1 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by MS4A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MS4A1 BINDING SITE, designated SEQ ID:5635, to the nucleotide sequence of VGAM2150 RNA, herein designated VGAM RNA, also designated SEQ ID:4861.

[74412] A function of VGAM2150 is therefore inhibition of Membrane-spanning 4-domains, Subfamily A, Member 1 (MS4A1, Accession NM_000139), a gene which may be involved in the regulation of b-cell activation and proliferation. Accordingly, utilities of VGAM2150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MS4A1. The function of MS4A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM362.DKFZp434F1719 (Accession NM_032248) is another VGAM2150 host target gene. DKFZp434F1719 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434F1719, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434F1719 BINDING SITE, designated SEQ ID:25987, to the nucleotide sequence of VGAM2150 RNA, herein designated VGAM RNA, also designated SEQ ID:4861.

[74413] Another function of VGAM2150 is therefore inhibition of DKFZp434F1719 (Accession NM_032248). Accordingly, utilities of VGAM2150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434F1719. FLJ14082 (Accession NM_025024) is another VGAM2150 host target gene. FLJ14082 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14082, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14082 BINDING SITE, designated SEQ ID:24607, to the nucleotide sequence of VGAM2150 RNA, herein designated VGAM RNA, also designated SEQ ID:4861.

[74414] Another function of VGAM2150 is therefore inhibition of FLJ14082 (Accession NM_025024). Accordingly, utilities of VGAM2150 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ14082. KIAA0471 (Accession NM_014857) is another VGAM2150 host target gene. KIAA0471 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0471, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0471 BINDING SITE, designated SEQ ID:16906, to the nucleotide sequence of VGAM2150 RNA, herein designated VGAM RNA, also designated SEQ ID:4861.

[74415] Another function of VGAM2150 is therefore inhibition of KIAA0471 (Accession NM_014857). Accordingly, utilities of VGAM2150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0471. KIAA0523 (Accession XM_041964) is another VGAM2150 host target gene. KIAA0523 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0523, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0523 BINDING SITE, designated SEQ ID:33645, to the

nucleotide sequence of VGAM2150 RNA, herein designated VGAM RNA, also designated SEQ ID:4861.

[74416] Another function of VGAM2150 is therefore inhibition of KIAA0523 (Accession XM_041964). Accordingly, utilities of VGAM2150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0523. KIAA1674 (Accession XM_044065) is another VGAM2150 host target gene. KIAA1674 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1674, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1674 BINDING SITE, designated SEQ ID:34101, to the nucleotide sequence of VGAM2150 RNA, herein designated VGAM RNA, also designated SEQ ID:4861.

[74417] Another function of VGAM2150 is therefore inhibition of KIAA1674 (Accession XM_044065). Accordingly, utilities of VGAM2150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1674. KIAA1775 (Accession NM_033100) is another VGAM2150 host target gene. KIAA1775 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1775, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1775 BINDING SITE, designated SEQ ID:26939, to the nucleotide sequence of VGAM2150 RNA, herein designated VGAM RNA, also designated SEQ ID:4861.

[74418] Another function of VGAM2150 is therefore inhibition of KIAA1775 (Accession NM_033100). Accordingly, utilities of VGAM2150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1775. LOC145135 (Accession XM_096721) is another VGAM2150 host target gene. LOC145135 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145135, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145135 BINDING SITE, designated SEQ ID:40497, to the nucleotide sequence of VGAM2150 RNA, herein designated VGAM RNA, also designated SEQ ID:4861.

[74419] Another function of VGAM2150 is therefore inhibition of LOC145135 (Accession XM_096721). Accordingly, utilities

of VGAM2150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145135. LOC92285 (Accession XM_044051) is another VGAM2150 host target gene. LOC92285 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92285, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92285 BINDING SITE, designated SEQ ID:34094, to the nucleotide sequence of VGAM2150 RNA, herein designated VGAM RNA, also designated SEQ ID:4861.

[74420] Another function of VGAM2150 is therefore inhibition of LOC92285 (Accession XM_044051). Accordingly, utilities of VGAM2150 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92285. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2151 (VGAM2151) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74421] VGAM2151 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2151 was detected is described hereinabove with reference to Figs. 1-8.

[74422] VGAM2151 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2151 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74423] VGAM2151 gene encodes a VGAM2151 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2151 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2151 precursor RNA is designated SEQ ID:2137, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2137 is located at position 54437 relative to the genome of Rana Tigrina Ranavirus.

[74424] VGAM2151 precursor RNA folds onto itself, forming VGAM2151 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74425] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2151 folded precursor RNA into VGAM2151 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2151 RNA is designated SEQ ID:4862, and is provided hereinbelow with reference to the sequence listing part.

[74426] VGAM2151 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2151 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2151 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[74427] VGAM2151 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2151 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2151 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2151 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2151 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74428] The complementary binding of VGAM2151 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2151 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2151 host target RNA into VGAM2151 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74429] It is appreciated that VGAM2151 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2151 host target genes. The mRNA of each one of this plurality of VGAM2151 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2151 RNA, herein designated VGAM RNA, and which when bound by VGAM2151 RNA causes inhibition of translation of respective one or more VGAM2151 host target proteins.

[74430] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2151 gene, herein designated VGAM GENE, on one or more VGAM2151 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74431] It is yet further appreciated that a function of VGAM2151 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2151 correlate with, and may be deduced from, the identity of the host target genes which VGAM2151 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74432] Nucleotide sequences of the VGAM2151 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2151 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2151 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2151 are further described hereinbelow with reference to Table 1.

[74433] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2151 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2151 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74434] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2151 gene, herein designated VGAM is inhibition of expression of VGAM2151 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2151 correlate with, and may be deduced from, the identity of the target genes which VGAM2151 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74435] A Disintegrin and Metalloproteinase Domain 10 (ADAM10, Accession NM_001110) is a VGAM2151 host target gene.

ADAM10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ADAM10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAM10 BINDING SITE, designated SEQ ID:6768, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74436] A function of VGAM2151 is therefore inhibition of A Disintegrin and Metalloproteinase Domain 10 (ADAM10, Accession NM_001110), a gene which Member of ADAM family of zinc metalloproteases. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAM10. The function of ADAM10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM706.ADP-ribosyltransferase (NAD+; poly (ADP-ribose) Polymerase) (ADPRT, Accession NM_001618) is another VGAM2151 host target gene. ADPRT BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ADPRT,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADPRT BINDING SITE, designated SEQ ID:7325, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74437] Another function of VGAM2151 is therefore inhibition of ADP-ribosyltransferase (NAD+; poly (ADP-ribose) Polymerase) (ADPRT, Accession NM_001618), a gene which catalyzes addition of mono-ADP-ribose to arginine residues of proteins, inhibits Pol II transcription. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADPRT. The function of ADPRT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM506.1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) (AGPAT2, Accession NM_006412) is another VGAM2151 host target gene. AGPAT2 BINDING SITE1 and AGPAT2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AGPAT2, corresponding to

HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AGPAT2 BINDING SITE1 and AGPAT2 BINDING SITE2, designated SEQ ID:13118 and SEQ ID:32745 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74438] Another function of VGAM2151 is therefore inhibition of 1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta) (AGPAT2, Accession NM_006412). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AGPAT2. V-raf Murine Sarcoma 3611 Viral Oncogene Homolog 1 (ARAF1, Accession XM_033884) is another VGAM2151 host target gene. ARAF1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARAF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARAF1 BINDING SITE, designated SEQ ID:31982, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ

ID:4862.

[74439] Another function of VGAM2151 is therefore inhibition of V-raf Murine Sarcoma 3611 Viral Oncogene Homolog 1 (ARAF1, Accession XM_033884), a gene which may play a critical role in cell growth and development. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARAF1. The function of ARAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM996.Achaete-scute Complex-like 2 (Drosophila) (ASCL2, Accession XM_113673) is another VGAM2151 host target gene. ASCL2 BINDING SITE1 and ASCL2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ASCL2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ASCL2 BINDING SITE1 and ASCL2 BINDING SITE2, designated SEQ ID:42324 and SEQ ID:11671 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74440] Another function of VGAM2151 is therefore inhibition of Achaete-scute Complex-like 2 (Drosophila) (ASCL2, Accession XM_113673), a gene which is involved in the determination of the neuronal precursors in the nervous system. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASCL2. The function of ASCL2 has been established by previous studies. The mammalian Achaete-Scute homologs are conserved mammalian cognates of the Drosophila Achaete-Scute complex. In rodents, 2 such genes have been identified: Mash1 (ASCL1; 100790) is expressed in neuronal progenita, while Mash2 (ASCL2) is expressed in spongiotrophoblast cells and their precursors. Both are members of the basic helix-loop-helix (bHLH) gene family, which includes MYC (OMIM Ref. No. 190080) and MYOD1 (OMIM Ref. No. 159970). Mash1 and Mash2 function as lineage-specific transcription factors essential for development of the neurectoderm and trophectoderm, respectively. Mice deficient for Mash2 die at 10 days postcoitum due to placental failure (Guillemot et al., 1994). In contrast, chimeric mice with heterozygous extraembryonic tissues and homozygous embryonic tissues are viable and normal, indicating that

this gene, although essential for development of a placenta, is not important for the development of the embryo proper. Alders et al. (1997) noted that in the mouse, the Mash2 gene is subject to genomic imprinting with only the maternal allele being active. Mice carrying the homozygously mutated Mash2 gene die at 10 days postcoitum, as do heterozygous mice who inherited the mutant allele from their mother. Heterozygous mice who inherited the mutant allele from their father are viable. This phenomenon of paternal imprinting of a gene being critical for development of a placenta is an exception to the common imprinting rule: nuclear transplantation studies in mice show that imprinting is biased toward embryonic versus extraembryonic tissues with preferential expression of the maternal and paternal alleles in the embryo and placenta, respectively. Mash2 in the mouse maps to distal chromosome 7 and is closely linked to 3 other imprinted genes, Ins2 (OMIM Ref. No. 176730), Igf2 (OMIM Ref. No. 147470), and H19 (OMIM Ref. No. 103280). The conserved syntenic human chromosome region is 11p15.5. Alders et al. (1997) took advantage of this fact to isolate the human homolog of the MASH2 gene, which they designated HASH2. They showed that the gene maps

proximal to, and in close proximity of, IGF2 and that the gene order in this region is HASH2-INS-IGF2-H19-tel. Expression studies showed that HASH2 is expressed in extravillus trophoblast cells only. The lack of expression in nonmalignant hydatidiform (androgenetic) moles indicated that HASH2 is also imprinted in man.

[74441] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74442] Alders, M.; Hodges, M.; Hadjantonakis, A.-K.; Postmus, J.; van Wijk, I.; Bliek, J.; de Meulemeester, M.; Westerveld, A.; Guillemot, F.; Oudejans, C.; Little, P.; Mannens, M. : The human Achaete-Scute homologue 2 (ASCL2,HASH2) maps to chromosome 11p15.5, close to IGF2 and is expressed in extravillus trophoblasts. Hum. Molec. Genet. 6: 859-867, 1997. ; and

[74443] Guillemot, F.; Nagy, A.; Auerbach, A.; Rossant, J.; Joyner, A. L. : Essential role of Mash-2 in extraembryonic development. Nature 371: 333-336, 1994.

[74444] Further studies establishing the function and utilities of ASCL2 are found in John Hopkins OMIM database record ID 601886, and in sited publications numbered 6701-6702 listed in the bibliography section hereinbelow,

which are also hereby incorporated by reference.B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_138576) is another VGAM2151 host target gene. BCL11B BINDING SITE1 and BCL11B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by BCL11B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL11B BINDING SITE1 and BCL11B BINDING SITE2, designated SEQ ID:28891 and SEQ ID:23167 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74445] Another function of VGAM2151 is therefore inhibition of B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_138576). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL11B. Breakpoint Cluster Region (BCR, Accession NM_004327) is another VGAM2151 host target gene. BCR BINDING SITE1 and BCR BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by BCR, corresponding to HOST TARGET binding

sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCR BINDING SITE1 and BCR BINDING SITE2, designated SEQ ID:10527 and SEQ ID:31989 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74446] Another function of VGAM2151 is therefore inhibition of Breakpoint Cluster Region (BCR, Accession NM_004327), a gene which is a serine/threonine kinase that involves in the t(9;22) translocation (Philadelphia chromosome). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCR. The function of BCR has been established by previous studies. The normal BCR gene occupies a region of about 135 kb on chromosome 22. It is expressed as mRNAs of 4.5- and 6.7-kb, which apparently encode for the same cytoplasmic 160-kD protein, and contains 23 exons as well as an unusual inverted repeat flanking the first exon. The BCR protein reportedly contains a unique serine/threonine kinase activity and at least two SH2 binding sites encoded in its first exon and a C-terminal domain that functions as a GTPase activating

protein for p21(rac) (Diekmann et al., 1991); see rac serine/threonine protein kinase (OMIM Ref. No. 164730). Chissoe et al. (1995) sequenced the complete BCR gene and greater than 80% of the human ABL gene, which are both involved in the t(9;22) translocation (Philadelphia chromosome) associated with more than 90% of chronic myelogenous leukemia, 25 to 30% of adult and 2 to 10% of childhood acute lymphoblastic leukemia, and rare cases of acute myelogenous leukemia. Comparison of the gene with its cDNA sequence revealed the positions of 23 BCR exons and putative alternative BCR first and second exons. From the sequence of 4 newly studied Philadelphia chromosome translocations and a review of several other previously sequenced breakpoints, Chissoe et al. (1995) could discern no consistent breakpoint features. No clear-cut mechanism for Philadelphia chromosome translocation was evident. Because tyrosine kinase activity is essential to the transforming function of BCR-ABL, Druker et al. (2001) reasoned that an inhibitor of the kinase may be an effective treatment for CML. They found that indeed a tyrosine kinase inhibitor (OMIM Ref. No. STI571) was well tolerated and had significant antileukemic activity in patients with CML in whom treatment with standard

chemotherapy had failed. This experience demonstrated the potential for the development of anticancer drugs based on the specific molecular abnormality present in a human cancer. Animal model experiments lend further support to the function of BCR. Cancer is thought to arise from multiple genetic events that establish irreversible malignancy. A different mechanism might be present in certain leukemias initiated by a chromosomal translocation. Huettner et al. (2000) adopted a new approach to determine if ablation of the genetic abnormality is sufficient for reversion. They generated a conditional transgenic model of BCR-ABL-induced leukemia. The most common form of the product of the fusion gene, p210 BCR-ABL1, is found in more than 90% of patients with chronic myelogenous leukemia and in up to 15% of adult patients with de novo acute lymphoblastic leukemia. Efforts to establish a useful transgenic model had been hampered by embryonic lethality when the oncogene is expressed during embryogenesis, by reduced penetrance, or by extremely long latency. Huettner et al. (2000) used the 'knock-in' approach to induce leukemia by p190 BCR-ABL1 (Castellanos et al., 1997). Lethal leukemia developed within an acceptable time frame in all animals, and com-

plete remission was achieved by suppression of BCR-ABL1 expression, even after multiple rounds of induction and reversion. The results demonstrated that BCR-ABL1 is required for both induction and maintenance of leukemia. The findings suggested that complete and lasting remissions can be achieved if the genetic abnormality is abolished or silenced before secondary mutations are acquired. The results have implications for therapies that directly target leukemia oncogenes, with a relevant example being the use of BCR-ABL1-specific tyrosine kinase inhibitors.

[74447] It is appreciated that the abovementioned animal model for BCR is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[74448] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74449] Chissoe, S. L.; Bodenteich, A.; Wang, Y.-F.; Wang, Y.-P.; Burian, D.; Clifton, S. W.; Crabtree, J.; Freeman, A.; Iyer, K.; Jian, L.; Ma, Y.; McLaury, H.-J.; Pan, H.-Q.; Sarhan, O. H.; Toth, S.; Wang, Z.; Zhang, G.; Heisterkamp, N.; Groffen, J.; Roe, B. A. : Sequence and analysis of the human ABL gene,

the BCR gene, and regions involved in the Philadelphia chromosomal translocation. Genomics 27: 67-82, 1995. ; and

[74450] Huettner, C. S.; Zhang, P.; Van Etten, R. A.; Tenen, D. G. : Reversibility of acute B-cell leukaemia induced by BCR-ABL1. Nature Genet. 24: 57-60, 2000.

[74451] Further studies establishing the function and utilities of BCR are found in John Hopkins OMIM database record ID 151410, and in sited publications numbered 11081-11088, 11375-11092, 11411, 11412-11416, 3659, 11417-11427, 3104, 11428-11441, 1135 and 11475-11496 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Cadherin Related 23 (CDH23, Accession NM_052836) is another VGAM2151 host target gene. CDH23 BINDING SITE1 and CDH23 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CDH23, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDH23 BINDING SITE1 and CDH23 BINDING SITE2, designated SEQ ID:27418 and SEQ ID:22670 respectively, to the nucleotide sequence of VGAM2151 RNA,

herein designated VGAM RNA, also designated SEQ ID:4862.

[74452] Another function of VGAM2151 is therefore inhibition of Cadherin Related 23 (CDH23, Accession NM_052836). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH23. DXYS155E (Accession NM_005088) is another VGAM2151 host target gene. DXYS155E BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DXYS155E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DXYS155E BINDING SITE, designated SEQ ID:11541, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74453] Another function of VGAM2151 is therefore inhibition of DXYS155E (Accession NM_005088), a gene which may be involved in b-cell activation. may also be involved in signal transduction and gene regulation. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

DXYS155E. The function of DXYS155E and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM766.Engrailed Homolog 2 (EN2, Accession NM_001427) is another VGAM2151 host target gene. EN2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EN2 BINDING SITE, designated SEQ ID:7146, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74454] Another function of VGAM2151 is therefore inhibition of Engrailed Homolog 2 (EN2, Accession NM_001427), a gene which may be required for normal cerebellar development; a homeobox protein, very strongly similar to murine En2. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EN2. The function of EN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM232.F-box

and Leucine-rich Repeat Protein 5 (FBXL5, Accession NM_033535) is another VGAM2151 host target gene. FBXL5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FBXL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXL5 BINDING SITE, designated SEQ ID:27304, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74455] Another function of VGAM2151 is therefore inhibition of F-box and Leucine-rich Repeat Protein 5 (FBXL5, Accession NM_033535), a gene which is a putative SCF ubiquitin ligase subunit involved in protein degradation. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXL5. The function of FBXL5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM61.F-box and Leucine-rich Repeat Protein 7 (FBXL7, Accession NM_012304) is another VGAM2151 host target gene. FBXL7 BINDING SITE is HOST

TARGET binding site found in the 5` untranslated region of mRNA encoded by FBXL7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXL7 BINDING SITE, designated SEQ ID:14672, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74456] Another function of VGAM2151 is therefore inhibition of F-box and Leucine-rich Repeat Protein 7 (FBXL7, Accession NM_012304), a gene which may be involved in in phosphorylation-dependent ubiquitination. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXL7. The function of FBXL7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1924.Forkhead Box D2 (FOXD2, Accession NM_004474) is another VGAM2151 host target gene. FOXD2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FOXD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of FOXD2 BINDING SITE, designated SEQ ID:10788, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74457] Another function of VGAM2151 is therefore inhibition of Forkhead Box D2 (FOXD2, Accession NM_004474). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXD2. Follistatin-like 1 (FSTL1, Accession NM_007085) is another VGAM2151 host target gene. FSTL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FSTL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FSTL1 BINDING SITE, designated SEQ ID:13951, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74458] Another function of VGAM2151 is therefore inhibition of Follistatin-like 1 (FSTL1, Accession NM_007085), a gene which may modulate the action of some growth factors on cell proliferation and differentiation. Accordingly, utilities

of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FSTL1. The function of FSTL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM791.HIR Histone Cell Cycle Regulation Defective Homolog A (S. cerevisiae) (HIRA, Accession NM_003325) is another VGAM2151 host target gene. HIRA BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HIRA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIRA BINDING SITE, designated SEQ ID:9326, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74459] Another function of VGAM2151 is therefore inhibition of HIR Histone Cell Cycle Regulation Defective Homolog A (S. cerevisiae) (HIRA, Accession NM_003325), a gene which could have a part in mechanisms of transcriptional regulation similar to that played by yeast hir1 and hir2 together. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical

conditions associated with HIRA. The function of HIRA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1259.Homeo Box A3 (HOXA3, Accession NM_030661) is another VGAM2151 host target gene. HOXA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HOXA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOXA3 BINDING SITE, designated SEQ ID:24994, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74460] Another function of VGAM2151 is therefore inhibition of Homeo Box A3 (HOXA3, Accession NM_030661). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXA3. IQ Motif Containing GTPase Activating Protein 2 (IQGAP2, Accession NM_006633) is another VGAM2151 host target gene. IQGAP2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IQGAP2, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IQGAP2 BINDING SITE, designated SEQ ID:13429, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74461] Another function of VGAM2151 is therefore inhibition of IQ Motif Containing GTPase Activating Protein 2 (IQGAP2, Accession NM_006633), a gene which Inhibits GTPase activity of Cdc42 and Rac1. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IQGAP2. The function of IQGAP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM110.Integrin, Alpha M (complement component receptor 3, alpha; also known as CD11b (p170), Macrophage Antigen Alpha Polypeptide) (ITGAM, Accession NM_000632) is another VGAM2151 host target gene. ITGAM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGAM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of ITGAM BINDING SITE, designated SEQ ID:6250, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74462] Another function of VGAM2151 is therefore inhibition of Integrin, Alpha M (complement component receptor 3, alpha; also known as CD11b (p170), Macrophage Antigen Alpha Polypeptide) (ITGAM, Accession NM_000632), a gene which is invovled in various adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAM. The function of ITGAM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1386.Inositol 1,4,5-triphosphate Receptor, Type 2 (ITPR2, Accession NM_002223) is another VGAM2151 host target gene. ITPR2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ITPR2, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITPR2 BINDING SITE, designated SEQ ID:7993, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74463] Another function of VGAM2151 is therefore inhibition of Inositol 1,4,5-triphosphate Receptor, Type 2 (ITPR2, Accession NM_002223). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPR2. Potassium Voltage-gated Channel, Shal-related Subfamily, Member 2 (KCND2, Accession NM_012281) is another VGAM2151 host target gene. KCND2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCND2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCND2 BINDING SITE, designated SEQ ID:14609, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74464] Another function of VGAM2151 is therefore inhibition of Potassium Voltage-gated Channel, Shal-related Subfamily,

Member 2 (KCND2, Accession NM_012281), a gene which is prominent in the repolarization phase of the action potential. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCND2. The function of KCND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM449.LIM Domain Only 2 (rhombotin-like 1) (LMO2, Accession NM_005574) is another VGAM2151 host target gene. LMO2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LMO2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LMO2 BINDING SITE, designated SEQ ID:12103, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74465] Another function of VGAM2151 is therefore inhibition of LIM Domain Only 2 (rhombotin-like 1) (LMO2, Accession NM_005574). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LMO2. Mitogen-activated

Protein Kinase Kinase Kinase 5 (MAP3K5, Accession NM_005923) is another VGAM2151 host target gene. MAP3K5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAP3K5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K5 BINDING SITE, designated SEQ ID:12547, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74466] Another function of VGAM2151 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 5 (MAP3K5, Accession NM_005923), a gene which phosphorylates and activates two different subgroups of map kinase kinases, mkk4/sek1 and mkk3/mapkk6 (or mkk6) .overexpression induces apoptotic cell death. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K5. The function of MAP3K5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1622.Mitogen-activated Protein

Kinase Kinase Kinase 7 Interacting Protein 2 (MAP3K7IP2, Accession NM_015093) is another VGAM2151 host target gene. MAP3K7IP2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAP3K7IP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K7IP2 BINDING SITE, designated SEQ ID:17486, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74467] Another function of VGAM2151 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 7 Interacting Protein 2 (MAP3K7IP2, Accession NM_015093). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K7IP2. Mitogen-activated Protein Kinase Kinase Kinase Kinase 5 (MAP4K5, Accession NM_006575) is another VGAM2151 host target gene. MAP4K5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAP4K5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of MAP4K5 BINDING SITE, designated SEQ ID:13342, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74468] Another function of VGAM2151 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase Kinase 5 (MAP4K5, Accession NM_006575). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP4K5. Mannose-P-dolichol Utilization Defect 1 (MPDU1, Accession NM_004870) is another VGAM2151 host target gene. MPDU1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MPDU1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MPDU1 BINDING SITE, designated SEQ ID:11298, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74469] Another function of VGAM2151 is therefore inhibition of Mannose-P-dolichol Utilization Defect 1 (MPDU1, Acces-

sion NM_004870), a gene which corrects the Lec15 mutant phenotype. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPDU1. The function of MPDU1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1187.8-oxoguanine DNA Glycosylase (OGG1, Accession NM_016819) is another VGAM2151 host target gene. OGG1 BINDING SITE1 through OGG1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by OGG1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OGG1 BINDING SITE1 through OGG1 BINDING SITE3, designated SEQ ID:18807, SEQ ID:18812 and SEQ ID:8390 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74470] Another function of VGAM2151 is therefore inhibition of 8-oxoguanine DNA Glycosylase (OGG1, Accession NM_016819), a gene which is involved in base excision DNA repair and removal of 8-oxyguanine. Accordingly,

utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OGG1. The function of OGG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM390.Protein Kinase (cAMP-dependent, catalytic) Inhibitor Alpha (PKIA, Accession NM_006823) is another VGAM2151 host target gene. PKIA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PKIA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PKIA BINDING SITE, designated SEQ ID:13702, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74471] Another function of VGAM2151 is therefore inhibition of Protein Kinase (cAMP-dependent, catalytic) Inhibitor Alpha (PKIA, Accession NM_006823). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKIA. POU Domain, Class 2, Transcription Factor 2 (POU2F2, Accession NM_002698) is another VGAM2151 host target

gene. POU2F2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POU2F2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POU2F2 BINDING SITE, designated SEQ ID:8549, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74472] Another function of VGAM2151 is therefore inhibition of POU Domain, Class 2, Transcription Factor 2 (POU2F2, Accession NM_002698), a gene which activates immunoglobulin gene expression. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU2F2. The function of POU2F2 has been established by previous studies. An understanding of development necessitates an understanding of the molecular mechanisms of cell type-specific gene expression. Using synthetic promoter constructions, it has been found that 2 sequences within immunoglobulin promoters are sufficient for lymphoid-specific promoter activity: an octamer, ATTTGCAT, and a TATA box. Staudt et al. (1988) isolated a cDNA

which hybridized with mRNA transcripts that were largely restricted to lymphoid cells. The level of expression of the gene, termed OCT2, within different lymphoid cell lines correlated well with the amount of a nuclear factor called NFA2 that had previously been detected only in lymphoid cells. Ko et al. (1988) determined the DNA sequence of the OCT2 cDNA and showed that its gene product contains a homeobox. Site-directed mutagenesis of the homeobox domain abolished DNA binding. They demonstrated, furthermore, that the gene is located on chromosome 19, using hybridization to a panel of somatic cell hybrid DNAs. By linkage studies in an interspecific backcross and by studies of recombinant inbred strains, Siracusa et al. (1991) assigned the Otf2 gene to mouse chromosome 7. Whereas the Otf1 and Otf2 molecular probes recognize single loci, members of the Otf3 family map to mouse chromosomes 1, 2, 3, 6, 14, 17, and the X chromosome. Schubart et al. (2001) noted that Oct2-deficient mice die at birth but have normal B-cell development and transcription of immunoglobulin (Ig) genes. Oct-binding factor-1 (Obf1; 601206)-deficient mice are viable with unaffected B-cell development in bone marrow and normal serum IgM but have reduced B-cell numbers in spleen

and low serum IgG. By creating double knockout mice, Schubart et al. (2001) confirmed that B-cell development and Ig gene transcription can proceed normally without these B-cell specific factors. However, in these animals the mature B-cell pool was strongly reduced, suggesting that these factors play an important role in controlling the expansion and/or maintenance of mature B cells.

[74473] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74474] Staudt, L. M.; Clerc, R. G.; Singh, H.; LeBowitz, J. H.; Sharp, P. A.; Baltimore, D. : Cloning of a lymphoid-specific cDNA encoding a protein binding the regulatory octamer DNA motif. Science 241: 577-580, 1988. ; and

[74475] Schubart, K.; Massa, S.; Schubart, D.; Corcoran, L. M.; Rolink, A. G.; Matthias, P. : B cell development and immunoglobulin gene transcription in the absence of Oct-2 and OBF-1. Nature Immu.

[74476] Further studies establishing the function and utilities of POU2F2 are found in John Hopkins OMIM database record ID 164176, and in sited publications numbered 1859, 10798-1079 and 10856 listed in the bibliography section hereinbelow, which are also hereby incorporated by refer-

ence.Protein Phosphatase 3 (formerly 2B), Catalytic Subunit, Gamma Isoform (calcineurin A gamma) (PPP3CC, Accession NM_005605) is another VGAM2151 host target gene. PPP3CC BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PPP3CC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP3CC BINDING SITE, designated SEQ ID:12127, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74477] Another function of VGAM2151 is therefore inhibition of Protein Phosphatase 3 (formerly 2B), Catalytic Subunit, Gamma Isoform (calcineurin A gamma) (PPP3CC, Accession NM_005605). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP3CC. Phosphatase and Tensin Homolog (mutated in multiple advanced cancers 1) (PTEN, Accession NM_000314) is another VGAM2151 host target gene. PTEN BINDING SITE1 through PTEN BINDING SITE5 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTEN,

corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTEN BINDING SITE1 through PTEN BINDING SITE5, designated SEQ ID:5854, SEQ ID:5855, SEQ ID:5856, SEQ ID:5857 and SEQ ID:5853 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74478] Another function of VGAM2151 is therefore inhibition of Phosphatase and Tensin Homolog (mutated in multiple advanced cancers 1) (PTEN, Accession NM_000314). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTEN. Protein Tyrosine Phosphatase Type IVA, Member 2 (PTP4A2, Accession NM_080392) is another VGAM2151 host target gene. PTP4A2 BINDING SITE1 and PTP4A2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTP4A2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTP4A2 BINDING SITE1 and PTP4A2 BINDING SITE2, designated SEQ ID:27830 and SEQ ID:34789 re-

spectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74479] Another function of VGAM2151 is therefore inhibition of Protein Tyrosine Phosphatase Type IVA, Member 2 (PTP4A2, Accession NM_080392), a gene which is a protein tyrosine phosphatase which has a C-terminal prenylation site. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTP4A2. The function of PTP4A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM217.RAD21 Homolog (S. pombe) (RAD21, Accession NM_006265) is another VGAM2151 host target gene. RAD21 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAD21, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD21 BINDING SITE, designated SEQ ID:12946, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ

ID:4862.

[74480] Another function of VGAM2151 is therefore inhibition of RAD21 Homolog (S. pombe) (RAD21, Accession NM_006265), a gene which may act in double strand break repair. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD21. The function of RAD21 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1928.RALBP1 Associated Eps Domain Containing 2 (REPS2, Accession NM_004726) is another VGAM2151 host target gene. REPS2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by REPS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of REPS2 BINDING SITE, designated SEQ ID:11098, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74481] Another function of VGAM2151 is therefore inhibition of RALBP1 Associated Eps Domain Containing 2 (REPS2, Ac-

cession NM_004726), a gene which interacts with the active form of RAS with adaptor protein GRB2 and binds calcium. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with REPS2. The function of REPS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM709.Replication Factor C (activator 1) 4, 37kDa (RFC4, Accession NM_002916) is another VGAM2151 host target gene. RFC4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RFC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RFC4 BINDING SITE, designated SEQ ID:8821, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74482] Another function of VGAM2151 is therefore inhibition of Replication Factor C (activator 1) 4, 37kDa (RFC4, Accession NM_002916), a gene which activates DNA polymerases for elongation of primed dna templates. Accord-

ingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFC4. The function of RFC4 has been established by previous studies. The elongation of primed DNA templates by DNA polymerase delta and DNA polymerase epsilon requires the action of 2 accessory proteins, proliferating cell nuclear antigen (PCNA; 176740) and activator 1 (A1; also called replication factor C). A1 is an enzyme that contains 5 different subunits of 140, 40, 38, 37, and 36 kD. Chen et al. (1992) isolated the gene encoding the 37-kD subunit from HeLa cells. The deduced amino acid sequence showed a high degree of homology to the 40-kD subunit of A1 but, unlike the 40-kD protein, the 37-kD expressed protein did not bind ATP. Other findings suggested that both the 37- and 40-kD subunits of A1 are required for the biologic role of A1 and that they may function differently in this process. See replication factor C, subunit 2 (RFC2; 600404). Wang et al. (2000) used immunoprecipitation and mass spectrometry analyses to identify BRCA1 (OMIM Ref. No. 113705)-associated proteins. They found that BRCA1 is part of a large multisubunit protein complex of tumor suppressors, DNA damage sensors, and signal transducers. They named this complex

BASC, for 'BRCA1-associated genome surveillance complex.' Among the DNA repair proteins identified in the complex were ATM (OMIM Ref. No. 208900), BLM (OMIM Ref. No. 604610), MSH2 (OMIM Ref. No. 120435), MSH6 (OMIM Ref. No. 600678), MLH1 (OMIM Ref. No. 120436), the RAD50 (OMIM Ref. No. 604040)-MRE11 (OMIM Ref. No. 600814)-NBS1 (OMIM Ref. No. 602667) complex, and the RFC1 (OMIM Ref. No. 102579)-RFC2-RFC4 complex. Wang et al. (2000) suggested that BASC may serve as a sensor of abnormal DNA structures and/or as a regulator of the postreplication repair process.

[74483] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74484] Chen, M.; Pan, Z.-Q.; Hurwitz, J. : Studies of the cloned 37-kDa subunit of activator 1 (replication factor C) of HeLa cells. Proc. Nat. Acad. Sci. 89: 5211-5215, 1992. ; and

[74485] Wang, Y.; Cortez, D.; Yazdi, P.; Neff, N.; Elledge, S. J.; Qin, J. : BASC, a super complex of BRCA1-associated proteins involved in the recognition and repair of aberrant DNA structures.

[74486] Further studies establishing the function and utilities of

RFC4 are found in John Hopkins OMIM database record ID 102577, and in sited publications numbered 427 and 7117-7118 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.RGL (Accession NM_015149) is another VGAM2151 host target gene. RGL BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RGL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RGL BINDING SITE, designated SEQ ID:17507, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74487] Another function of VGAM2151 is therefore inhibition of RGL (Accession NM_015149), a gene which is involved in nucleotide exchange factor. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGL. The function of RGL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM861.Rho-associated, Coiled-coil Containing Protein Kinase 2 (ROCK2, Accession XM_038377) is another

VGAM2151 host target gene. ROCK2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ROCK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ROCK2 BINDING SITE, designated SEQ ID:32841, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74488] Another function of VGAM2151 is therefore inhibition of Rho-associated, Coiled-coil Containing Protein Kinase 2 (ROCK2, Accession XM_038377), a gene which regulates cytokinesis, smooth muscle contraction, the formation of actin stress fibers and focal adhesions. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ROCK2. The function of ROCK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM273.Tafazzin (cardiomyopathy, dilated 3A (X-linked); Endocardial Fibroelastosis 2; Barth Syndrome) (TAZ, Accession NM_015472) is another VGAM2151 host target gene. TAZ BINDING SITE is HOST

TARGET binding site found in the 5` untranslated region of mRNA encoded by TAZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAZ BINDING SITE, designated SEQ ID:17753, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74489] Another function of VGAM2151 is therefore inhibition of Tafazzin (cardiomyopathy, dilated 3A (X-linked); Endocardial Fibroelastosis 2; Barth Syndrome) (TAZ, Accession NM_015472). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAZ. TRK-fused Gene (TFG, Accession NM_006070) is another VGAM2151 host target gene. TFG BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TFG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TFG BINDING SITE, designated SEQ ID:12713, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74490] Another function of VGAM2151 is therefore inhibition of TRK-fused Gene (TFG, Accession NM_006070), a gene which is a chimeric protein that forms multimeric complexes in vivo. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TFG. The function of TFG has been established by previous studies. See 188550. Greco et al. (1995) stated that approximately 50% of papillary thyroid carcinomas are associated with rearrangements of the RET (OMIM Ref. No. 164761) and NTRK1 (OMIM Ref. No. 191315) transmembrane receptor tyrosine kinase protooncogenes. The rearrangements juxtapose the tyrosine kinase domain to 5-prime sequences from unrelated loci, yielding chimeric proteins with ectopic, constitutive tyrosine kinase activity. In one tumor, Greco et al. (1995) found a chimeric oncogene, designated TRKT3, in which 1,412 nucleotides of NTRK1 are fused to 598 nucleotides from a novel gene called TFG (TRK-fused gene). TRKT3 encodes a predicted 592-amino acid chimeric protein that forms multimeric complexes in vivo. Mencinger et al. (1997) identified the complete TFG gene by searching for ESTs that were similar to the N-terminal regions of EWS (OMIM Ref. No. 133450) and FUS (OMIM

Ref. No. 137070). TFG encodes a predicted 400-amino acid protein with a putative N-terminal coiled-coil region. On Northern blots, the 2.2-kb TFG mRNA was expressed in all tissues tested. Greco et al. (1995) stated that a coiled-coil structure and ubiquitous expression are features shared by all NTRK1-activating genes as well as genes that activate other tyrosine kinase protooncogenes.

[74491] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74492] Greco, A.; Mariani, C.; Miranda, C.; Lupas, A.; Pagliardini, S.; Pomati, M.; Pierotti, M. A. : The DNA rearrangement that generates the TRK-T3 oncogene involves a novel gene on chromosome 3 whose product has a potential coiled-coil domain. Molec. Cell Biol. 15: 6118-6127, 1995. ; and

[74493] Mencinger, M.; Panagopoulos, I.; Andreasson, P.; Lassen, C.; Mitelman, F.; Aman, P. : Characterization and chromosomal mapping of the human TFG gene involved in thyroid carcinoma. Genom.

[74494] Further studies establishing the function and utilities of TFG are found in John Hopkins OMIM database record ID 602498, and in sited publications numbered 8252-8253

listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Translin (TSN, Accession NM_004622) is another VGAM2151 host target gene. TSN BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TSN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TSN BINDING SITE, designated SEQ ID:10986, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74495] Another function of VGAM2151 is therefore inhibition of Translin (TSN, Accession NM_004622), a gene which is a DNA binding protein and involved in DNA repair, replication, or recombination. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSN. The function of TSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM98.Wolf-Hirschhorn Syndrome Candidate 1-like 1 (WHSC1L1, Accession NM_017778) is another VGAM2151 host target gene. WHSC1L1 BINDING SITE1 and WHSC1L1

BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WHSC1L1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WHSC1L1 BINDING SITE1 and WHSC1L1 BINDING SITE2, designated SEQ ID:19410 and SEQ ID:23317 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74496] Another function of VGAM2151 is therefore inhibition of Wolf-Hirschhorn Syndrome Candidate 1-like 1 (WHSC1L1, Accession NM_017778), a gene which restores repair of base-base and single- nucleotide insertion-deletion mismatches, and increases the proficiency to process heteroduplexes with insertion-deletion mismatches. Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WHSC1L1. The function of WHSC1L1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM475.Zinc Finger Protein 6 (CMPX1) (ZNF6, Accession NM_021998) is another VGAM2151 host target gene. ZNF6 BINDING SITE is HOST

TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF6 BINDING SITE, designated SEQ ID:22536, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74497] Another function of VGAM2151 is therefore inhibition of Zinc Finger Protein 6 (CMPX1) (ZNF6, Accession NM_021998). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF6. BDG-29 (Accession XM_051343) is another VGAM2151 host target gene. BDG-29 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BDG-29, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BDG-29 BINDING SITE, designated SEQ ID:35818, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74498] Another function of VGAM2151 is therefore inhibition of BDG-29 (Accession XM_051343). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BDG-29. C3IP1 (Accession NM_021633) is another VGAM2151 host target gene. C3IP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C3IP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C3IP1 BINDING SITE, designated SEQ ID:22276, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74499] Another function of VGAM2151 is therefore inhibition of C3IP1 (Accession NM_021633). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C3IP1. CASPR3 (Accession NM_033655) is another VGAM2151 host target gene. CASPR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CASPR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASPR3 BINDING SITE, designated SEQ ID:27384, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74500] Another function of VGAM2151 is therefore inhibition of CASPR3 (Accession NM_033655). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASPR3. Centaurin, Gamma 2 (CENTG2, Accession NM_014914) is another VGAM2151 host target gene. CENTG2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CENTG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CENTG2 BINDING SITE, designated SEQ ID:17160, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74501] Another function of VGAM2151 is therefore inhibition of Centaurin, Gamma 2 (CENTG2, Accession NM_014914). Accordingly, utilities of VGAM2151 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with CENTG2. COASTER (Accession NM_015555) is another VGAM2151 host target gene. COASTER BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by COASTER, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COASTER BINDING SITE, designated SEQ ID:17823, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74502] Another function of VGAM2151 is therefore inhibition of COASTER (Accession NM_015555). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COASTER. Collagen, Type IV, Alpha 3 (Goodpasture antigen) Binding Protein (COL4A3BP, Accession NM_005713) is another VGAM2151 host target gene. COL4A3BP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by COL4A3BP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of COL4A3BP BINDING SITE, designated SEQ ID:12267, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74503] Another function of VGAM2151 is therefore inhibition of Collagen, Type IV, Alpha 3 (Goodpasture antigen) Binding Protein (COL4A3BP, Accession NM_005713). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A3BP. D123 (Accession NM_006023) is another VGAM2151 host target gene. D123 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by D123, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of D123 BINDING SITE, designated SEQ ID:12641, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74504] Another function of VGAM2151 is therefore inhibition of D123 (Accession NM_006023). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with D123.

Death-associated Protein Kinase 2 (DAPK2, Accession NM_014326) is another VGAM2151 host target gene. DAPK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DAPK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAPK2 BINDING SITE, designated SEQ ID:15635, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74505] Another function of VGAM2151 is therefore inhibition of Death-associated Protein Kinase 2 (DAPK2, Accession NM_014326). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAPK2. DKFZP434M154 (Accession XM_051330) is another VGAM2151 host target gene. DKFZP434M154 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434M154, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434M154

BINDING SITE, designated SEQ ID:35808, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74506] Another function of VGAM2151 is therefore inhibition of DKFZP434M154 (Accession XM_051330). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434M154. DKFZp434O0320 (Accession XM_097012) is another VGAM2151 host target gene. DKFZp434O0320 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp434O0320, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434O0320 BINDING SITE, designated SEQ ID:40707, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74507] Another function of VGAM2151 is therefore inhibition of DKFZp434O0320 (Accession XM_097012). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434O0320. DKFZP566K1924 (Accession

XM_057469) is another VGAM2151 host target gene. DKFZP566K1924 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP566K1924, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566K1924 BINDING SITE, designated SEQ ID:36521, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74508] Another function of VGAM2151 is therefore inhibition of DKFZP566K1924 (Accession XM_057469). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566K1924. Dlc2 (Accession NM_080677) is another VGAM2151 host target gene. Dlc2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by Dlc2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Dlc2 BINDING SITE, designated SEQ ID:27970, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA,

also designated SEQ ID:4862.

[74509] Another function of VGAM2151 is therefore inhibition of Dlc2 (Accession NM_080677). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Dlc2. EHM2 (Accession NM_019114) is another VGAM2151 host target gene. EHM2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EHM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EHM2 BINDING SITE, designated SEQ ID:21188, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74510] Another function of VGAM2151 is therefore inhibition of EHM2 (Accession NM_019114). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHM2. ELKS (Accession NM_015064) is another VGAM2151 host target gene. ELKS BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ELKS, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELKS BINDING SITE, designated SEQ ID:17421, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74511] Another function of VGAM2151 is therefore inhibition of ELKS (Accession NM_015064). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELKS. EZFIT (Accession NM_021216) is another VGAM2151 host target gene. EZFIT BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EZFIT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EZFIT BINDING SITE, designated SEQ ID:22196, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74512] Another function of VGAM2151 is therefore inhibition of EZFIT (Accession NM_021216). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with EZFIT. Fem-1 Homolog B (C. elegans) (FEM1B, Accession NM_015322) is another VGAM2151 host target gene. FEM1B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FEM1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FEM1B BINDING SITE, designated SEQ ID:17642, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74513] Another function of VGAM2151 is therefore inhibition of Fem-1 Homolog B (C. elegans) (FEM1B, Accession NM_015322). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FEM1B. FLJ10101 (Accession NM_024718) is another VGAM2151 host target gene. FLJ10101 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10101, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of FLJ10101 BINDING SITE, designated SEQ ID:24049, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74514] Another function of VGAM2151 is therefore inhibition of FLJ10101 (Accession NM_024718). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10101. FLJ10244 (Accession NM_018037) is another VGAM2151 host target gene. FLJ10244 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10244, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10244 BINDING SITE, designated SEQ ID:19781, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74515] Another function of VGAM2151 is therefore inhibition of FLJ10244 (Accession NM_018037). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10244. FLJ12076 (Accession NM_025187) is another

VGAM2151 host target gene. FLJ12076 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12076, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12076 BINDING SITE, designated SEQ ID:24824, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74516] Another function of VGAM2151 is therefore inhibition of FLJ12076 (Accession NM_025187). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12076. FLJ13204 (Accession NM_024761) is another VGAM2151 host target gene. FLJ13204 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13204, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13204 BINDING SITE, designated SEQ ID:24117, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74517] Another function of VGAM2151 is therefore inhibition of FLJ13204 (Accession NM_024761). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13204. FLJ13621 (Accession NM_025009) is another VGAM2151 host target gene. FLJ13621 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13621, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13621 BINDING SITE, designated SEQ ID:24581, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74518] Another function of VGAM2151 is therefore inhibition of FLJ13621 (Accession NM_025009). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13621. FLJ14356 (Accession NM_030824) is another VGAM2151 host target gene. FLJ14356 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ14356, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14356 BINDING SITE, designated SEQ ID:25153, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74519] Another function of VGAM2151 is therefore inhibition of FLJ14356 (Accession NM_030824). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14356. FLJ20080 (Accession NM_017657) is another VGAM2151 host target gene. FLJ20080 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20080, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20080 BINDING SITE, designated SEQ ID:19180, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74520] Another function of VGAM2151 is therefore inhibition of FLJ20080 (Accession NM_017657). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20080. FLJ20435 (Accession NM_017821) is another VGAM2151 host target gene. FLJ20435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20435 BINDING SITE, designated SEQ ID:19471, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74521] Another function of VGAM2151 is therefore inhibition of FLJ20435 (Accession NM_017821). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20435. FLJ20718 (Accession NM_017939) is another VGAM2151 host target gene. FLJ20718 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20718, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20718 BINDING SITE, designated SEQ ID:19635, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM

RNA, also designated SEQ ID:4862.

[74522] Another function of VGAM2151 is therefore inhibition of FLJ20718 (Accession NM_017939). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20718. FLJ22393 (Accession NM_025106) is another VGAM2151 host target gene. FLJ22393 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22393, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22393 BINDING SITE, designated SEQ ID:24756, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74523] Another function of VGAM2151 is therefore inhibition of FLJ22393 (Accession NM_025106). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22393. FLJ22405 (Accession NM_022485) is another VGAM2151 host target gene. FLJ22405 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22405, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22405 BINDING SITE, designated SEQ ID:22866, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74524] Another function of VGAM2151 is therefore inhibition of FLJ22405 (Accession NM_022485). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22405. FLJ22457 (Accession NM_024901) is another VGAM2151 host target gene. FLJ22457 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22457, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22457 BINDING SITE, designated SEQ ID:24389, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74525] Another function of VGAM2151 is therefore inhibition of FLJ22457 (Accession NM_024901). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ22457. Fused Toes Homolog (mouse) (FTS, Accession NM_022476) is another VGAM2151 host target gene. FTS BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FTS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FTS BINDING SITE, designated SEQ ID:22843, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74526] Another function of VGAM2151 is therefore inhibition of Fused Toes Homolog (mouse) (FTS, Accession NM_022476). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FTS. GDBR1 (Accession NM_016172) is another VGAM2151 host target gene. GDBR1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GDBR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GDBR1 BINDING SITE, designated SEQ

ID:18262, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74527] Another function of VGAM2151 is therefore inhibition of GDBR1 (Accession NM_016172). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GDBR1. HSPC195 (Accession XM_087785) is another VGAM2151 host target gene. HSPC195 BINDING SITE1 and HSPC195 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HSPC195, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPC195 BINDING SITE1 and HSPC195 BINDING SITE2, designated SEQ ID:39424 and SEQ ID:39423 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74528] Another function of VGAM2151 is therefore inhibition of HSPC195 (Accession XM_087785). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC195. Insulin-like Growth Factor 2, Antisense (IGF2AS,

Accession NM_016412) is another VGAM2151 host target gene. IGF2AS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IGF2AS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IGF2AS BINDING SITE, designated SEQ ID:18541, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74529] Another function of VGAM2151 is therefore inhibition of Insulin-like Growth Factor 2, Antisense (IGF2AS, Accession NM_016412). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IGF2AS. Inositol 1,3,4-triphosphate 5/6 Kinase (ITPK1, Accession NM_014216) is another VGAM2151 host target gene. ITPK1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ITPK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITPK1 BINDING SITE, designated SEQ ID:15482,

to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74530] Another function of VGAM2151 is therefore inhibition of Inositol 1,3,4-triphosphate 5/6 Kinase (ITPK1, Accession NM_014216). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPK1. JIK (Accession NM_016281) is another VGAM2151 host target gene. JIK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by JIK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JIK BINDING SITE, designated SEQ ID:18406, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74531] Another function of VGAM2151 is therefore inhibition of JIK (Accession NM_016281). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JIK. KIAA0191 (Accession XM_038288) is another VGAM2151 host target gene. KIAA0191 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA

encoded by KIAA0191, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0191 BINDING SITE, designated SEQ ID:32788, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74532] Another function of VGAM2151 is therefore inhibition of KIAA0191 (Accession XM_038288). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0191. KIAA0210 (Accession NM_014744) is another VGAM2151 host target gene. KIAA0210 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0210, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0210 BINDING SITE, designated SEQ ID:16426, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74533] Another function of VGAM2151 is therefore inhibition of KIAA0210 (Accession NM_014744). Accordingly, utilities

of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0210. KIAA0227 (Accession XM_027236) is another VGAM2151 host target gene. KIAA0227 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0227, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0227 BINDING SITE, designated SEQ ID:30454, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74534] Another function of VGAM2151 is therefore inhibition of KIAA0227 (Accession XM_027236). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0227. KIAA0544 (Accession XM_048119) is another VGAM2151 host target gene. KIAA0544 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0544, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0544 BINDING SITE, designated SEQ ID:35115, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74535] Another function of VGAM2151 is therefore inhibition of KIAA0544 (Accession XM_048119). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0544. KIAA0607 (Accession XM_051931) is another VGAM2151 host target gene. KIAA0607 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0607, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0607 BINDING SITE, designated SEQ ID:35926, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74536] Another function of VGAM2151 is therefore inhibition of KIAA0607 (Accession XM_051931). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0607. KIAA0701 (Accession XM_045423) is another VGAM2151 host target gene. KIAA0701 BINDING SITE1

and KIAA0701 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0701, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0701 BINDING SITE1 and KIAA0701 BINDING SITE2, designated SEQ ID:34458 and SEQ ID:34459 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74537] Another function of VGAM2151 is therefore inhibition of KIAA0701 (Accession XM_045423). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0701. KIAA0721 (Accession NM_021648) is another VGAM2151 host target gene. KIAA0721 BINDING SITE1 and KIAA0721 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0721, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0721 BINDING SITE1 and KIAA0721 BINDING SITE2, designated SEQ ID:22321 and SEQ

ID:36066 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74538] Another function of VGAM2151 is therefore inhibition of KIAA0721 (Accession NM_021648). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0721. KIAA1233 (Accession XM_032181) is another VGAM2151 host target gene. KIAA1233 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1233, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1233 BINDING SITE, designated SEQ ID:31591, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74539] Another function of VGAM2151 is therefore inhibition of KIAA1233 (Accession XM_032181). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1233. KIAA1322 (Accession XM_052626) is another VGAM2151 host target gene. KIAA1322 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1322, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1322 BINDING SITE, designated SEQ ID:36031, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74540] Another function of VGAM2151 is therefore inhibition of KIAA1322 (Accession XM_052626). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1322. KIAA1822 (Accession XM_041566) is another VGAM2151 host target gene. KIAA1822 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1822, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1822 BINDING SITE, designated SEQ ID:33553, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74541] Another function of VGAM2151 is therefore inhibition of

KIAA1822 (Accession XM_041566). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1822. KIAA1940 (Accession XM_086981) is another VGAM2151 host target gene. KIAA1940 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1940, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1940 BINDING SITE, designated SEQ ID:39008, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74542] Another function of VGAM2151 is therefore inhibition of KIAA1940 (Accession XM_086981). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1940. KIAA1987 (Accession XM_113870) is another VGAM2151 host target gene. KIAA1987 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1987, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1987 BINDING SITE, designated SEQ ID:42499, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74543] Another function of VGAM2151 is therefore inhibition of KIAA1987 (Accession XM_113870). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1987. Kelch-like 4 (Drosophila) (KLHL4, Accession NM_019117) is another VGAM2151 host target gene. KLHL4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLHL4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLHL4 BINDING SITE, designated SEQ ID:21192, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74544] Another function of VGAM2151 is therefore inhibition of Kelch-like 4 (Drosophila) (KLHL4, Accession NM_019117). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with KLHL4. LSR68 (Accession NM_018678) is another VGAM2151 host target gene. LSR68 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LSR68, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LSR68 BINDING SITE, designated SEQ ID:20752, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74545] Another function of VGAM2151 is therefore inhibition of LSR68 (Accession NM_018678). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LSR68. Mesoderm Development Candidate 1 (MESDC1, Accession NM_022566) is another VGAM2151 host target gene. MESDC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MESDC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MESDC1 BINDING SITE, designated SEQ

ID:22883, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74546] Another function of VGAM2151 is therefore inhibition of Mesoderm Development Candidate 1 (MESDC1, Accession NM_022566). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MESDC1. MGC11296 (Accession NM_032352) is another VGAM2151 host target gene. MGC11296 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC11296, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11296 BINDING SITE, designated SEQ ID:26141, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74547] Another function of VGAM2151 is therefore inhibition of MGC11296 (Accession NM_032352). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11296. MGC11324 (Accession NM_032717) is an-

other VGAM2151 host target gene. MGC11324 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC11324, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11324 BINDING SITE, designated SEQ ID:26445, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74548] Another function of VGAM2151 is therefore inhibition of MGC11324 (Accession NM_032717). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11324. MGC26684 (Accession NM_144568) is another VGAM2151 host target gene. MGC26684 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC26684, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC26684 BINDING SITE, designated SEQ ID:29373, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74549] Another function of VGAM2151 is therefore inhibition of MGC26684 (Accession NM_144568). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC26684. MGC3265 (Accession NM_024028) is another VGAM2151 host target gene. MGC3265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC3265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC3265 BINDING SITE, designated SEQ ID:23459, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74550] Another function of VGAM2151 is therefore inhibition of MGC3265 (Accession NM_024028). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3265. MGC4368 (Accession NM_024510) is another VGAM2151 host target gene. MGC4368 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC4368, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4368 BINDING SITE, designated SEQ ID:23701, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74551] Another function of VGAM2151 is therefore inhibition of MGC4368 (Accession NM_024510). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4368. MIR (Accession XM_165739) is another VGAM2151 host target gene. MIR BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MIR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MIR BINDING SITE, designated SEQ ID:43739, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74552] Another function of VGAM2151 is therefore inhibition of MIR (Accession XM_165739). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIR.

Myelin Protein Zero-like 1 (MPZL1, Accession NM_003953) is another VGAM2151 host target gene. MPZL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MPZL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MPZL1 BINDING SITE, designated SEQ ID:10088, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74553] Another function of VGAM2151 is therefore inhibition of Myelin Protein Zero-like 1 (MPZL1, Accession NM_003953). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPZL1. MY014 (Accession NM_030918) is another VGAM2151 host target gene. MY014 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MY014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MY014 BINDING SITE, designated SEQ ID:25191, to the nucleotide sequence of VGAM2151 RNA,

herein designated VGAM RNA, also designated SEQ ID:4862.

[74554] Another function of VGAM2151 is therefore inhibition of MY014 (Accession NM_030918). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MY014. Nuclear Receptor Co-repressor 1 (NCOR1, Accession NM_006311) is another VGAM2151 host target gene. NCOR1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NCOR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOR1 BINDING SITE, designated SEQ ID:13002, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74555] Another function of VGAM2151 is therefore inhibition of Nuclear Receptor Co-repressor 1 (NCOR1, Accession NM_006311). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOR1. Netrin 4 (NTN4, Accession XM_031896) is another VGAM2151 host target

gene. NTN4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NTN4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NTN4 BINDING SITE, designated SEQ ID:31515, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74556] Another function of VGAM2151 is therefore inhibition of Netrin 4 (NTN4, Accession XM_031896). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTN4. Nucleoredoxin (NXN, Accession NM_022463) is another VGAM2151 host target gene. NXN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NXN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NXN BINDING SITE, designated SEQ ID:22811, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74557] Another function of VGAM2151 is therefore inhibition of

Nucleoredoxin (NXN, Accession NM_022463). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXN. Olfactory Receptor, Family 2, Subfamily C, Member 3 (OR2C3, Accession XM_060575) is another VGAM2151 host target gene. OR2C3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OR2C3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OR2C3 BINDING SITE, designated SEQ ID:37175, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74558] Another function of VGAM2151 is therefore inhibition of Olfactory Receptor, Family 2, Subfamily C, Member 3 (OR2C3, Accession XM_060575). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OR2C3. Oxysterol Binding Protein-like 5 (OSBPL5, Accession XM_052567) is another VGAM2151 host target gene. OSBPL5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL5,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL5 BINDING SITE, designated SEQ ID:35990, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74559] Another function of VGAM2151 is therefore inhibition of Oxysterol Binding Protein-like 5 (OSBPL5, Accession XM_052567). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL5. P5-1 (Accession NM_006674) is another VGAM2151 host target gene. P5-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P5-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P5-1 BINDING SITE, designated SEQ ID:13499, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74560] Another function of VGAM2151 is therefore inhibition of P5-1 (Accession NM_006674). Accordingly, utilities of

VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P5-1. P300/CBP-associated Factor (PCAF, Accession NM_003884) is another VGAM2151 host target gene. PCAF BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PCAF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCAF BINDING SITE, designated SEQ ID:9964, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74561] Another function of VGAM2151 is therefore inhibition of P300/CBP-associated Factor (PCAF, Accession NM_003884). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCAF. Proprotein Convertase Subtilisin/kexin Type 7 (PCSK7, Accession NM_004716) is another VGAM2151 host target gene. PCSK7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PCSK7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of PCSK7 BINDING SITE, designated SEQ ID:11076, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74562] Another function of VGAM2151 is therefore inhibition of Proprotein Convertase Subtilisin/kexin Type 7 (PCSK7, Accession NM_004716). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCSK7. Programmed Cell Death 7 (PDCD7, Accession XM_050977) is another VGAM2151 host target gene. PDCD7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDCD7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDCD7 BINDING SITE, designated SEQ ID:35696, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74563] Another function of VGAM2151 is therefore inhibition of Programmed Cell Death 7 (PDCD7, Accession XM_050977). Accordingly, utilities of VGAM2151 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with PDCD7. PEGASUS (Accession NM_022466) is another VGAM2151 host target gene. PEGASUS BINDING SITE1 and PEGASUS BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PEGASUS, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEGASUS BINDING SITE1 and PEGASUS BINDING SITE2, designated SEQ ID:22814 and SEQ ID:22815 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74564] Another function of VGAM2151 is therefore inhibition of PEGASUS (Accession NM_022466). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEGASUS. PF1 (Accession XM_170828) is another VGAM2151 host target gene. PF1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of PF1 BINDING SITE, designated SEQ ID:45604, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74565] Another function of VGAM2151 is therefore inhibition of PF1 (Accession XM_170828). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PF1. PPI5PIV (Accession NM_019892) is another VGAM2151 host target gene. PPI5PIV BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPI5PIV, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPI5PIV BINDING SITE, designated SEQ ID:21277, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74566] Another function of VGAM2151 is therefore inhibition of PPI5PIV (Accession NM_019892). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPI5PIV. Protein Tyrosine Phosphatase, Non-receptor Type Sub-

strate 1 (PTPNS1, Accession NM_080792) is another VGAM2151 host target gene. PTPNS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPNS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPNS1 BINDING SITE, designated SEQ ID:28056, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74567] Another function of VGAM2151 is therefore inhibition of Protein Tyrosine Phosphatase, Non-receptor Type Substrate 1 (PTPNS1, Accession NM_080792). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPNS1. PTR4 (Accession XM_058546) is another VGAM2151 host target gene. PTR4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PTR4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTR4 BINDING SITE, designated SEQ ID:36654, to the nucleotide sequence of

VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74568] Another function of VGAM2151 is therefore inhibition of PTR4 (Accession XM_058546). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTR4. RPH3A (Accession NM_014954) is another VGAM2151 host target gene. RPH3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPH3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPH3A BINDING SITE, designated SEQ ID:17307, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74569] Another function of VGAM2151 is therefore inhibition of RPH3A (Accession NM_014954). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPH3A. Solute Carrier Family 21 (organic anion transporter), Member 11 (SLC21A11, Accession XM_035268) is another VGAM2151 host target gene. SLC21A11 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC21A11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC21A11 BINDING SITE, designated SEQ ID:32208, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74570] Another function of VGAM2151 is therefore inhibition of Solute Carrier Family 21 (organic anion transporter), Member 11 (SLC21A11, Accession XM_035268). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC21A11. Slit Homolog 1 (Drosophila) (SLIT1, Accession NM_003061) is another VGAM2151 host target gene. SLIT1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLIT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLIT1 BINDING SITE, designated SEQ ID:9030, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74571] Another function of VGAM2151 is therefore inhibition of Slit Homolog 1 (Drosophila) (SLIT1, Accession NM_003061). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLIT1. Serum Response Factor (c-fos serum response element-binding transcription factor) (SRF, Accession NM_003131) is another VGAM2151 host target gene. SRF BINDING SITE1 and SRF BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SRF, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SRF BINDING SITE1 and SRF BINDING SITE2, designated SEQ ID:9101 and SEQ ID:9102 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74572] Another function of VGAM2151 is therefore inhibition of Serum Response Factor (c-fos serum response element-binding transcription factor) (SRF, Accession NM_003131). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRF. Serine Threonine Kinase 39

(STE20/SPS1 homolog, yeast) (STK39, Accession NM_013233) is another VGAM2151 host target gene. STK39 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by STK39, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STK39 BINDING SITE, designated SEQ ID:14894, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74573] Another function of VGAM2151 is therefore inhibition of Serine Threonine Kinase 39 (STE20/SPS1 homolog, yeast) (STK39, Accession NM_013233). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK39. TU12B1-TY (Accession NM_016575) is another VGAM2151 host target gene. TU12B1-TY BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TU12B1-TY, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

TU12B1-TY BINDING SITE, designated SEQ ID:18649, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74574] Another function of VGAM2151 is therefore inhibition of TU12B1-TY (Accession NM_016575). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TU12B1-TY. TUSP (Accession NM_020245) is another VGAM2151 host target gene. TUSP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUSP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUSP BINDING SITE, designated SEQ ID:21530, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74575] Another function of VGAM2151 is therefore inhibition of TUSP (Accession NM_020245). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUSP. Unc-51-like Kinase 2 (C. elegans) (ULK2, Accession NM_014683) is another VGAM2151 host target gene.

ULK2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ULK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ULK2 BINDING SITE, designated SEQ ID:16182, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74576] Another function of VGAM2151 is therefore inhibition of Unc-51-like Kinase 2 (C. elegans) (ULK2, Accession NM_014683). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ULK2. WIT-1 (Accession NM_015855) is another VGAM2151 host target gene. WIT-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WIT-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WIT-1 BINDING SITE, designated SEQ ID:17991, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74577] Another function of VGAM2151 is therefore inhibition of

WIT-1 (Accession NM_015855). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WIT-1. Zinc Finger, DHHC Domain Containing 3 (ZDHHC3, Accession NM_016598) is another VGAM2151 host target gene. ZDHHC3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZDHHC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZDHHC3 BINDING SITE, designated SEQ ID:18689, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74578] Another function of VGAM2151 is therefore inhibition of Zinc Finger, DHHC Domain Containing 3 (ZDHHC3, Accession NM_016598). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZDHHC3. ZF (Accession NM_021212) is another VGAM2151 host target gene. ZF BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZF, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZF BINDING SITE, designated SEQ ID:22191, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74579] Another function of VGAM2151 is therefore inhibition of ZF (Accession NM_021212). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZF. Zinc Finger Protein 238 (ZNF238, Accession NM_006352) is another VGAM2151 host target gene. ZNF238 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF238, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF238 BINDING SITE, designated SEQ ID:13044, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74580] Another function of VGAM2151 is therefore inhibition of Zinc Finger Protein 238 (ZNF238, Accession NM_006352). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with ZNF238. ZTL1 (Accession NM_024055) is another VGAM2151 host target gene. ZTL1 BINDING SITE1 and ZTL1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ZTL1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZTL1 BINDING SITE1 and ZTL1 BINDING SITE2, designated SEQ ID:23492 and SEQ ID:23188 respectively, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74581] Another function of VGAM2151 is therefore inhibition of ZTL1 (Accession NM_024055). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZTL1. LOC118851 (Accession XM_061180) is another VGAM2151 host target gene. LOC118851 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC118851, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC118851 BINDING SITE, designated SEQ ID:37202, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74582] Another function of VGAM2151 is therefore inhibition of LOC118851 (Accession XM_061180). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118851. LOC121536 (Accession XM_058567) is another VGAM2151 host target gene. LOC121536 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC121536, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC121536 BINDING SITE, designated SEQ ID:36665, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74583] Another function of VGAM2151 is therefore inhibition of LOC121536 (Accession XM_058567). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121536. LOC122553 (Accession XM_058630) is another VGAM2151 host target gene. LOC122553 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC122553, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122553 BINDING SITE, designated SEQ ID:36690, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74584] Another function of VGAM2151 is therefore inhibition of LOC122553 (Accession XM_058630). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122553. LOC122792 (Accession NM_145251) is another VGAM2151 host target gene. LOC122792 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC122792, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122792 BINDING SITE, designated SEQ ID:29764, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74585] Another function of VGAM2151 is therefore inhibition of

LOC122792 (Accession NM_145251). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122792. LOC125228 (Accession XM_058913) is another VGAM2151 host target gene. LOC125228 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC125228, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC125228 BINDING SITE, designated SEQ ID:36792, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74586] Another function of VGAM2151 is therefore inhibition of LOC125228 (Accession XM_058913). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC125228. LOC126432 (Accession XM_059046) is another VGAM2151 host target gene. LOC126432 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC126432, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC126432 BINDING SITE, designated SEQ ID:36842, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74587] Another function of VGAM2151 is therefore inhibition of LOC126432 (Accession XM_059046). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126432. LOC134553 (Accession XM_059723) is another VGAM2151 host target gene. LOC134553 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC134553, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC134553 BINDING SITE, designated SEQ ID:37077, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74588] Another function of VGAM2151 is therefore inhibition of LOC134553 (Accession XM_059723). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC134553. LOC146057 (Accession XM_085302) is an-

other VGAM2151 host target gene. LOC146057 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146057 BINDING SITE, designated SEQ ID:38058, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74589] Another function of VGAM2151 is therefore inhibition of LOC146057 (Accession XM_085302). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146057. LOC146439 (Accession XM_085463) is another VGAM2151 host target gene. LOC146439 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146439, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146439 BINDING SITE, designated SEQ ID:38151, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74590] Another function of VGAM2151 is therefore inhibition of LOC146439 (Accession XM_085463). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146439. LOC147895 (Accession XM_097339) is another VGAM2151 host target gene. LOC147895 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147895, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147895 BINDING SITE, designated SEQ ID:40861, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74591] Another function of VGAM2151 is therefore inhibition of LOC147895 (Accession XM_097339). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147895. LOC150113 (Accession XM_104532) is another VGAM2151 host target gene. LOC150113 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150113, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150113 BINDING SITE, designated SEQ ID:42168, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74592] Another function of VGAM2151 is therefore inhibition of LOC150113 (Accession XM_104532). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150113. LOC151610 (Accession XM_087245) is another VGAM2151 host target gene. LOC151610 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151610, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151610 BINDING SITE, designated SEQ ID:39136, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74593] Another function of VGAM2151 is therefore inhibition of LOC151610 (Accession XM_087245). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC151610. LOC152059 (Accession XM_087372) is another VGAM2151 host target gene. LOC152059 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152059, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152059 BINDING SITE, designated SEQ ID:39208, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74594] Another function of VGAM2151 is therefore inhibition of LOC152059 (Accession XM_087372). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152059. LOC158654 (Accession XM_088632) is another VGAM2151 host target gene. LOC158654 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158654, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158654 BINDING SITE, designated SEQ ID:39878, to the nucleotide sequence of VGAM2151 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4862.

[74595] Another function of VGAM2151 is therefore inhibition of LOC158654 (Accession XM_088632). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158654. LOC162022 (Accession XM_091293) is another VGAM2151 host target gene. LOC162022 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC162022, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162022 BINDING SITE, designated SEQ ID:40044, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74596] Another function of VGAM2151 is therefore inhibition of LOC162022 (Accession XM_091293). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162022. LOC199796 (Accession XM_058994) is another VGAM2151 host target gene. LOC199796 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC199796, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199796 BINDING SITE, designated SEQ ID:36813, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74597] Another function of VGAM2151 is therefore inhibition of LOC199796 (Accession XM_058994). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199796. LOC203069 (Accession XM_114618) is another VGAM2151 host target gene. LOC203069 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203069, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203069 BINDING SITE, designated SEQ ID:43001, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74598] Another function of VGAM2151 is therefore inhibition of LOC203069 (Accession XM_114618). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC203069. LOC221583 (Accession XM_166396) is another VGAM2151 host target gene. LOC221583 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221583, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221583 BINDING SITE, designated SEQ ID:44247, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74599] Another function of VGAM2151 is therefore inhibition of LOC221583 (Accession XM_166396). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221583. LOC254181 (Accession XM_174526) is another VGAM2151 host target gene. LOC254181 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254181, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254181 BINDING SITE, designated SEQ ID:46598, to

the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74600] Another function of VGAM2151 is therefore inhibition of LOC254181 (Accession XM_174526). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254181. LOC256586 (Accession XM_170759) is another VGAM2151 host target gene. LOC256586 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256586, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256586 BINDING SITE, designated SEQ ID:45514, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74601] Another function of VGAM2151 is therefore inhibition of LOC256586 (Accession XM_170759). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256586. LOC257438 (Accession XM_168338) is another VGAM2151 host target gene. LOC257438 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC257438, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257438 BINDING SITE, designated SEQ ID:45108, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74602] Another function of VGAM2151 is therefore inhibition of LOC257438 (Accession XM_168338). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257438. LOC257612 (Accession XM_175270) is another VGAM2151 host target gene. LOC257612 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257612, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257612 BINDING SITE, designated SEQ ID:46742, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74603] Another function of VGAM2151 is therefore inhibition of LOC257612 (Accession XM_175270). Accordingly, utilities

of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257612. LOC51015 (Accession NM_016048) is another VGAM2151 host target gene. LOC51015 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51015, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51015 BINDING SITE, designated SEQ ID:18127, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74604] Another function of VGAM2151 is therefore inhibition of LOC51015 (Accession NM_016048). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51015. LOC57107 (Accession NM_020381) is another VGAM2151 host target gene. LOC57107 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57107, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC57107 BINDING SITE, designated SEQ ID:21651, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74605] Another function of VGAM2151 is therefore inhibition of LOC57107 (Accession NM_020381). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57107. LOC84548 (Accession XM_048904) is another VGAM2151 host target gene. LOC84548 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC84548, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC84548 BINDING SITE, designated SEQ ID:35298, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74606] Another function of VGAM2151 is therefore inhibition of LOC84548 (Accession XM_048904). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC84548. LOC90620 (Accession XM_032986) is another VGAM2151 host target gene. LOC90620 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90620, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90620 BINDING SITE, designated SEQ ID:31804, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74607] Another function of VGAM2151 is therefore inhibition of LOC90620 (Accession XM_032986). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90620. LOC90835 (Accession XM_034371) is another VGAM2151 host target gene. LOC90835 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90835, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90835 BINDING SITE, designated SEQ ID:32073, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74608] Another function of VGAM2151 is therefore inhibition of

LOC90835 (Accession XM_034371). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90835. LOC90874 (Accession XM_034660) is another VGAM2151 host target gene. LOC90874 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90874, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90874 BINDING SITE, designated SEQ ID:32135, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74609] Another function of VGAM2151 is therefore inhibition of LOC90874 (Accession XM_034660). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90874. LOC91156 (Accession XM_036558) is another VGAM2151 host target gene. LOC91156 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91156, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC91156 BINDING SITE, designated SEQ ID:32465, to the nucleotide sequence of VGAM2151 RNA, herein designated VGAM RNA, also designated SEQ ID:4862.

[74610] Another function of VGAM2151 is therefore inhibition of LOC91156 (Accession XM_036558). Accordingly, utilities of VGAM2151 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91156. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2152 (VGAM2152) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74611] VGAM2152 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2152 was detected is described hereinabove with reference to Figs. 1-8.

[74612] VGAM2152 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2152 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[74613] VGAM2152 gene encodes a VGAM2152 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2152 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2152 precursor RNA is designated SEQ ID:2138, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2138 is located at position 44423 relative to the genome of Rana Tigrina Ranavirus.

[74614] VGAM2152 precursor RNA folds onto itself, forming VGAM2152 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74615] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2152 folded precursor RNA into VGAM2152 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2152 RNA is designated SEQ ID:4863, and is provided hereinbelow with reference to the sequence listing part.

[74616] VGAM2152 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2152 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2152 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74617] VGAM2152 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2152 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2152 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2152 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2152 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74618] The complementary binding of VGAM2152 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2152 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2152 host target RNA into VGAM2152 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74619] It is appreciated that VGAM2152 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2152 host target genes. The mRNA of each one of this plurality of VGAM2152 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2152 RNA, herein designated VGAM RNA, and which when bound by VGAM2152 RNA causes inhibition of translation of respective one or more VGAM2152 host target proteins.

[74620] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2152 gene, herein designated VGAM GENE, on one or more VGAM2152 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74621] It is yet further appreciated that a function of VGAM2152 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2152 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2152 correlate with, and may be deduced from, the identity of the host target genes which VGAM2152 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74622] Nucleotide sequences of the VGAM2152 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2152 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2152 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2152 are further described hereinbelow with reference to Table 1.

[74623] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2152 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2152 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74624] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2152 gene, herein designated VGAM is inhibition of expression of VGAM2152 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2152 correlate with, and may be deduced from, the identity of the target genes which VGAM2152 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74625] FLJ10748 (Accession NM_018203) is a VGAM2152 host target gene. FLJ10748 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10748, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10748 BINDING SITE, designated SEQ ID:20087, to the nucleotide sequence of VGAM2152 RNA, herein designated VGAM RNA, also designated SEQ ID:4863.

[74626] A function of VGAM2152 is therefore inhibition of FLJ10748 (Accession NM_018203). Accordingly, utilities of VGAM2152 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10748. LOC112937 (Accession XM_166199) is another VGAM2152 host target gene. LOC112937 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC112937, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112937 BINDING SITE, designated SEQ ID:44006, to the nucleotide sequence of VGAM2152 RNA, herein designated VGAM RNA, also designated SEQ ID:4863.

[74627] Another function of VGAM2152 is therefore inhibition of LOC112937 (Accession XM_166199). Accordingly, utilities of VGAM2152 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112937. LOC158301 (Accession XM_088543) is another VGAM2152 host target gene. LOC158301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158301, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158301 BINDING SITE, designated SEQ ID:39811, to the nucleotide sequence of VGAM2152 RNA, herein designated VGAM RNA, also designated SEQ ID:4863.

[74628] Another function of VGAM2152 is therefore inhibition of LOC158301 (Accession XM_088543). Accordingly, utilities of VGAM2152 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158301. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2153 (VGAM2153) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74629] VGAM2153 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2153 was detected is described hereinabove with reference to Figs. 1-8.

[74630] VGAM2153 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2153 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[74631] VGAM2153 gene encodes a VGAM2153 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2153 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2153 precursor RNA is designated SEQ ID:2139, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2139 is located at position 59440 relative to the genome of Rana Tigrina Ranavirus.

[74632] VGAM2153 precursor RNA folds onto itself, forming VGAM2153 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74633] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2153 folded precursor RNA into VGAM2153

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2153 RNA is designated SEQ ID:4864, and is provided hereinbelow with reference to the sequence listing part.

[74634] VGAM2153 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2153 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2153 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74635] VGAM2153 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2153 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2153 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2153 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2153 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74636] The complementary binding of VGAM2153 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2153 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2153 host target RNA into VGAM2153 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[74637] It is appreciated that VGAM2153 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2153 host target genes. The mRNA of each one of this plurality of VGAM2153 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2153 RNA, herein designated VGAM RNA, and which when bound by VGAM2153 RNA causes inhibition of translation of respective one or more VGAM2153 host target proteins.

[74638] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2153 gene, herein designated VGAM GENE, on one or more VGAM2153 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74639] It is yet further appreciated that a function of VGAM2153 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2153 correlate with, and may be deduced from, the identity of the host target genes which VGAM2153 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74640] Nucleotide sequences of the VGAM2153 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2153 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2153 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2153 are further described hereinbelow with reference to Table 1.

[74641] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2153 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2153 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74642] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2153 gene, herein designated VGAM is inhibition of expression of VGAM2153 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2153 correlate with, and may be deduced from, the identity of the target genes which VGAM2153 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74643] Core-binding Factor, Runt Domain, Alpha Subunit 2; Translocated To, 3 (CBFA2T3, Accession NM_005187) is a VGAM2153 host target gene. CBFA2T3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CBFA2T3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBFA2T3 BINDING SITE, designated SEQ ID:11692, to the nucleotide

sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74644] A function of VGAM2153 is therefore inhibition of Core-binding Factor, Runt Domain, Alpha Subunit 2; Translocated To, 3 (CBFA2T3, Accession NM_005187). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T3. Cytoplasmic Linker Associated Protein 1 (CLASP1, Accession XM_037105) is another VGAM2153 host target gene. CLASP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CLASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLASP1 BINDING SITE, designated SEQ ID:32540, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74645] Another function of VGAM2153 is therefore inhibition of Cytoplasmic Linker Associated Protein 1 (CLASP1, Accession XM_037105), a gene which plays a role in the local regulation of microtubule dynamics . Accordingly, utilities of VGAM2153 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with CLASP1. The function of CLASP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM298.Interleukin 13 Receptor, Alpha 1 (IL13RA1, Accession NM_001560) is another VGAM2153 host target gene. IL13RA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL13RA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL13RA1 BINDING SITE, designated SEQ ID:7284, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74646] Another function of VGAM2153 is therefore inhibition of Interleukin 13 Receptor, Alpha 1 (IL13RA1, Accession NM_001560), a gene which binds il-13 with a low affinity. together with il-4r- alpha can form a functional receptor for il-13. Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL13RA1. The function of IL13RA1 and its association with various diseases and

clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM144.Inositol 1,4,5-triphosphate Receptor, Type 1 (ITPR1, Accession NM_002222) is another VGAM2153 host target gene. ITPR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITPR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITPR1 BINDING SITE, designated SEQ ID:7984, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74647] Another function of VGAM2153 is therefore inhibition of Inositol 1,4,5-triphosphate Receptor, Type 1 (ITPR1, Accession NM_002222), a gene which couples cell membrane receptors to Ca2+ signal transduction pathways. Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPR1. The function of ITPR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM106.Nijmegen Break-

age Syndrome 1 (nibrin) (NBS1, Accession XM_045343) is another VGAM2153 host target gene. NBS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NBS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NBS1 BINDING SITE, designated SEQ ID:34435, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74648] Another function of VGAM2153 is therefore inhibition of Nijmegen Breakage Syndrome 1 (nibrin) (NBS1, Accession XM_045343), a gene which may be involved in repair of DNA double-strand breaks. Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NBS1. The function of NBS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM450.NDRG Family Member 3 (NDRG3, Accession NM_032013) is another VGAM2153 host target gene. NDRG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

NDRG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDRG3 BINDING SITE, designated SEQ ID:25725, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74649] Another function of VGAM2153 is therefore inhibition of NDRG Family Member 3 (NDRG3, Accession NM_032013). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG3. Nuclear Receptor Subfamily 2, Group E, Member 3 (NR2E3, Accession NM_016346) is another VGAM2153 host target gene. NR2E3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NR2E3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR2E3 BINDING SITE, designated SEQ ID:18471, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74650] Another function of VGAM2153 is therefore inhibition of

Nuclear Receptor Subfamily 2, Group E, Member 3 (NR2E3, Accession NM_016346). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR2E3. RIG (Accession NM_006394) is another VGAM2153 host target gene. RIG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RIG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RIG BINDING SITE, designated SEQ ID:13103, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74651] Another function of VGAM2153 is therefore inhibition of RIG (Accession NM_006394), a gene which is ribosomal protein S15. Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RIG. The function of RIG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977) is another

VGAM2153 host target gene. SLC22A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC22A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC22A3 BINDING SITE, designated SEQ ID:22507, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74652] Another function of VGAM2153 is therefore inhibition of Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977), a gene which is a sodium-ion dependent, high affinity carnitine transporter. also transports organic cations without the involvement of sodium. involved in the active cellular uptake of carnitine. Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC22A3. The function of SLC22A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2147.WIG1 (Accession XM_170497) is another VGAM2153 host target gene. WIG1 BINDING SITE is HOST

TARGET binding site found in the 5` untranslated region of mRNA encoded by WIG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WIG1 BINDING SITE, designated SEQ ID:45336, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74653] Another function of VGAM2153 is therefore inhibition of WIG1 (Accession XM_170497), a gene which is a sensor of cellular stress conditions including oncogenic activation, DNA damage and hypoxia. Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WIG1. The function of WIG1 has been established by previous studies. 1. Hellborg, F.; Qian, W.; Mendez-Vidal, C.; Asker, C.; Kost-Alimova, M.; Wilhelm, M.; Imreh, S.; Wiman, K. G. : Human wig-1, a p53 target gene that encodes a growth inhibitory zinc finger protein. Oncogene 20: 5466-5474, 2001. PubMed ID : 11571644 2. Varmeh-Ziaie, S.; Okan, I.; Wang, Y.; Magnusson, K. P.; Warthoe, P.; Strauss, M.; Wiman, K. G. : Wig-1, a new p53-induced gene encoding a zinc finger protein. Oncogene 15: 2699-2704, 1997.

PubMed ID : 9400996

[74654] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74655] Hellborg, F.; Qian, W.; Mendez-Vidal, C.; Asker, C.; Kost-Alimova, M.; Wilhelm, M.; Imreh, S.; Wiman, K. G. : Human wig-1, a p53 target gene that encodes a growth inhibitory zinc finger protein. Oncogene 20: 5466-5474, 2001. ; and

[74656] Varmeh-Ziaie, S.; Okan, I.; Wang, Y.; Magnusson, K. P.; Warthoe, P.; Strauss, M.; Wiman, K. G. : Wig-1, a new p53-induced gene encoding a zinc finger protein. Onco-gene 15: 2699-2704, 1.

[74657] Further studies establishing the function and utilities of WIG1 are found in John Hopkins OMIM database record ID 606452, and in sited publications numbered 6272-6273 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Zinc Finger Protein 202 (ZNF202, Accession NM_003455) is another VGAM2153 host target gene. ZNF202 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF202, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF202 BINDING SITE, designated SEQ ID:9509, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74658] Another function of VGAM2153 is therefore inhibition of Zinc Finger Protein 202 (ZNF202, Accession NM_003455). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF202. Chromosome 9 Open Reading Frame 5 (C9orf5, Accession NM_032012) is another VGAM2153 host target gene. C9orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C9orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C9orf5 BINDING SITE, designated SEQ ID:25715, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74659] Another function of VGAM2153 is therefore inhibition of Chromosome 9 Open Reading Frame 5 (C9orf5, Accession NM_032012). Accordingly, utilities of VGAM2153 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf5. Chondrolectin (CHODL, Accession NM_024944) is another VGAM2153 host target gene. CHODL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHODL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHODL BINDING SITE, designated SEQ ID:24490, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74660] Another function of VGAM2153 is therefore inhibition of Chondrolectin (CHODL, Accession NM_024944). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHODL. CPR2 (Accession NM_030900) is another VGAM2153 host target gene. CPR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CPR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPR2 BIND-

ING SITE, designated SEQ ID:25173, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74661] Another function of VGAM2153 is therefore inhibition of CPR2 (Accession NM_030900). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPR2. DKFZP586M1120 (Accession NM_031294) is another VGAM2153 host target gene. DKFZP586M1120 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586M1120, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586M1120 BINDING SITE, designated SEQ ID:25323, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74662] Another function of VGAM2153 is therefore inhibition of DKFZP586M1120 (Accession NM_031294). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586M1120. DKFZp761K1423 (Accession

NM_018422) is another VGAM2153 host target gene. DKFZp761K1423 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp761K1423, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp761K1423 BINDING SITE, designated SEQ ID:20470, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74663] Another function of VGAM2153 is therefore inhibition of DKFZp761K1423 (Accession NM_018422). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761K1423. DKFZp762E1312 (Accession NM_018410) is another VGAM2153 host target gene. DKFZp762E1312 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp762E1312, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp762E1312 BINDING SITE, designated SEQ ID:20451, to the nucleotide sequence of

VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74664] Another function of VGAM2153 is therefore inhibition of DKFZp762E1312 (Accession NM_018410). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762E1312. EZF-2 (Accession NM_018337) is another VGAM2153 host target gene. EZF-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EZF-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EZF-2 BINDING SITE, designated SEQ ID:20341, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74665] Another function of VGAM2153 is therefore inhibition of EZF-2 (Accession NM_018337). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EZF-2. FLJ10520 (Accession NM_018124) is another VGAM2153 host target gene. FLJ10520 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA

encoded by FLJ10520, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10520 BINDING SITE, designated SEQ ID:19906, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74666] Another function of VGAM2153 is therefore inhibition of FLJ10520 (Accession NM_018124). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10520. FLJ13110 (Accession NM_022912) is another VGAM2153 host target gene. FLJ13110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13110 BINDING SITE, designated SEQ ID:23222, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74667] Another function of VGAM2153 is therefore inhibition of FLJ13110 (Accession NM_022912). Accordingly, utilities of

VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13110. FLJ13769 (Accession NM_025012) is another VGAM2153 host target gene. FLJ13769 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13769, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13769 BINDING SITE, designated SEQ ID:24596, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74668] Another function of VGAM2153 is therefore inhibition of FLJ13769 (Accession NM_025012). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13769. FLJ20081 (Accession NM_017658) is another VGAM2153 host target gene. FLJ20081 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20081, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20081

BINDING SITE, designated SEQ ID:19182, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74669] Another function of VGAM2153 is therefore inhibition of FLJ20081 (Accession NM_017658). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20081. FLJ20139 (Accession NM_017685) is another VGAM2153 host target gene. FLJ20139 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20139 BINDING SITE, designated SEQ ID:19234, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74670] Another function of VGAM2153 is therefore inhibition of FLJ20139 (Accession NM_017685). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20139. FLJ20477 (Accession NM_017837) is another VGAM2153 host target gene. FLJ20477 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20477, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20477 BINDING SITE, designated SEQ ID:19503, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74671] Another function of VGAM2153 is therefore inhibition of FLJ20477 (Accession NM_017837). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20477. FLJ21916 (Accession NM_023112) is another VGAM2153 host target gene. FLJ21916 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21916, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21916 BINDING SITE, designated SEQ ID:23381, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74672] Another function of VGAM2153 is therefore inhibition of

FLJ21916 (Accession NM_023112). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21916. FLJ23510 (Accession NM_024720) is another VGAM2153 host target gene. FLJ23510 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23510, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23510 BINDING SITE, designated SEQ ID:24053, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74673] Another function of VGAM2153 is therefore inhibition of FLJ23510 (Accession NM_024720). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23510. FLJ30294 (Accession NM_144632) is another VGAM2153 host target gene. FLJ30294 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ30294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ30294 BINDING SITE, designated SEQ ID:29451, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74674] Another function of VGAM2153 is therefore inhibition of FLJ30294 (Accession NM_144632). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30294. IKKE (Accession NM_014002) is another VGAM2153 host target gene. IKKE BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IKKE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IKKE BINDING SITE, designated SEQ ID:15204, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74675] Another function of VGAM2153 is therefore inhibition of IKKE (Accession NM_014002). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IKKE. KIAA0237 (Accession NM_014747) is another VGAM2153

host target gene. KIAA0237 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0237, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0237 BINDING SITE, designated SEQ ID:16458, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74676] Another function of VGAM2153 is therefore inhibition of KIAA0237 (Accession NM_014747). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0237. KIAA0337 (Accession NM_014786) is another VGAM2153 host target gene. KIAA0337 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0337, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0337 BINDING SITE, designated SEQ ID:16656, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74677] Another function of VGAM2153 is therefore inhibition of KIAA0337 (Accession NM_014786). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0337. KIAA0390 (Accession NM_014717) is another VGAM2153 host target gene. KIAA0390 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0390, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0390 BINDING SITE, designated SEQ ID:16271, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74678] Another function of VGAM2153 is therefore inhibition of KIAA0390 (Accession NM_014717). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0390. KIAA0451 (Accession NM_014826) is another VGAM2153 host target gene. KIAA0451 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0451, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0451 BINDING SITE, designated SEQ ID:16809, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74679] Another function of VGAM2153 is therefore inhibition of KIAA0451 (Accession NM_014826). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0451. KIAA0662 (Accession XM_088539) is another VGAM2153 host target gene. KIAA0662 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0662, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0662 BINDING SITE, designated SEQ ID:39804, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74680] Another function of VGAM2153 is therefore inhibition of KIAA0662 (Accession XM_088539). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0662. KIAA1318 (Accession XM_041080) is another VGAM2153 host target gene. KIAA1318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1318 BINDING SITE, designated SEQ ID:33434, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74681] Another function of VGAM2153 is therefore inhibition of KIAA1318 (Accession XM_041080). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1318. KIAA1503 (Accession XM_043197) is another VGAM2153 host target gene. KIAA1503 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1503, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1503 BINDING SITE, designated SEQ ID:33917, to the nucleotide sequence of VGAM2153 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4864.

[74682] Another function of VGAM2153 is therefore inhibition of KIAA1503 (Accession XM_043197). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1503. KIAA1582 (Accession XM_037262) is another VGAM2153 host target gene. KIAA1582 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1582, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1582 BINDING SITE, designated SEQ ID:32580, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74683] Another function of VGAM2153 is therefore inhibition of KIAA1582 (Accession XM_037262). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1582. KIAA1817 (Accession XM_042978) is another VGAM2153 host target gene. KIAA1817 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1817, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1817 BINDING SITE, designated SEQ ID:33863, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74684] Another function of VGAM2153 is therefore inhibition of KIAA1817 (Accession XM_042978). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1817. MGC10765 (Accession NM_024345) is another VGAM2153 host target gene. MGC10765 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC10765, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10765 BINDING SITE, designated SEQ ID:23645, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74685] Another function of VGAM2153 is therefore inhibition of MGC10765 (Accession NM_024345). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC10765. MGC13053 (Accession NM_032710) is another VGAM2153 host target gene. MGC13053 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC13053, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13053 BINDING SITE, designated SEQ ID:26422, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74686] Another function of VGAM2153 is therefore inhibition of MGC13053 (Accession NM_032710). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13053. MGC13168 (Accession NM_032735) is another VGAM2153 host target gene. MGC13168 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC13168, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13168 BINDING SITE, designated SEQ ID:26460, to

the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74687] Another function of VGAM2153 is therefore inhibition of MGC13168 (Accession NM_032735). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13168. MGC2508 (Accession NM_024327) is another VGAM2153 host target gene. MGC2508 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2508, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2508 BINDING SITE, designated SEQ ID:23619, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74688] Another function of VGAM2153 is therefore inhibition of MGC2508 (Accession NM_024327). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2508. MGC2663 (Accession NM_024106) is another VGAM2153 host target gene. MGC2663 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by MGC2663, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2663 BINDING SITE, designated SEQ ID:23550, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74689] Another function of VGAM2153 is therefore inhibition of MGC2663 (Accession NM_024106). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2663. PP1628 (Accession NM_025201) is another VGAM2153 host target gene. PP1628 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PP1628, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP1628 BINDING SITE, designated SEQ ID:24859, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74690] Another function of VGAM2153 is therefore inhibition of PP1628 (Accession NM_025201). Accordingly, utilities of

VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1628. Polyglutamine Binding Protein 1 (PQBP1, Accession NM_005710) is another VGAM2153 host target gene. PQBP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PQBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PQBP1 BINDING SITE, designated SEQ ID:12262, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74691] Another function of VGAM2153 is therefore inhibition of Polyglutamine Binding Protein 1 (PQBP1, Accession NM_005710). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PQBP1. RAB3-GAP150 (Accession NM_012414) is another VGAM2153 host target gene. RAB3-GAP150 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB3-GAP150, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB3-GAP150 BINDING SITE, designated SEQ ID:14790, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74692] Another function of VGAM2153 is therefore inhibition of RAB3-GAP150 (Accession NM_012414). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB3-GAP150. Suppressor of Ty 4 Homolog 1 (S. cerevisiae) (SUPT4H1, Accession NM_003168) is another VGAM2153 host target gene. SUPT4H1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SUPT4H1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SUPT4H1 BINDING SITE, designated SEQ ID:9145, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74693] Another function of VGAM2153 is therefore inhibition of Suppressor of Ty 4 Homolog 1 (S. cerevisiae) (SUPT4H1, Accession NM_003168). Accordingly, utilities of

VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUPT4H1. VILL (Accession XM_043435) is another VGAM2153 host target gene. VILL BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by VILL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VILL BINDING SITE, designated SEQ ID:33948, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74694] Another function of VGAM2153 is therefore inhibition of VILL (Accession XM_043435). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VILL. WSB1 (Accession NM_134264) is another VGAM2153 host target gene. WSB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WSB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WSB1 BINDING SITE, designated SEQ

ID:28619, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74695] Another function of VGAM2153 is therefore inhibition of WSB1 (Accession NM_134264). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WSB1. YKT6 (Accession NM_006555) is another VGAM2153 host target gene. YKT6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by YKT6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YKT6 BINDING SITE, designated SEQ ID:13322, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74696] Another function of VGAM2153 is therefore inhibition of YKT6 (Accession NM_006555). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YKT6. Zinc Finger Protein 271 (ZNF271, Accession XM_170865) is another VGAM2153 host target gene. ZNF271 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF271 BINDING SITE, designated SEQ ID:45636, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74697] Another function of VGAM2153 is therefore inhibition of Zinc Finger Protein 271 (ZNF271, Accession XM_170865). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF271. LOC126392 (Accession XM_065057) is another VGAM2153 host target gene. LOC126392 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC126392, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126392 BINDING SITE, designated SEQ ID:37275, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74698] Another function of VGAM2153 is therefore inhibition of LOC126392 (Accession XM_065057). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126392. LOC144519 (Accession XM_084890) is another VGAM2153 host target gene. LOC144519 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144519, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144519 BINDING SITE, designated SEQ ID:37760, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74699] Another function of VGAM2153 is therefore inhibition of LOC144519 (Accession XM_084890). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144519. LOC145899 (Accession XM_096899) is another VGAM2153 host target gene. LOC145899 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145899, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145899 BINDING SITE, designated SEQ ID:40625, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74700] Another function of VGAM2153 is therefore inhibition of LOC145899 (Accession XM_096899). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145899. LOC146243 (Accession XM_096956) is another VGAM2153 host target gene. LOC146243 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146243, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146243 BINDING SITE, designated SEQ ID:40678, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74701] Another function of VGAM2153 is therefore inhibition of LOC146243 (Accession XM_096956). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC146243. LOC146802 (Accession XM_085595) is another VGAM2153 host target gene. LOC146802 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146802, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146802 BINDING SITE, designated SEQ ID:38246, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74702] Another function of VGAM2153 is therefore inhibition of LOC146802 (Accession XM_085595). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146802. LOC147645 (Accession XM_085831) is another VGAM2153 host target gene. LOC147645 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147645, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147645 BINDING SITE, designated SEQ ID:38359, to the nucleotide sequence of VGAM2153 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4864.

[74703] Another function of VGAM2153 is therefore inhibition of LOC147645 (Accession XM_085831). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147645. LOC155038 (Accession XM_088130) is another VGAM2153 host target gene. LOC155038 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155038, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155038 BINDING SITE, designated SEQ ID:39533, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74704] Another function of VGAM2153 is therefore inhibition of LOC155038 (Accession XM_088130). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155038. LOC158117 (Accession XM_088483) is another VGAM2153 host target gene. LOC158117 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158117, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158117 BINDING SITE, designated SEQ ID:39728, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74705] Another function of VGAM2153 is therefore inhibition of LOC158117 (Accession XM_088483). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158117. LOC159199 (Accession XM_089441) is another VGAM2153 host target gene. LOC159199 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC159199, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159199 BINDING SITE, designated SEQ ID:39982, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74706] Another function of VGAM2153 is therefore inhibition of LOC159199 (Accession XM_089441). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC159199. LOC161536 (Accession XM_090967) is another VGAM2153 host target gene. LOC161536 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC161536, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161536 BINDING SITE, designated SEQ ID:40021, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74707] Another function of VGAM2153 is therefore inhibition of LOC161536 (Accession XM_090967). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161536. LOC201514 (Accession XM_113975) is another VGAM2153 host target gene. LOC201514 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201514, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201514 BINDING SITE, designated SEQ ID:42583, to

the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74708] Another function of VGAM2153 is therefore inhibition of LOC201514 (Accession XM_113975). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201514. LOC201707 (Accession XM_114369) is another VGAM2153 host target gene. LOC201707 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201707, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201707 BINDING SITE, designated SEQ ID:42903, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74709] Another function of VGAM2153 is therefore inhibition of LOC201707 (Accession XM_114369). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201707. LOC203275 (Accession XM_114667) is another VGAM2153 host target gene. LOC203275 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC203275, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203275 BINDING SITE, designated SEQ ID:43025, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74710] Another function of VGAM2153 is therefore inhibition of LOC203275 (Accession XM_114667). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203275. LOC221583 (Accession XM_166396) is another VGAM2153 host target gene. LOC221583 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221583, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221583 BINDING SITE, designated SEQ ID:44244, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74711] Another function of VGAM2153 is therefore inhibition of LOC221583 (Accession XM_166396). Accordingly, utilities

of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221583. LOC253936 (Accession XM_170637) is another VGAM2153 host target gene. LOC253936 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253936, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253936 BINDING SITE, designated SEQ ID:45408, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74712] Another function of VGAM2153 is therefore inhibition of LOC253936 (Accession XM_170637). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253936. LOC255565 (Accession XM_170811) is another VGAM2153 host target gene. LOC255565 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255565, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC255565 BINDING SITE, designated SEQ ID:45587, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74713] Another function of VGAM2153 is therefore inhibition of LOC255565 (Accession XM_170811). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255565. LOC255974 (Accession XM_173706) is another VGAM2153 host target gene. LOC255974 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255974, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255974 BINDING SITE, designated SEQ ID:46557, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74714] Another function of VGAM2153 is therefore inhibition of LOC255974 (Accession XM_173706). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255974. LOC256021 (Accession XM_172884) is another VGAM2153 host target gene. LOC256021 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256021, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256021 BINDING SITE, designated SEQ ID:46167, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74715] Another function of VGAM2153 is therefore inhibition of LOC256021 (Accession XM_172884). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256021. LOC90010 (Accession XM_028150) is another VGAM2153 host target gene. LOC90010 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90010, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90010 BINDING SITE, designated SEQ ID:30620, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74716] Another function of VGAM2153 is therefore inhibition of

LOC90010 (Accession XM_028150). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90010. LOC90499 (Accession XM_032170) is another VGAM2153 host target gene. LOC90499 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90499, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90499 BINDING SITE, designated SEQ ID:31585, to the nucleotide sequence of VGAM2153 RNA, herein designated VGAM RNA, also designated SEQ ID:4864.

[74717] Another function of VGAM2153 is therefore inhibition of LOC90499 (Accession XM_032170). Accordingly, utilities of VGAM2153 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90499. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2154 (VGAM2154) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[74718] VGAM2154 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2154 was detected is described hereinabove with reference to Figs. 1-8.

[74719] VGAM2154 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2154 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74720] VGAM2154 gene encodes a VGAM2154 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2154 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2154 precursor RNA is designated SEQ ID:2140, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2140 is located at position 48817 relative to the genome of Rana Tigrina Ranavirus.

[74721] VGAM2154 precursor RNA folds onto itself, forming VGAM2154 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74722] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2154 folded precursor RNA into VGAM2154 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2154 RNA is designated SEQ ID:4865, and is provided hereinbelow with reference to the sequence listing part.

[74723] VGAM2154 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2154 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2154 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74724] VGAM2154 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2154 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2154 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2154 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2154 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[74725] The complementary binding of VGAM2154 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2154 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2154 host target RNA into VGAM2154 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74726] It is appreciated that VGAM2154 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2154 host target genes. The mRNA of each one of this plurality of VGAM2154 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2154 RNA, herein designated VGAM RNA, and which when bound by VGAM2154 RNA causes inhibition of translation of respective one or more VGAM2154 host target proteins.

[74727] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2154 gene, herein designated VGAM GENE, on one

or more VGAM2154 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74728] It is yet further appreciated that a function of VGAM2154 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2154 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2154 correlate with, and may be deduced from, the identity of the host target genes which VGAM2154 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74729] Nucleotide sequences of the VGAM2154 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2154 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2154 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2154 are further described hereinbelow with reference to Table 1.

[74730] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2154 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2154 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74731] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2154 gene, herein designated VGAM is inhibition of expression of VGAM2154 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2154 correlate with, and may be deduced from, the identity of the target genes which VGAM2154 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74732] Tumor-associated Calcium Signal Transducer 2

(TACSTD2, Accession NM_002353) is a VGAM2154 host target gene. TACSTD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TACSTD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TACSTD2 BINDING SITE, designated SEQ ID:8162, to the nucleotide sequence of VGAM2154 RNA, herein designated VGAM RNA, also designated SEQ ID:4865.

[74733] A function of VGAM2154 is therefore inhibition of Tumor-associated Calcium Signal Transducer 2 (TACSTD2, Accession NM_002353), a gene which belongs to ga733 tumor-associated antigen gene family and may function as growth factor receptors. Accordingly, utilities of VGAM2154 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TACSTD2. The function of TACSTD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM210.E74-like Factor 1 (ets domain transcription factor) (ELF1, Accession XM_049376) is another VGAM2154 host target gene. ELF1 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELF1 BINDING SITE, designated SEQ ID:35401, to the nucleotide sequence of VGAM2154 RNA, herein designated VGAM RNA, also designated SEQ ID:4865.

[74734] Another function of VGAM2154 is therefore inhibition of E74-like Factor 1 (ets domain transcription factor) (ELF1, Accession XM_049376). Accordingly, utilities of VGAM2154 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELF1. MGC16202 (Accession NM_032373) is another VGAM2154 host target gene. MGC16202 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC16202, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16202 BINDING SITE, designated SEQ ID:26161, to the nucleotide sequence of VGAM2154 RNA, herein designated VGAM RNA, also designated SEQ ID:4865.

[74735] Another function of VGAM2154 is therefore inhibition of MGC16202 (Accession NM_032373). Accordingly, utilities of VGAM2154 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16202. LOC147219 (Accession XM_097214) is another VGAM2154 host target gene. LOC147219 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147219 BINDING SITE, designated SEQ ID:40824, to the nucleotide sequence of VGAM2154 RNA, herein designated VGAM RNA, also designated SEQ ID:4865.

[74736] Another function of VGAM2154 is therefore inhibition of LOC147219 (Accession XM_097214). Accordingly, utilities of VGAM2154 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147219. LOC153114 (Accession XM_098313) is another VGAM2154 host target gene. LOC153114 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153114, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153114 BINDING SITE, designated SEQ ID:41574, to the nucleotide sequence of VGAM2154 RNA, herein designated VGAM RNA, also designated SEQ ID:4865.

[74737] Another function of VGAM2154 is therefore inhibition of LOC153114 (Accession XM_098313). Accordingly, utilities of VGAM2154 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153114. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2155 (VGAM2155) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74738] VGAM2155 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2155 was detected is described hereinabove with reference to Figs. 1-8.

[74739] VGAM2155 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2155 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[74740] VGAM2155 gene encodes a VGAM2155 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2155 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2155 precursor RNA is designated SEQ ID:2141, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2141 is located at position 168488 relative to the genome of Monkeypox Virus.

[74741] VGAM2155 precursor RNA folds onto itself, forming VGAM2155 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74742] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2155 folded precursor RNA into VGAM2155

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2155 RNA is designated SEQ ID:4866, and is provided hereinbelow with reference to the sequence listing part.

[74743] VGAM2155 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2155 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2155 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74744] VGAM2155 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2155 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2155 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2155 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2155 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74745] The complementary binding of VGAM2155 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2155 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2155 host target RNA into VGAM2155 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[74746] It is appreciated that VGAM2155 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2155 host target genes. The mRNA of each one of this plurality of VGAM2155 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2155 RNA, herein designated VGAM RNA, and which when bound by VGAM2155 RNA causes inhibition of translation of respective one or more VGAM2155 host target proteins.

[74747] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2155 gene, herein designated VGAM GENE, on one or more VGAM2155 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74748] It is yet further appreciated that a function of VGAM2155 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2155 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2155 correlate with, and may be deduced from, the identity of the host target genes which VGAM2155 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74749] Nucleotide sequences of the VGAM2155 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2155 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2155 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2155 are further described hereinbelow with reference to Table 1.

[74750] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2155 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2155 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74751] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2155 gene, herein designated VGAM is inhibition of expression of VGAM2155 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2155 correlate with, and may be deduced from, the identity of the target genes which VGAM2155 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74752] Fibroblast Growth Factor Receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) (FGFR2, Accession NM_000141) is a VGAM2155 host target gene. FGFR2 BINDING SITE1 through FGFR2 BINDING SITE6 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FGFR2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Ta-

ble 2 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE1 through FGFR2 BINDING SITE6, designated SEQ ID:5641, SEQ ID:23237, SEQ ID:23244, SEQ ID:23291, SEQ ID:23297 and SEQ ID:23303 respectively, to the nucleotide sequence of VGAM2155 RNA, herein designated VGAM RNA, also designated SEQ ID:4866.

[74753] A function of VGAM2155 is therefore inhibition of Fibroblast Growth Factor Receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) (FGFR2, Accession NM_000141). Accordingly, utilities of VGAM2155 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFR2. Potassium Inwardly-rectifying Channel, Subfamily J, Member 6 (KCNJ6, Accession NM_002240) is another VGAM2155 host target gene. KCNJ6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNJ6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNJ6 BINDING SITE, designated SEQ ID:8023, to the nucleotide se-

quence of VGAM2155 RNA, herein designated VGAM RNA, also designated SEQ ID:4866.

[74754] Another function of VGAM2155 is therefore inhibition of Potassium Inwardly-rectifying Channel, Subfamily J, Member 6 (KCNJ6, Accession NM_002240), a gene which may be involved in the regulation of insulin secretion by glucose and/or neurotransmitters. Accordingly, utilities of VGAM2155 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ6. The function of KCNJ6 has been established by previous studies. ATP-sensitive potassium channels, also called K(ATP) channels, are closed by an increase in the intracellular ATP concentration of the cell and thereby provide a means of linking cellular metabolism to the electrical excitability of the plasma membrane. Sakura et al. (1995) stated that their physiologic function is best understood in the pancreatic beta-cell where they play a key role in the regulation of insulin secretion in response to nutrients. Closure of K(ATP) channels, as the result of metabolically generated ATP, produces membrane depolarization. This leads to activation of voltage-sensitive Ca(2+) channels, Ca(2+) influx, and ultimately insulin release. Sakura et al. (1995) cloned the KCNJ6 gene, which

encodes a putative subunit of a human ATP-sensitive K-channel expressed in brain and beta cells, and characterized its exon/intron structure. By screening of a somatic cell mapping panel and fluorescence in situ hybridization, they placed the gene on 21q22.1-q22.2. Analysis of SSCPs revealed the presence of 2 silent polymorphisms (pro149: CCG-CCA and asp328: GAC-GAT) with similar frequencies in normal and noninsulin-dependent diabetic patients. The weaver mutation, discovered by Lane (1964), had been studied intensively for more than 25 years (Rakic and Sidman, 1973) for insights into the normal processes of neural development and differentiation. Homozygous animals suffer from severe ataxia that is obvious by about the second postnatal week. The cerebellum of these animals is drastically reduced in size due to depletion of the major cell type of cerebellum, the granule cell neuron. Heterozygous animals are not ataxic but have an intermediate number of surviving granule cells. Patil et al. (1995), and other workers before them, found that the overall expression pattern of the Girk2 gene corresponds closely to the pattern of phenotypic effects in weaver mice. Expression in the cerebellum, substantia nigra, and testes is associated with a developmental loss of cells in

those tissues. Expression of Girk2 in the cortex is consistent with seizures that affect weaver mice. Goldowitz and Smeyne (1995) diagrammed the developmental events in the early postnatal cerebellum in wildtype and weaver mice, the expression pattern of Girk2 mRNA in adult brain, and the proposed role of Girk2 in normal and abnormal granule cell differentiation.

[74755] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74756] Bandmann, O.; Davis, M. B.; Marsden, C. D.; Wood, N. W. : The human homologue of the Weaver mouse gene in familial and sporadic Parkinson's disease. Neuroscience 72: 877-879, 1996. ; and

[74757] Goldowitz, D.; Smeyne, R. J. : Tune into the weaver channel. Nature Genet. 11: 107-109, 1995.

[74758] Further studies establishing the function and utilities of KCNJ6 are found in John Hopkins OMIM database record ID 600877, and in sited publications numbered 3274, 6844-684 and 10066-6851 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.FLJ14075 (Accession NM_024894) is another VGAM2155 host target gene. FLJ14075 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14075, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14075 BINDING SITE, designated SEQ ID:24373, to the nucleotide sequence of VGAM2155 RNA, herein designated VGAM RNA, also designated SEQ ID:4866.

[74759] Another function of VGAM2155 is therefore inhibition of FLJ14075 (Accession NM_024894). Accordingly, utilities of VGAM2155 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14075. KIAA0626 (Accession NM_021647) is another VGAM2155 host target gene. KIAA0626 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0626, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0626 BINDING SITE, designated SEQ ID:22314, to the nucleotide sequence of VGAM2155 RNA, herein designated VGAM RNA, also designated SEQ ID:4866.

[74760] Another function of VGAM2155 is therefore inhibition of

KIAA0626 (Accession NM_021647). Accordingly, utilities of VGAM2155 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0626. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2156 (VGAM2156) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74761] VGAM2156 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2156 was detected is described hereinabove with reference to Figs. 1-8.

[74762] VGAM2156 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2156 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74763] VGAM2156 gene encodes a VGAM2156 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2156 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2156 precursor RNA is designated SEQ ID:2142, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2142 is located at position 170622 relative to the genome of Monkeypox Virus.

[74764] VGAM2156 precursor RNA folds onto itself, forming VGAM2156 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74765] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2156 folded precursor RNA into VGAM2156 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide se-

quence of VGAM2156 RNA is designated SEQ ID:4867, and is provided hereinbelow with reference to the sequence listing part.

[74766] VGAM2156 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2156 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2156 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74767] VGAM2156 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2156 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2156 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2156 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2156 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74768] The complementary binding of VGAM2156 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2156 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2156 host target RNA into VGAM2156 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74769] It is appreciated that VGAM2156 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2156 host target genes. The mRNA of each one of this plurality of VGAM2156 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2156 RNA, herein designated VGAM RNA, and which when bound by VGAM2156 RNA causes inhibition of translation of respective one or more VGAM2156 host target proteins.

[74770] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2156 gene, herein designated VGAM GENE, on one or more VGAM2156 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74771] It is yet further appreciated that a function of VGAM2156

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2156 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2156 correlate with, and may be deduced from, the identity of the host target genes which VGAM2156 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74772] Nucleotide sequences of the VGAM2156 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2156 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2156 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2156 are further described hereinbelow with reference to Table 1.

[74773] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2156 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2156 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74774] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2156 gene, herein designated VGAM is inhibition of expression of VGAM2156 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2156 correlate with, and may be deduced from, the identity of the target genes which VGAM2156 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74775] FLJ22283 (Accession NM_032220) is a VGAM2156 host target gene. FLJ22283 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22283, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22283 BINDING SITE, designated SEQ ID:25947, to the nucleotide sequence of VGAM2156 RNA, herein designated VGAM RNA, also designated SEQ ID:4867.

[74776] A function of VGAM2156 is therefore inhibition of FLJ22283 (Accession NM_032220). Accordingly, utilities of VGAM2156 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22283. LOC219686 (Accession XM_165544) is another

VGAM2156 host target gene. LOC219686 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219686, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219686 BINDING SITE, designated SEQ ID:43676, to the nucleotide sequence of VGAM2156 RNA, herein designated VGAM RNA, also designated SEQ ID:4867.

[74777] Another function of VGAM2156 is therefore inhibition of LOC219686 (Accession XM_165544). Accordingly, utilities of VGAM2156 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219686. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2157 (VGAM2157) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74778] VGAM2157 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2157 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[74779] VGAM2157 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2157 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74780] VGAM2157 gene encodes a VGAM2157 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2157 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2157 precursor RNA is designated SEQ ID:2143, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2143 is located at position 162621 relative to the genome of Monkeypox Virus.

[74781] VGAM2157 precursor RNA folds onto itself, forming VGAM2157 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74782] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2157 folded precursor RNA into VGAM2157 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2157 RNA is designated SEQ ID:4868, and is provided hereinbelow with reference to the sequence listing part.

[74783] VGAM2157 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2157 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2157 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74784] VGAM2157 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2157 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2157 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2157 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2157 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74785] The complementary binding of VGAM2157 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2157 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2157 host target RNA into VGAM2157 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74786] It is appreciated that VGAM2157 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2157 host target genes. The mRNA of each one of this plurality of VGAM2157 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2157 RNA, herein designated VGAM RNA, and which when bound by VGAM2157 RNA causes inhibition of translation of respective one or more VGAM2157 host target proteins.

[74787] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2157 gene, herein designated VGAM GENE, on one or more VGAM2157 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74788] It is yet further appreciated that a function of VGAM2157 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2157 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2157 correlate with, and may be deduced from, the identity of the host target genes which VGAM2157 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74789] Nucleotide sequences of the VGAM2157 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2157 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2157 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2157 are further described hereinbelow with reference to Table 1.

[74790] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2157 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2157 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74791] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2157 gene, herein designated VGAM is inhibition of expression of VGAM2157 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2157 correlate with, and may be deduced from, the identity of the target genes which VGAM2157 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74792] Ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2, Accession NM_015838) is a VGAM2157 host target gene. FCN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FCN2, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FCN2 BINDING SITE, designated SEQ ID:17950, to the nucleotide sequence of VGAM2157 RNA, herein designated VGAM RNA, also designated SEQ ID:4868.

[74793] A function of VGAM2157 is therefore inhibition of Ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2, Accession NM_015838), a gene which is involved in phagocytosis of pathogens. Accordingly, utilities of VGAM2157 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCN2. The function of FCN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM493.LOC90148 (Accession XM_029430) is another VGAM2157 host target gene. LOC90148 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90148, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90148 BINDING SITE, designated SEQ ID:30890, to the

nucleotide sequence of VGAM2157 RNA, herein designated VGAM RNA, also designated SEQ ID:4868.

[74794] Another function of VGAM2157 is therefore inhibition of LOC90148 (Accession XM_029430). Accordingly, utilities of VGAM2157 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90148. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2158 (VGAM2158) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74795] VGAM2158 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2158 was detected is described hereinabove with reference to Figs. 1-8.

[74796] VGAM2158 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2158 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74797] VGAM2158 gene encodes a VGAM2158 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2158 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2158 precursor RNA is designated SEQ ID:2144, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2144 is located at position 165985 relative to the genome of Monkeypox Virus.

[74798] VGAM2158 precursor RNA folds onto itself, forming VGAM2158 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74799] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2158 folded precursor RNA into VGAM2158 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2158 RNA is designated SEQ ID:4869, and is provided hereinbelow with reference to the sequence listing part.

[74800] VGAM2158 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2158 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2158 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74801] VGAM2158 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2158 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2158 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2158 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2158 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74802] The complementary binding of VGAM2158 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2158 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2158 host target RNA into VGAM2158 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74803] It is appreciated that VGAM2158 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2158 host target genes. The mRNA of each one of this plurality of VGAM2158 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2158 RNA, herein designated VGAM RNA, and which when bound by VGAM2158 RNA causes inhibition of translation of respective one or more VGAM2158 host target proteins.

[74804] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2158 gene, herein designated VGAM GENE, on one or more VGAM2158 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74805] It is yet further appreciated that a function of VGAM2158 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2158 correlate with, and may be deduced from, the identity of the host target genes which VGAM2158 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74806] Nucleotide sequences of the VGAM2158 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2158 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2158 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2158 are further described hereinbelow with reference to Table 1.

[74807] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2158 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2158 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74808] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2158 gene, herein designated VGAM is inhibition of expression of VGAM2158 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2158 correlate with, and may be deduced from, the identity of the target genes which VGAM2158 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74809] Dopachrome Tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT, Accession NM_001922) is a VGAM2158 host target gene. DCT BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DCT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCT BINDING SITE, designated SEQ ID:7638, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74810] A function of VGAM2158 is therefore inhibition of

Dopachrome Tautomerase (dopachrome delta-isomerase, tyrosine-related protein 2) (DCT, Accession NM_001922), a gene which regulates eumelanin and phaeomelanin levels. Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCT. The function of DCT has been established by previous studies. Sturm et al. (1995) showed that the TYRP1 protein is encoded in 7 exons spread over 24 kb of genomic DNA. By contrast, the TYRP2 protein is encoded by 8 exons. TYRP1, TYRP2, and the tyrosinase gene share a common C-terminal membrane spanning exon. The position of intron junctions suggested that TYRP1 was derived from a TYR duplication and then was itself duplicated to give rise to the TYRP2 gene. The comparisons also suggested that at least some of the introns within the TYR, TYRP1, and TYRP2 coding regions were gained after duplication and that intron slippage was unlikely to have occurred. NYESO1 (CTAG; 300156) is expressed on tumor cells of many different types, including melanoma. TRP2 is a melanoma-differentiation antigen. In a melanoma vaccine trial in patients with metastatic disease, Khong and Rosenberg (2002) identified tumor-infiltrating lymphocytes (TILs)

that recognized NYESO1, TRP2, and a TRP2 splice variant from a patient who experienced dramatic tumor regression. The TILs expressed immunologic reactivity against these antigens before vaccination with antigens, none of which she had been vaccinated against. Khong and Rosenberg (2002) proposed that NYESO1 and TRP2 may be useful in the active immunotherapy of patients with melanoma.

[74811] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[74812] Khong, H. T.; Rosenberg, S. A. : Pre-existing immunity to tyrosinase-related protein (TRP)-2, a new TRP-2 isoform, and the NY-ESO-1 melanoma antigen in a patient with a dramatic response to immunotherapy. J. Immun. 168: 951-956, 2002. ; and

[74813] Sturm, R. A.; O'Sullivan B. J.; Box, N. F.; Smith, A. G.; Smit, S. E.; Puttick, E. R. J.; Parsons, P. G.; Dunn, I. S. : Chromosomal structure of the human TYRP1 and TYRP2 loci and compa.

[74814] Further studies establishing the function and utilities of DCT are found in John Hopkins OMIM database record ID 191275, and in sited publications numbered 2559-2566

listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838) is another VGAM2158 host target gene. EGFL5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EGFL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGFL5 BINDING SITE, designated SEQ ID:41876, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74815] Another function of VGAM2158 is therefore inhibition of EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGFL5. Hypoxia-inducible Factor 1, Alpha Subunit (basic helix-loop-helix transcription factor) (HIF1A, Accession NM_001530) is another VGAM2158 host target gene. HIF1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HIF1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIF1A BINDING SITE, designated SEQ ID:7267, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74816] Another function of VGAM2158 is therefore inhibition of Hypoxia-inducible Factor 1, Alpha Subunit (basic helix-loop-helix transcription factor) (HIF1A, Accession NM_001530), a gene which is a basic helix-loop-helix transcription factor and mediates transcriptional responses to hypoxia and dioxin-signaling. Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIF1A. The function of HIF1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM229.Potassium Large Conductance Calcium-activated Channel, Subfamily M Beta Member 3 (KCNMB3, Accession NM_014407) is another VGAM2158 host target gene. KCNMB3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCNMB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNMB3 BINDING SITE, designated SEQ ID:15749, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74817] Another function of VGAM2158 is therefore inhibition of Potassium Large Conductance Calcium-activated Channel, Subfamily M Beta Member 3 (KCNMB3, Accession NM_014407), a gene which is similar to a regulatory subunit of Ca-activated potassium channel. Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNMB3. The function of KCNMB3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM111.Membrane Component, Chromosome 17, Surface Marker 2 (ovarian carcinoma antigen CA125) (M17S2, Accession NM_031858) is another VGAM2158 host target gene. M17S2 BINDING SITE1 through M17S2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by M17S2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of M17S2 BINDING SITE1 through M17S2 BINDING SITE3, designated SEQ ID:25609, SEQ ID:25622 and SEQ ID:12520 respectively, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74818] Another function of VGAM2158 is therefore inhibition of Membrane Component, Chromosome 17, Surface Marker 2 (ovarian carcinoma antigen CA125) (M17S2, Accession NM_031858), a gene which Contains a B-box/coiled coil motif. Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with M17S2. The function of M17S2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1081.Tumor Necrosis Factor Receptor Superfamily, Member 9 (TNFRSF9, Accession NM_001561) is another VGAM2158 host target gene. TNFRSF9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFRSF9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of TNFRSF9 BINDING SITE, designated SEQ ID:7288, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74819] Another function of VGAM2158 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 9 (TNFRSF9, Accession NM_001561), a gene which inhibits proliferation of activated T lymphocytes. Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF9. The function of TNFRSF9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1954.Chromosome 13 Open Reading Frame 1 (C13orf1, Accession NM_020456) is another VGAM2158 host target gene. C13orf1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C13orf1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C13orf1 BINDING SITE, designated SEQ ID:21693, to the nucleotide sequence of VGAM2158 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4869.

[74820] Another function of VGAM2158 is therefore inhibition of Chromosome 13 Open Reading Frame 1 (C13orf1, Accession NM_020456). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C13orf1. C3IP1 (Accession NM_021633) is another VGAM2158 host target gene. C3IP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C3IP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C3IP1 BINDING SITE, designated SEQ ID:22275, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74821] Another function of VGAM2158 is therefore inhibition of C3IP1 (Accession NM_021633). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C3IP1. Chromosome 5 Open Reading Frame 5 (C5orf5, Accession NM_016603) is another VGAM2158 host target gene. C5orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

C5orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5orf5 BINDING SITE, designated SEQ ID:18699, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74822] Another function of VGAM2158 is therefore inhibition of Chromosome 5 Open Reading Frame 5 (C5orf5, Accession NM_016603). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf5. Histidine Triad Nucleotide Binding Protein 3 (HINT3, Accession NM_138571) is another VGAM2158 host target gene. HINT3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HINT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HINT3 BINDING SITE, designated SEQ ID:28878, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74823] Another function of VGAM2158 is therefore inhibition of

Histidine Triad Nucleotide Binding Protein 3 (HINT3, Accession NM_138571). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HINT3. KIAA0416 (Accession NM_015564) is another VGAM2158 host target gene. KIAA0416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0416 BINDING SITE, designated SEQ ID:17837, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74824] Another function of VGAM2158 is therefore inhibition of KIAA0416 (Accession NM_015564). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0416. KIAA0781 (Accession XM_041314) is another VGAM2158 host target gene. KIAA0781 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0781, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0781 BINDING SITE, designated SEQ ID:33499, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74825] Another function of VGAM2158 is therefore inhibition of KIAA0781 (Accession XM_041314). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0781. KIAA0871 (Accession NM_014961) is another VGAM2158 host target gene. KIAA0871 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0871 BINDING SITE, designated SEQ ID:17332, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74826] Another function of VGAM2158 is therefore inhibition of KIAA0871 (Accession NM_014961). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0871. KIAA1505 (Accession XM_168469) is another VGAM2158 host target gene. KIAA1505 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1505, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1505 BINDING SITE, designated SEQ ID:45190, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74827] Another function of VGAM2158 is therefore inhibition of KIAA1505 (Accession XM_168469). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1505. KIAA1678 (Accession XM_051221) is another VGAM2158 host target gene. KIAA1678 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1678, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1678 BINDING SITE, designated SEQ ID:35787, to the nucleotide sequence of VGAM2158 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4869.

[74828] Another function of VGAM2158 is therefore inhibition of KIAA1678 (Accession XM_051221). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1678. MGC16063 (Accession NM_053047) is another VGAM2158 host target gene. MGC16063 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC16063, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16063 BINDING SITE, designated SEQ ID:27590, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74829] Another function of VGAM2158 is therefore inhibition of MGC16063 (Accession NM_053047). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16063. MSTP031 (Accession NM_032035) is another VGAM2158 host target gene. MSTP031 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MSTP031, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MSTP031 BINDING SITE, designated SEQ ID:25734, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74830] Another function of VGAM2158 is therefore inhibition of MSTP031 (Accession NM_032035). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSTP031. Neuron Navigator 3 (NAV3, Accession NM_014903) is another VGAM2158 host target gene. NAV3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NAV3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAV3 BINDING SITE, designated SEQ ID:17088, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74831] Another function of VGAM2158 is therefore inhibition of Neuron Navigator 3 (NAV3, Accession NM_014903). Accordingly, utilities of VGAM2158 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with NAV3. LOC51212 (Accession NM_016380) is another VGAM2158 host target gene. LOC51212 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51212, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51212 BINDING SITE, designated SEQ ID:18518, to the nucleotide sequence of VGAM2158 RNA, herein designated VGAM RNA, also designated SEQ ID:4869.

[74832] Another function of VGAM2158 is therefore inhibition of LOC51212 (Accession NM_016380). Accordingly, utilities of VGAM2158 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51212. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2159 (VGAM2159) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74833] VGAM2159 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2159 was detected is described hereinabove with reference to Figs. 1-8.

[74834] VGAM2159 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2159 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74835] VGAM2159 gene encodes a VGAM2159 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2159 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2159 precursor RNA is designated SEQ ID:2145, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2145 is located at position 155355 relative to the genome of Monkeypox Virus.

[74836] VGAM2159 precursor RNA folds onto itself, forming VGAM2159 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74837] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2159 folded precursor RNA into VGAM2159 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2159 RNA is designated SEQ ID:4870, and is provided hereinbelow with reference to the sequence listing part.

[74838] VGAM2159 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2159 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2159 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74839] VGAM2159 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2159 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2159 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2159 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2159 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74840] The complementary binding of VGAM2159 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2159 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2159 host target RNA into VGAM2159 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74841] It is appreciated that VGAM2159 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2159 host target genes. The mRNA of each one of this plurality of VGAM2159 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2159 RNA, herein designated VGAM RNA, and which when bound by VGAM2159 RNA causes inhibition of translation of respective one or more VGAM2159 host target proteins.

[74842] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2159 gene, herein designated VGAM GENE, on one or more VGAM2159 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74843] It is yet further appreciated that a function of VGAM2159 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2159 correlate with, and may be deduced from, the identity of the host target genes which VGAM2159 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74844] Nucleotide sequences of the VGAM2159 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2159 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2159 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2159 are further described hereinbelow with reference to Table 1.

[74845] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2159 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2159 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74846] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2159 gene, herein designated VGAM is inhibition of expression of VGAM2159 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2159 correlate with, and may be deduced from, the identity of the target genes which VGAM2159 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74847] Espin (ESPN, Accession NM_031475) is a VGAM2159 host target gene. ESPN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by ESPN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESPN BINDING SITE, designated SEQ ID:25548, to the nucleotide sequence of VGAM2159 RNA, herein designated VGAM RNA, also designated SEQ ID:4870.

[74848] A function of VGAM2159 is therefore inhibition of Espin (ESPN, Accession NM_031475), a gene which a membrane-cytoskeletal assemblages . Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESPN. The function of ESPN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1006.Glucocorticoid Receptor DNA Binding Factor 1 (GRLF1, Accession XM_085943) is another VGAM2159 host target gene. GRLF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRLF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRLF1 BINDING SITE, des-

ignated SEQ ID:38407, to the nucleotide sequence of VGAM2159 RNA, herein designated VGAM RNA, also designated SEQ ID:4870.

[74849] Another function of VGAM2159 is therefore inhibition of Glucocorticoid Receptor DNA Binding Factor 1 (GRLF1, Accession XM_085943), a gene which inhibits transcription of the glucocorticoid receptor gene. Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRLF1. The function of GRLF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Integrin, Alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) (ITGA2, Accession NM_002203) is another VGAM2159 host target gene. ITGA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA2 BINDING SITE, designated SEQ ID:7962, to the nucleotide sequence of VGAM2159 RNA, herein designated VGAM RNA, also designated SEQ ID:4870.

[74850] Another function of VGAM2159 is therefore inhibition of Integrin, Alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) (ITGA2, Accession NM_002203), a gene which has roles in blood clotting and angiogenesis, acts as a collagen and laminin receptor. Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA2. The function of ITGA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM827.Wilms Tumor 1 (WT1, Accession NM_024424) is another VGAM2159 host target gene. WT1 BINDING SITE1 through WT1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WT1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WT1 BINDING SITE1 through WT1 BINDING SITE4, designated SEQ ID:23667, SEQ ID:23675, SEQ ID:23671 and SEQ ID:5951 respectively, to the nucleotide sequence of VGAM2159 RNA, herein designated VGAM RNA, also designated SEQ ID:4870.

[74851] Another function of VGAM2159 is therefore inhibition of

Wilms Tumor 1 (WT1, Accession NM_024424). Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WT1. KIAA0993 (Accession XM_034413) is another VGAM2159 host target gene. KIAA0993 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0993, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0993 BINDING SITE, designated SEQ ID:32083, to the nucleotide sequence of VGAM2159 RNA, herein designated VGAM RNA, also designated SEQ ID:4870.

[74852] Another function of VGAM2159 is therefore inhibition of KIAA0993 (Accession XM_034413). Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0993. KIAA1416 (Accession XM_098762) is another VGAM2159 host target gene. KIAA1416 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1416 BINDING SITE, designated SEQ ID:41797, to the nucleotide sequence of VGAM2159 RNA, herein designated VGAM RNA, also designated SEQ ID:4870.

[74853] Another function of VGAM2159 is therefore inhibition of KIAA1416 (Accession XM_098762). Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1416. My015 (Accession XM_039512) is another VGAM2159 host target gene. My015 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by My015, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of My015 BINDING SITE, designated SEQ ID:33103, to the nucleotide sequence of VGAM2159 RNA, herein designated VGAM RNA, also designated SEQ ID:4870.

[74854] Another function of VGAM2159 is therefore inhibition of My015 (Accession XM_039512). Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with My015. Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2,

Accession NM_014737) is another VGAM2159 host target gene. RASSF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RASSF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:16388, to the nucleotide sequence of VGAM2159 RNA, herein designated VGAM RNA, also designated SEQ ID:4870.

[74855] Another function of VGAM2159 is therefore inhibition of Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2, Accession NM_014737). Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2. Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession XM_053740) is another VGAM2159 host target gene. TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TP53INP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2, designated SEQ ID:36112 and SEQ ID:27101 respectively, to the nucleotide sequence of VGAM2159 RNA, herein designated VGAM RNA, also designated SEQ ID:4870.

[74856] Another function of VGAM2159 is therefore inhibition of Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession XM_053740). Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53INP1. LOC157503 (Accession XM_098767) is another VGAM2159 host target gene. LOC157503 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157503, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157503 BINDING SITE, designated SEQ ID:41815, to the nucleotide sequence of VGAM2159 RNA, herein designated VGAM RNA, also designated SEQ ID:4870.

[74857] Another function of VGAM2159 is therefore inhibition of LOC157503 (Accession XM_098767). Accordingly, utilities of VGAM2159 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC157503. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2160 (VGAM2160) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74858] VGAM2160 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2160 was detected is described hereinabove with reference to Figs. 1-8.

[74859] VGAM2160 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2160 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74860] VGAM2160 gene encodes a VGAM2160 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2160 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2160 precursor RNA is designated SEQ ID:2146, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2146 is located at position 168205 relative to the genome of Monkeypox Virus.

[74861] VGAM2160 precursor RNA folds onto itself, forming VGAM2160 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74862] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2160 folded precursor RNA into VGAM2160 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2160 RNA is designated SEQ ID:4871, and is provided hereinbelow with reference to the sequence listing part.

[74863] VGAM2160 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2160 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2160 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74864] VGAM2160 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2160 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2160 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2160 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2160 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74865] The complementary binding of VGAM2160 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2160 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2160 host target RNA into VGAM2160 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74866] It is appreciated that VGAM2160 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2160 host target genes. The mRNA of each one of this plurality of VGAM2160 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2160 RNA, herein designated VGAM RNA, and which when bound by VGAM2160 RNA causes

inhibition of translation of respective one or more VGAM2160 host target proteins.

[74867] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2160 gene, herein designated VGAM GENE, on one or more VGAM2160 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74868] It is yet further appreciated that a function of VGAM2160 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2160 include diagnosis, prevention and

treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2160 correlate with, and may be deduced from, the identity of the host target genes which VGAM2160 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74869] Nucleotide sequences of the VGAM2160 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2160 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2160 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2160 are further described hereinbelow with reference to Table 1.

[74870] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2160 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2160 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74871] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2160 gene, herein designated VGAM is inhibition of expression of VGAM2160 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2160 correlate with, and may be deduced from, the identity of the target genes which VGAM2160 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74872] Hormonally Upregulated Neu-associated Kinase (HUNK, Accession NM_014586) is a VGAM2160 host target gene. HUNK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HUNK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HUNK BINDING SITE, designated SEQ ID:15954, to the nucleotide sequence of VGAM2160 RNA, herein designated VGAM RNA, also designated SEQ ID:4871.

[74873] A function of VGAM2160 is therefore inhibition of Hormonally Upregulated Neu-associated Kinase (HUNK, Accession NM_014586). Accordingly, utilities of VGAM2160 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HUNK. Splicing Factor, Arginine/serine-rich 7, 35kDa (SFRS7, Accession XM_002575) is another VGAM2160 host target gene. SFRS7 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by SFRS7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRS7 BINDING SITE, designated SEQ ID:29900, to the nucleotide sequence of VGAM2160 RNA, herein designated VGAM RNA, also designated SEQ ID:4871.

[74874] Another function of VGAM2160 is therefore inhibition of Splicing Factor, Arginine/serine-rich 7, 35kDa (SFRS7, Accession XM_002575), a gene which is required for pre-mnra splicing. Accordingly, utilities of VGAM2160 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRS7. The function of SFRS7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM191.ARNTL2 (Accession NM_020183) is another VGAM2160 host target gene. ARNTL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARNTL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARNTL2

BINDING SITE, designated SEQ ID:21412, to the nucleotide sequence of VGAM2160 RNA, herein designated VGAM RNA, also designated SEQ ID:4871.

[74875] Another function of VGAM2160 is therefore inhibition of ARNTL2 (Accession NM_020183). Accordingly, utilities of VGAM2160 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARNTL2. FLJ12592 (Accession NM_032169) is another VGAM2160 host target gene. FLJ12592 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12592, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12592 BINDING SITE, designated SEQ ID:25875, to the nucleotide sequence of VGAM2160 RNA, herein designated VGAM RNA, also designated SEQ ID:4871.

[74876] Another function of VGAM2160 is therefore inhibition of FLJ12592 (Accession NM_032169). Accordingly, utilities of VGAM2160 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12592. Hepatitis B Virus X Associated Protein (HBXAP, Accession NM_016578) is another VGAM2160 host target

gene. HBXAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HBXAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HBXAP BINDING SITE, designated SEQ ID:18657, to the nucleotide sequence of VGAM2160 RNA, herein designated VGAM RNA, also designated SEQ ID:4871.

[74877] Another function of VGAM2160 is therefore inhibition of Hepatitis B Virus X Associated Protein (HBXAP, Accession NM_016578). Accordingly, utilities of VGAM2160 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HBXAP. KIAA0776 (Accession XM_035970) is another VGAM2160 host target gene. KIAA0776 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0776, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0776 BINDING SITE, designated SEQ ID:32363, to the nucleotide sequence of VGAM2160 RNA, herein designated VGAM RNA, also designated SEQ

ID:4871.

[74878] Another function of VGAM2160 is therefore inhibition of KIAA0776 (Accession XM_035970). Accordingly, utilities of VGAM2160 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0776. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2161 (VGAM2161) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74879] VGAM2161 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2161 was detected is described hereinabove with reference to Figs. 1-8.

[74880] VGAM2161 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2161 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74881] VGAM2161 gene encodes a VGAM2161 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2161 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2161 precursor RNA is designated SEQ ID:2147, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2147 is located at position 194827 relative to the genome of Camelpox Virus.

[74882] VGAM2161 precursor RNA folds onto itself, forming VGAM2161 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74883] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2161 folded precursor RNA into VGAM2161 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2161 RNA is designated SEQ ID:4872, and is provided hereinbelow with reference to the sequence listing part.

[74884] VGAM2161 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2161 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2161 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74885] VGAM2161 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2161 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2161 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2161 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2161 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74886] The complementary binding of VGAM2161 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2161 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2161 host target RNA into VGAM2161 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74887] It is appreciated that VGAM2161 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2161 host target genes. The mRNA of

each one of this plurality of VGAM2161 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2161 RNA, herein designated VGAM RNA, and which when bound by VGAM2161 RNA causes inhibition of translation of respective one or more VGAM2161 host target proteins.

[74888] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2161 gene, herein designated VGAM GENE, on one or more VGAM2161 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[74889] It is yet further appreciated that a function of VGAM2161 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2161 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2161 correlate with, and may be deduced from, the identity of the host target genes which VGAM2161 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74890] Nucleotide sequences of the VGAM2161 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2161 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2161 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2161 are further described hereinbelow with reference to Table 1.

[74891] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2161 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2161 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74892] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2161 gene, herein designated VGAM is inhibition of expression of VGAM2161 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2161 correlate with, and may be deduced from, the identity of the target genes which VGAM2161 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74893] DKFZp566D133 (Accession XM_050005) is a VGAM2161 host target gene. DKFZp566D133 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp566D133, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp566D133 BINDING SITE, designated SEQ ID:35545, to the nucleotide sequence of VGAM2161 RNA, herein designated VGAM RNA, also designated SEQ ID:4872.

[74894] A function of VGAM2161 is therefore inhibition of DKFZp566D133 (Accession XM_050005). Accordingly, utilities of VGAM2161 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZp566D133. SBBI31 (Accession NM_014035) is another VGAM2161 host target gene. SBBI31 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SBBI31, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SBBI31 BINDING SITE, designated SEQ ID:15264, to the nucleotide sequence of VGAM2161 RNA, herein designated VGAM RNA, also designated SEQ ID:4872.

[74895] Another function of VGAM2161 is therefore inhibition of SBBI31 (Accession NM_014035). Accordingly, utilities of VGAM2161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SBBI31. LOC253959 (Accession XM_170749) is another VGAM2161 host target gene. LOC253959 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253959, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253959 BINDING SITE, designated SEQ ID:45511, to

the nucleotide sequence of VGAM2161 RNA, herein designated VGAM RNA, also designated SEQ ID:4872.

[74896] Another function of VGAM2161 is therefore inhibition of LOC253959 (Accession XM_170749). Accordingly, utilities of VGAM2161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253959. LOC57107 (Accession NM_020381) is another VGAM2161 host target gene. LOC57107 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57107, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57107 BINDING SITE, designated SEQ ID:21647, to the nucleotide sequence of VGAM2161 RNA, herein designated VGAM RNA, also designated SEQ ID:4872.

[74897] Another function of VGAM2161 is therefore inhibition of LOC57107 (Accession NM_020381). Accordingly, utilities of VGAM2161 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57107. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2162 (VGAM2162) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74898] VGAM2162 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2162 was detected is described hereinabove with reference to Figs. 1-8.

[74899] VGAM2162 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2162 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74900] VGAM2162 gene encodes a VGAM2162 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2162 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2162 precursor RNA is designated SEQ ID:2148, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2148 is located at position 195253 relative to the genome of Camelpox Virus.

[74901] VGAM2162 precursor RNA folds onto itself, forming VGAM2162 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74902] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2162 folded precursor RNA into VGAM2162 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2162 RNA is designated SEQ ID:4873, and is provided hereinbelow with reference to the sequence listing part.

[74903] VGAM2162 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2162 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2162 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74904] VGAM2162 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2162 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2162 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2162 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2162 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74905] The complementary binding of VGAM2162 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2162 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2162 host target RNA into VGAM2162 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74906] It is appreciated that VGAM2162 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2162 host target genes. The mRNA of each one of this plurality of VGAM2162 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2162 RNA, herein designated VGAM RNA, and which when bound by VGAM2162 RNA causes inhibition of translation of respective one or more VGAM2162 host target proteins.

[74907] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2162 gene, herein designated VGAM GENE, on one or more VGAM2162 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74908] It is yet further appreciated that a function of VGAM2162 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2162 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2162 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74909] Nucleotide sequences of the VGAM2162 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2162 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2162 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2162 are further described hereinbelow with reference to Table 1.

[74910] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2162 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2162 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74911] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2162 gene, herein designated VGAM is inhibition of expression of VGAM2162 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2162 correlate with, and may be deduced from, the identity of the target genes which VGAM2162

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74912] Estrogen-related Receptor Gamma (ESRRG, Accession XM_039053) is a VGAM2162 host target gene. ESRRG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ESRRG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESRRG BINDING SITE, designated SEQ ID:32999, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74913] A function of VGAM2162 is therefore inhibition of Estrogen-related Receptor Gamma (ESRRG, Accession XM_039053), a gene which Estrogen-related receptor gamma. Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESRRG. The function of ESRRG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM359.Integrin, Alpha L (antigen CD11A (p180), Lymphocyte Function-associated Antigen 1; Alpha Polypeptide) (ITGAL, Acces-

sion NM_002209) is another VGAM2162 host target gene. ITGAL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGAL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGAL BINDING SITE, designated SEQ ID:7972, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74914] Another function of VGAM2162 is therefore inhibition of Integrin, Alpha L (antigen CD11A (p180), Lymphocyte Function-associated Antigen 1; Alpha Polypeptide) (ITGAL, Accession NM_002209), a gene which s a receptor for icam1, icam2, icam3 and icam4. it is involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, cytotoxic t-cell mediated killing, and antibody dependent killing by granulocytes and monocytes. Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAL. The function of ITGAL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Nuclear Fragile X

Mental Retardation Protein Interacting Protein 1 (NUFIP1, Accession NM_012345) is another VGAM2162 host target gene. NUFIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUFIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUFIP1 BINDING SITE, designated SEQ ID:14737, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74915] Another function of VGAM2162 is therefore inhibition of Nuclear Fragile X Mental Retardation Protein Interacting Protein 1 (NUFIP1, Accession NM_012345), a gene which binds and colocalizes with nuclear fragile X mental retardation protein. Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUFIP1. The function of NUFIP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM733.POU Domain, Class 2, Associating Factor 1 (POU2AF1, Accession NM_006235) is another VGAM2162 host target gene.

POU2AF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POU2AF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POU2AF1 BINDING SITE, designated SEQ ID:12892, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74916] Another function of VGAM2162 is therefore inhibition of POU Domain, Class 2, Associating Factor 1 (POU2AF1, Accession NM_006235), a gene which is a transcriptional coactivator that specifically associates with either oct1 or oct2. Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU2AF1. The function of POU2AF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM171.Recombination Activating Gene 2 (RAG2, Accession XM_089839) is another VGAM2162 host target gene. RAG2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

RAG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAG2 BINDING SITE, designated SEQ ID:39985, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74917] Another function of VGAM2162 is therefore inhibition of Recombination Activating Gene 2 (RAG2, Accession XM_089839). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAG2. Tensin (TNS, Accession NM_022648) is another VGAM2162 host target gene. TNS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNS BINDING SITE, designated SEQ ID:22903, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74918] Another function of VGAM2162 is therefore inhibition of Tensin (TNS, Accession NM_022648). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with TNS. DKFZP434I092 (Accession XM_042042) is another VGAM2162 host target gene. DKFZP434I092 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434I092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434I092 BINDING SITE, designated SEQ ID:33673, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74919] Another function of VGAM2162 is therefore inhibition of DKFZP434I092 (Accession XM_042042). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434I092. FLJ10656 (Accession NM_018170) is another VGAM2162 host target gene. FLJ10656 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10656, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10656 BINDING SITE, designated SEQ ID:19988, to the

nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74920] Another function of VGAM2162 is therefore inhibition of FLJ10656 (Accession NM_018170). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10656. GABA(A) Receptor-associated Protein Like 1 (GABARAPL1, Accession NM_031412) is another VGAM2162 host target gene. GABARAPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABARAPL1 BINDING SITE, designated SEQ ID:25392, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74921] Another function of VGAM2162 is therefore inhibition of GABA(A) Receptor-associated Protein Like 1 (GABARAPL1, Accession NM_031412). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL1. GABA(A) Receptors Associated Protein Like 3

(GABARAPL3, Accession NM_032568) is another VGAM2162 host target gene. GABARAPL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABARAPL3 BINDING SITE, designated SEQ ID:26300, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74922] Another function of VGAM2162 is therefore inhibition of GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL3. HT002 (Accession NM_014066) is another VGAM2162 host target gene. HT002 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HT002, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HT002 BINDING SITE, designated SEQ ID:15281, to the nucleotide sequence of

VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74923] Another function of VGAM2162 is therefore inhibition of HT002 (Accession NM_014066). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HT002. KIAA0475 (Accession NM_014864) is another VGAM2162 host target gene. KIAA0475 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:16949, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74924] Another function of VGAM2162 is therefore inhibition of KIAA0475 (Accession NM_014864). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0475. KIAA0712 (Accession NM_014715) is another VGAM2162 host target gene. KIAA0712 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by KIAA0712, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0712 BINDING SITE, designated SEQ ID:16262, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74925] Another function of VGAM2162 is therefore inhibition of KIAA0712 (Accession NM_014715). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0712. KIAA1301 (Accession XM_038999) is another VGAM2162 host target gene. KIAA1301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1301 BINDING SITE, designated SEQ ID:32978, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74926] Another function of VGAM2162 is therefore inhibition of KIAA1301 (Accession XM_038999). Accordingly, utilities

of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1301. Seizure Related 6 Homolog (mouse) (SEZ6, Accession XM_058869) is another VGAM2162 host target gene. SEZ6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEZ6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEZ6 BINDING SITE, designated SEQ ID:36774, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74927] Another function of VGAM2162 is therefore inhibition of Seizure Related 6 Homolog (mouse) (SEZ6, Accession XM_058869). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEZ6. VMP1 (Accession NM_030938) is another VGAM2162 host target gene. VMP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VMP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of VMP1 BINDING SITE, designated SEQ ID:25204, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74928] Another function of VGAM2162 is therefore inhibition of VMP1 (Accession NM_030938). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VMP1. LOC115110 (Accession XM_049825) is another VGAM2162 host target gene. LOC115110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115110 BINDING SITE, designated SEQ ID:35503, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74929] Another function of VGAM2162 is therefore inhibition of LOC115110 (Accession XM_049825). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115110. LOC132235 (Accession XM_072302) is another VGAM2162 host target gene. LOC132235 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC132235, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132235 BINDING SITE, designated SEQ ID:37483, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74930] Another function of VGAM2162 is therefore inhibition of LOC132235 (Accession XM_072302). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132235. LOC142941 (Accession XM_096363) is another VGAM2162 host target gene. LOC142941 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC142941, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC142941 BINDING SITE, designated SEQ ID:40322, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74931] Another function of VGAM2162 is therefore inhibition of

LOC142941 (Accession XM_096363). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142941. LOC158549 (Accession XM_098963) is another VGAM2162 host target gene. LOC158549 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158549, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158549 BINDING SITE, designated SEQ ID:42007, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74932] Another function of VGAM2162 is therefore inhibition of LOC158549 (Accession XM_098963). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158549. LOC221882 (Accession XM_166507) is another VGAM2162 host target gene. LOC221882 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221882, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC221882 BINDING SITE, designated SEQ ID:44434, to the nucleotide sequence of VGAM2162 RNA, herein designated VGAM RNA, also designated SEQ ID:4873.

[74933] Another function of VGAM2162 is therefore inhibition of LOC221882 (Accession XM_166507). Accordingly, utilities of VGAM2162 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221882. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2163 (VGAM2163) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74934] VGAM2163 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2163 was detected is described hereinabove with reference to Figs. 1-8.

[74935] VGAM2163 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2163 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[74936] VGAM2163 gene encodes a VGAM2163 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2163 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2163 precursor RNA is designated SEQ ID:2149, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2149 is located at position 184394 relative to the genome of Camelpox Virus.

[74937] VGAM2163 precursor RNA folds onto itself, forming VGAM2163 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74938] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2163 folded precursor RNA into VGAM2163 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2163 RNA is designated SEQ ID:4874, and is provided hereinbelow with reference to the sequence listing part.

[74939] VGAM2163 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2163 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2163 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74940] VGAM2163 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2163 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2163 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2163 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2163 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74941] The complementary binding of VGAM2163 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2163 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2163 host target RNA into VGAM2163 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74942] It is appreciated that VGAM2163 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2163 host target genes. The mRNA of each one of this plurality of VGAM2163 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2163 RNA, herein designated VGAM RNA, and which when bound by VGAM2163 RNA causes inhibition of translation of respective one or more VGAM2163 host target proteins.

[74943] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2163 gene, herein designated VGAM GENE, on one or more VGAM2163 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74944] It is yet further appreciated that a function of VGAM2163 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2163 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2163 correlate with, and may be deduced from, the identity of the host target genes which VGAM2163 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74945] Nucleotide sequences of the VGAM2163 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2163 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2163 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2163 are further described hereinbelow with reference to Table 1.

[74946] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2163 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2163 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74947] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2163 gene, herein designated VGAM is inhibition of expression of VGAM2163 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2163 correlate with, and may be deduced from, the identity of the target genes which VGAM2163 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74948] Chromosome 9 Open Reading Frame 12 (C9orf12, Accession NM_022755) is a VGAM2163 host target gene. C9orf12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C9orf12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C9orf12 BINDING SITE, designated SEQ ID:22990, to the nucleotide sequence of VGAM2163 RNA, herein designated VGAM RNA, also designated SEQ

ID:4874.

[74949] A function of VGAM2163 is therefore inhibition of Chromosome 9 Open Reading Frame 12 (C9orf12, Accession NM_022755). Accordingly, utilities of VGAM2163 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf12. DKFZP564F013 (Accession XM_168479) is another VGAM2163 host target gene. DKFZP564F013 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564F013, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564F013 BINDING SITE, designated SEQ ID:45205, to the nucleotide sequence of VGAM2163 RNA, herein designated VGAM RNA, also designated SEQ ID:4874.

[74950] Another function of VGAM2163 is therefore inhibition of DKFZP564F013 (Accession XM_168479). Accordingly, utilities of VGAM2163 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564F013. LOC199923 (Accession XM_114057) is another VGAM2163 host target gene. LOC199923 BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by LOC199923, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199923 BINDING SITE, designated SEQ ID:42665, to the nucleotide sequence of VGAM2163 RNA, herein designated VGAM RNA, also designated SEQ ID:4874.

[74951] Another function of VGAM2163 is therefore inhibition of LOC199923 (Accession XM_114057). Accordingly, utilities of VGAM2163 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199923. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2164 (VGAM2164) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74952] VGAM2164 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2164 was detected is described hereinabove with reference to Figs. 1-8.

[74953] VGAM2164 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip Yellow Fleck Virus. VGAM2164 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74954] VGAM2164 gene encodes a VGAM2164 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2164 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2164 precursor RNA is designated SEQ ID:2150, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2150 is located at position 4805 relative to the genome of Parsnip Yellow Fleck Virus.

[74955] VGAM2164 precursor RNA folds onto itself, forming VGAM2164 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[74956] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2164 folded precursor RNA into VGAM2164 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2164 RNA is designated SEQ ID:4875, and is provided hereinbelow with reference to the sequence listing part.

[74957] VGAM2164 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2164 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2164 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74958] VGAM2164 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2164 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2164 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2164 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2164 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74959] The complementary binding of VGAM2164 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2164 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2164 host target RNA into VGAM2164 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74960] It is appreciated that VGAM2164 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2164 host target genes. The mRNA of each one of this plurality of VGAM2164 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2164 RNA, herein designated VGAM RNA, and which when bound by VGAM2164 RNA causes inhibition of translation of respective one or more VGAM2164 host target proteins.

[74961] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2164 gene, herein designated VGAM GENE, on one or more VGAM2164 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74962] It is yet further appreciated that a function of VGAM2164 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2164 include diagnosis, prevention and treatment of viral infection by Parsnip Yellow Fleck Virus. Specific functions, and accordingly utilities, of VGAM2164 correlate with, and may be deduced from, the identity of the host target genes which VGAM2164 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74963] Nucleotide sequences of the VGAM2164 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2164 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2164 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2164 are further described hereinbelow with reference to Table 1.

[74964] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2164 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2164 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74965] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2164 gene, herein designated VGAM is inhibition of expression of VGAM2164 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2164 correlate with, and may be deduced from, the identity of the target genes which VGAM2164 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74966] Interleukin 6 Receptor (IL6R, Accession NM_000565) is a VGAM2164 host target gene. IL6R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL6R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of IL6R BINDING SITE, designated SEQ ID:6171, to the nucleotide sequence of VGAM2164 RNA, herein designated VGAM RNA, also designated SEQ ID:4875.

[74967] A function of VGAM2164 is therefore inhibition of Interleukin 6 Receptor (IL6R, Accession NM_000565), a gene which is essential to the regulation of the immune response, hematopoiesis, and acute-phase reactions. Accordingly, utilities of VGAM2164 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL6R. The function of IL6R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1189.XT3 (Accession NM_020208) is another VGAM2164 host target gene. XT3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XT3 BINDING SITE, designated SEQ ID:21441, to the nucleotide sequence of VGAM2164 RNA, herein designated VGAM RNA, also designated SEQ ID:4875.

[74968] Another function of VGAM2164 is therefore inhibition of XT3 (Accession NM_020208), a gene which is a Kidney-specific orphan transporter. Accordingly, utilities of VGAM2164 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XT3. The function of XT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM21.F-box Only Protein 9 (FBXO9, Accession NM_033480) is another VGAM2164 host target gene. FBXO9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXO9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXO9 BINDING SITE, designated SEQ ID:27257, to the nucleotide sequence of VGAM2164 RNA, herein designated VGAM RNA, also designated SEQ ID:4875.

[74969] Another function of VGAM2164 is therefore inhibition of F-box Only Protein 9 (FBXO9, Accession NM_033480). Accordingly, utilities of VGAM2164 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with FBXO9. FLJ14840 (Accession NM_032850) is another VGAM2164 host target gene. FLJ14840 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ14840, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14840 BINDING SITE, designated SEQ ID:26644, to the nucleotide sequence of VGAM2164 RNA, herein designated VGAM RNA, also designated SEQ ID:4875.

[74970] Another function of VGAM2164 is therefore inhibition of FLJ14840 (Accession NM_032850). Accordingly, utilities of VGAM2164 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14840. Nup43 (Accession NM_024647) is another VGAM2164 host target gene. Nup43 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Nup43, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Nup43 BINDING SITE, designated SEQ ID:23932, to the nucleotide sequence of VGAM2164 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4875.

[74971] Another function of VGAM2164 is therefore inhibition of Nup43 (Accession NM_024647). Accordingly, utilities of VGAM2164 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Nup43. PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335) is another VGAM2164 host target gene. PRPF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRPF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRPF8 BINDING SITE, designated SEQ ID:30684, to the nucleotide sequence of VGAM2164 RNA, herein designated VGAM RNA, also designated SEQ ID:4875.

[74972] Another function of VGAM2164 is therefore inhibition of PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335). Accordingly, utilities of VGAM2164 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRPF8. YME1-like 1 (S. cerevisiae) (YME1L1, Accession NM_139312) is another VGAM2164 host target gene.

YME1L1 BINDING SITE1 and YME1L1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by YME1L1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YME1L1 BINDING SITE1 and YME1L1 BINDING SITE2, designated SEQ ID:29292 and SEQ ID:15536 respectively, to the nucleotide sequence of VGAM2164 RNA, herein designated VGAM RNA, also designated SEQ ID:4875.

[74973] Another function of VGAM2164 is therefore inhibition of YME1-like 1 (S. cerevisiae) (YME1L1, Accession NM_139312). Accordingly, utilities of VGAM2164 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YME1L1. LOC147664 (Accession XM_085826) is another VGAM2164 host target gene. LOC147664 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147664, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147664 BINDING SITE, designated SEQ ID:38352, to the nucleotide sequence of

VGAM2164 RNA, herein designated VGAM RNA, also designated SEQ ID:4875.

[74974] Another function of VGAM2164 is therefore inhibition of LOC147664 (Accession XM_085826). Accordingly, utilities of VGAM2164 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147664. LOC51336 (Accession NM_016646) is another VGAM2164 host target gene. LOC51336 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51336, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51336 BINDING SITE, designated SEQ ID:18755, to the nucleotide sequence of VGAM2164 RNA, herein designated VGAM RNA, also designated SEQ ID:4875.

[74975] Another function of VGAM2164 is therefore inhibition of LOC51336 (Accession NM_016646). Accordingly, utilities of VGAM2164 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51336. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2165 (VGAM2165) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[74976] VGAM2165 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2165 was detected is described hereinabove with reference to Figs. 1-8.

[74977] VGAM2165 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2165 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[74978] VGAM2165 gene encodes a VGAM2165 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2165 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2165 precursor RNA is designated SEQ ID:2151, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2151 is located at position 196786 relative to the genome of Camelpox Virus.

[74979] VGAM2165 precursor RNA folds onto itself, forming VGAM2165 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[74980] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2165 folded precursor RNA into VGAM2165 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2165 RNA is designated SEQ ID:4876, and is provided hereinbelow with reference to the sequence listing part.

[74981] VGAM2165 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2165 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2165 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[74982] VGAM2165 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2165 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2165 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2165 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2165 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[74983] The complementary binding of VGAM2165 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2165 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2165 host target RNA into VGAM2165 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[74984] It is appreciated that VGAM2165 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2165 host target genes. The mRNA of each one of this plurality of VGAM2165 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2165 RNA, herein designated VGAM RNA, and which when bound by VGAM2165 RNA causes inhibition of translation of respective one or more VGAM2165 host target proteins.

[74985] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2165 gene, herein designated VGAM GENE, on one or more VGAM2165 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[74986] It is yet further appreciated that a function of VGAM2165 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2165 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2165 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2165 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[74987] Nucleotide sequences of the VGAM2165 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2165 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2165 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2165 are further described hereinbelow with reference to Table 1.

[74988] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2165 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2165 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[74989] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2165 gene, herein designated VGAM is inhibition of expression of VGAM2165 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2165 correlate with, and may be deduced from, the identity of the target genes which VGAM2165

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[74990] Ephrin-B2 (EFNB2, Accession NM_004093) is a VGAM2165 host target gene. EFNB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EFNB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFNB2 BINDING SITE, designated SEQ ID:10295, to the nucleotide sequence of VGAM2165 RNA, herein designated VGAM RNA, also designated SEQ ID:4876.

[74991] A function of VGAM2165 is therefore inhibition of Ephrin-B2 (EFNB2, Accession NM_004093). Accordingly, utilities of VGAM2165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFNB2. Erythrocyte Membrane Protein Band 4.1-like 1 (EPB41L1, Accession XM_047295) is another VGAM2165 host target gene. EPB41L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPB41L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of EPB41L1 BINDING SITE, designated SEQ ID:34938, to the nucleotide sequence of VGAM2165 RNA, herein designated VGAM RNA, also designated SEQ ID:4876.

[74992] Another function of VGAM2165 is therefore inhibition of Erythrocyte Membrane Protein Band 4.1-like 1 (EPB41L1, Accession XM_047295). Accordingly, utilities of VGAM2165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPB41L1. GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568) is another VGAM2165 host target gene. GABARAPL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABARAPL3 BINDING SITE, designated SEQ ID:26295, to the nucleotide sequence of VGAM2165 RNA, herein designated VGAM RNA, also designated SEQ ID:4876.

[74993] Another function of VGAM2165 is therefore inhibition of GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568). Accordingly, utilities of

VGAM2165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL3. KIAA0265 (Accession XM_045954) is another VGAM2165 host target gene. KIAA0265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0265 BINDING SITE, designated SEQ ID:34621, to the nucleotide sequence of VGAM2165 RNA, herein designated VGAM RNA, also designated SEQ ID:4876.

[74994] Another function of VGAM2165 is therefore inhibition of KIAA0265 (Accession XM_045954). Accordingly, utilities of VGAM2165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0265. MGC13105 (Accession XM_049394) is another VGAM2165 host target gene. MGC13105 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC13105, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

MGC13105 BINDING SITE, designated SEQ ID:35407, to the nucleotide sequence of VGAM2165 RNA, herein designated VGAM RNA, also designated SEQ ID:4876.

[74995] Another function of VGAM2165 is therefore inhibition of MGC13105 (Accession XM_049394). Accordingly, utilities of VGAM2165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13105. LOC222681 (Accession XM_167116) is another VGAM2165 host target gene. LOC222681 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222681, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222681 BINDING SITE, designated SEQ ID:44606, to the nucleotide sequence of VGAM2165 RNA, herein designated VGAM RNA, also designated SEQ ID:4876.

[74996] Another function of VGAM2165 is therefore inhibition of LOC222681 (Accession XM_167116). Accordingly, utilities of VGAM2165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222681. LOC255995 (Accession XM_173071) is another VGAM2165 host target gene. LOC255995 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255995, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255995 BINDING SITE, designated SEQ ID:46323, to the nucleotide sequence of VGAM2165 RNA, herein designated VGAM RNA, also designated SEQ ID:4876.

[74997] Another function of VGAM2165 is therefore inhibition of LOC255995 (Accession XM_173071). Accordingly, utilities of VGAM2165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255995. LOC257507 (Accession XM_175204) is another VGAM2165 host target gene. LOC257507 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257507, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257507 BINDING SITE, designated SEQ ID:46672, to the nucleotide sequence of VGAM2165 RNA, herein designated VGAM RNA, also designated SEQ ID:4876.

[74998] Another function of VGAM2165 is therefore inhibition of

LOC257507 (Accession XM_175204). Accordingly, utilities of VGAM2165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257507. LOC257625 (Accession XM_175267) is another VGAM2165 host target gene. LOC257625 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257625, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257625 BINDING SITE, designated SEQ ID:46728, to the nucleotide sequence of VGAM2165 RNA, herein designated VGAM RNA, also designated SEQ ID:4876.

[74999] Another function of VGAM2165 is therefore inhibition of LOC257625 (Accession XM_175267). Accordingly, utilities of VGAM2165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257625. LOC90777 (Accession XM_034052) is another VGAM2165 host target gene. LOC90777 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90777, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of LOC90777 BINDING SITE, designated SEQ ID:31991, to the nucleotide sequence of VGAM2165 RNA, herein designated VGAM RNA, also designated SEQ ID:4876.

[75000] Another function of VGAM2165 is therefore inhibition of LOC90777 (Accession XM_034052). Accordingly, utilities of VGAM2165 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90777. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2166 (VGAM2166) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75001] VGAM2166 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2166 was detected is described hereinabove with reference to Figs. 1-8.

[75002] VGAM2166 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2166 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[75003] VGAM2166 gene encodes a VGAM2166 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2166 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2166 precursor RNA is designated SEQ ID:2152, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2152 is located at position 186373 relative to the genome of Camelpox Virus.

[75004] VGAM2166 precursor RNA folds onto itself, forming VGAM2166 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75005] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2166 folded precursor RNA into VGAM2166 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2166 RNA is designated SEQ ID:4877, and is provided hereinbelow with reference to the sequence listing part.

[75006] VGAM2166 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2166 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2166 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75007] VGAM2166 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2166 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2166 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2166 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2166 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75008] The complementary binding of VGAM2166 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2166 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2166 host target RNA into VGAM2166 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75009] It is appreciated that VGAM2166 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2166 host target genes. The mRNA of each one of this plurality of VGAM2166 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2166 RNA, herein designated VGAM RNA, and which when bound by VGAM2166 RNA causes inhibition of translation of respective one or more VGAM2166 host target proteins.

[75010] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2166 gene, herein designated VGAM GENE, on one or more VGAM2166 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75011] It is yet further appreciated that a function of VGAM2166 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2166 correlate with, and may be deduced from, the identity of the host target genes which VGAM2166 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75012] Nucleotide sequences of the VGAM2166 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2166 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2166 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2166 are further described hereinbelow with reference to Table 1.

[75013] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2166 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2166 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75014] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2166 gene, herein designated VGAM is inhibition of expression of VGAM2166 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2166 correlate with, and may be deduced from, the identity of the target genes which VGAM2166 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75015] BIG1 (Accession NM_006421) is a VGAM2166 host target gene. BIG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BIG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIG1 BINDING SITE, designated SEQ ID:13138, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75016] A function of VGAM2166 is therefore inhibition of BIG1

(Accession NM_006421), a gene which is a guanine nucleotide-exchange protein, has a role in vesicular transport. Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIG1. The function of BIG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1190.E2F Transcription Factor 3 (E2F3, Accession NM_001949) is another VGAM2166 host target gene. E2F3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by E2F3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of E2F3 BINDING SITE, designated SEQ ID:7669, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75017] Another function of VGAM2166 is therefore inhibition of E2F Transcription Factor 3 (E2F3, Accession NM_001949), a gene which binds dna and controls cell-cycle progression from g1 to s phase. Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with E2F3. The function of E2F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM475.Potassium Channel, Subfamily K, Member 6 (KCNK6, Accession NM_004823) is another VGAM2166 host target gene. KCNK6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNK6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNK6 BINDING SITE, designated SEQ ID:11239, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75018] Another function of VGAM2166 is therefore inhibition of Potassium Channel, Subfamily K, Member 6 (KCNK6, Accession NM_004823), a gene which is an inward rectifying potassium channel protein. Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK6. The function of KCNK6 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to VGAM1190.RNA Binding Motif Protein 8A (RBM8A, Accession NM_005105) is another VGAM2166 host target gene. RBM8A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBM8A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBM8A BINDING SITE, designated SEQ ID:11577, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75019] Another function of VGAM2166 is therefore inhibition of RNA Binding Motif Protein 8A (RBM8A, Accession NM_005105), a gene which involves in the pathway of gene expression postsplicing nuclear preexport mRNPs, and newly exported cytoplasmic mRNPs. Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBM8A. The function of RBM8A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1864.Stearoyl-CoA Desaturase

(delta-9-desaturase) (SCD, Accession NM_005063) is another VGAM2166 host target gene. SCD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCD BINDING SITE, designated SEQ ID:11494, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75020] Another function of VGAM2166 is therefore inhibition of Stearoyl-CoA Desaturase (delta-9-desaturase) (SCD, Accession NM_005063), a gene which functions in the synthesis of unsaturated fatty acids. Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCD. The function of SCD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM314.H2AV (Accession NM_138635) is another VGAM2166 host target gene. H2AV BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by H2AV, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H2AV BINDING SITE, designated SEQ ID:28909, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75021] Another function of VGAM2166 is therefore inhibition of H2AV (Accession NM_138635). Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H2AV. KIAA0410 (Accession NM_014778) is another VGAM2166 host target gene. KIAA0410 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0410, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0410 BINDING SITE, designated SEQ ID:16621, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75022] Another function of VGAM2166 is therefore inhibition of KIAA0410 (Accession NM_014778). Accordingly, utilities of VGAM2166 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0410. KIAA0795 (Accession NM_025010) is another VGAM2166 host target gene. KIAA0795 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0795, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0795 BINDING SITE, designated SEQ ID:24582, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75023] Another function of VGAM2166 is therefore inhibition of KIAA0795 (Accession NM_025010). Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0795. KIAA1786 (Accession XM_038436) is another VGAM2166 host target gene. KIAA1786 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1786 BINDING SITE, designated SEQ ID:32846, to the

nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75024] Another function of VGAM2166 is therefore inhibition of KIAA1786 (Accession XM_038436). Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1786. KIAA1900 (Accession XM_055299) is another VGAM2166 host target gene. KIAA1900 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1900, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1900 BINDING SITE, designated SEQ ID:36262, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75025] Another function of VGAM2166 is therefore inhibition of KIAA1900 (Accession XM_055299). Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1900. RAP140 (Accession NM_015224) is another VGAM2166 host target gene. RAP140 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by RAP140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAP140 BINDING SITE, designated SEQ ID:17559, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75026] Another function of VGAM2166 is therefore inhibition of RAP140 (Accession NM_015224). Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP140. RNA Binding Motif Protein 7 (RBM7, Accession NM_016090) is another VGAM2166 host target gene. RBM7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBM7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBM7 BINDING SITE, designated SEQ ID:18179, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75027] Another function of VGAM2166 is therefore inhibition of RNA Binding Motif Protein 7 (RBM7, Accession

NM_016090). Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBM7. LOC145820 (Accession XM_085246) is another VGAM2166 host target gene. LOC145820 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145820, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145820 BINDING SITE, designated SEQ ID:37988, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75028] Another function of VGAM2166 is therefore inhibition of LOC145820 (Accession XM_085246). Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145820. LOC150587 (Accession XM_097917) is another VGAM2166 host target gene. LOC150587 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150587, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC150587 BINDING SITE, designated SEQ ID:41213, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75029] Another function of VGAM2166 is therefore inhibition of LOC150587 (Accession XM_097917). Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150587. LOC197003 (Accession XM_113798) is another VGAM2166 host target gene. LOC197003 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197003, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197003 BINDING SITE, designated SEQ ID:42443, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75030] Another function of VGAM2166 is therefore inhibition of LOC197003 (Accession XM_113798). Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197003. LOC54505 (Accession XM_042110) is an-

other VGAM2166 host target gene. LOC54505 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC54505, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC54505 BINDING SITE, designated SEQ ID:33696, to the nucleotide sequence of VGAM2166 RNA, herein designated VGAM RNA, also designated SEQ ID:4877.

[75031] Another function of VGAM2166 is therefore inhibition of LOC54505 (Accession XM_042110). Accordingly, utilities of VGAM2166 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC54505. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2167 (VGAM2167) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75032] VGAM2167 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2167 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[75033] VGAM2167 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip Yellow Fleck Virus. VGAM2167 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75034] VGAM2167 gene encodes a VGAM2167 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2167 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2167 precursor RNA is designated SEQ ID:2153, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2153 is located at position 7389 relative to the genome of Parsnip Yellow Fleck Virus.

[75035] VGAM2167 precursor RNA folds onto itself, forming VGAM2167 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75036] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2167 folded precursor RNA into VGAM2167 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2167 RNA is designated SEQ ID:4878, and is provided hereinbelow with reference to the sequence listing part.

[75037] VGAM2167 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2167 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2167 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75038] VGAM2167 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2167 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2167 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2167 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2167 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75039] The complementary binding of VGAM2167 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2167 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2167 host target RNA into VGAM2167 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75040] It is appreciated that VGAM2167 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2167 host target genes. The mRNA of each one of this plurality of VGAM2167 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2167 RNA, herein designated VGAM RNA, and which when bound by VGAM2167 RNA causes inhibition of translation of respective one or more VGAM2167 host target proteins.

[75041] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2167 gene, herein designated VGAM GENE, on one or more VGAM2167 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75042] It is yet further appreciated that a function of VGAM2167 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2167 include diagnosis, prevention and treatment of viral infection by Parsnip Yellow Fleck Virus. Specific functions, and accordingly utilities, of VGAM2167 correlate with, and may be deduced from, the identity of the host target genes which VGAM2167 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75043] Nucleotide sequences of the VGAM2167 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2167 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2167 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2167 are further described hereinbelow with reference to Table 1.

[75044] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2167 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2167 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75045] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2167 gene, herein designated VGAM is inhibition of expression of VGAM2167 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2167 correlate with, and may be deduced from, the identity of the target genes which VGAM2167 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75046] Fibroblast Growth Factor 12 (FGF12, Accession NM_021032) is a VGAM2167 host target gene. FGF12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGF12, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF12 BINDING SITE, designated SEQ ID:22020, to the nucleotide sequence of VGAM2167 RNA, herein designated VGAM RNA, also designated SEQ ID:4878.

[75047] A function of VGAM2167 is therefore inhibition of Fibroblast Growth Factor 12 (FGF12, Accession NM_021032), a gene which probably involved in nervous system development and function. Accordingly, utilities of VGAM2167 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF12. The function of FGF12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1025.DKFZP434G1411 (Accession XM_166383) is another VGAM2167 host target gene. DKFZP434G1411 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434G1411, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434G1411 BINDING SITE, designated SEQ ID:44233, to the nucleotide sequence of

VGAM2167 RNA, herein designated VGAM RNA, also designated SEQ ID:4878.

[75048] Another function of VGAM2167 is therefore inhibition of DKFZP434G1411 (Accession XM_166383). Accordingly, utilities of VGAM2167 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434G1411. Golgi Reassembly Stacking Protein 2, 55kDa (GORASP2, Accession NM_015530) is another VGAM2167 host target gene. GORASP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GORASP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GORASP2 BINDING SITE, designated SEQ ID:17797, to the nucleotide sequence of VGAM2167 RNA, herein designated VGAM RNA, also designated SEQ ID:4878.

[75049] Another function of VGAM2167 is therefore inhibition of Golgi Reassembly Stacking Protein 2, 55kDa (GORASP2, Accession NM_015530). Accordingly, utilities of VGAM2167 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GORASP2. KIAA1396 (Accession XM_032054) is another

VGAM2167 host target gene. KIAA1396 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1396, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1396 BINDING SITE, designated SEQ ID:31545, to the nucleotide sequence of VGAM2167 RNA, herein designated VGAM RNA, also designated SEQ ID:4878.

[75050] Another function of VGAM2167 is therefore inhibition of KIAA1396 (Accession XM_032054). Accordingly, utilities of VGAM2167 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1396. LOC220936 (Accession XM_166137) is another VGAM2167 host target gene. LOC220936 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220936, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220936 BINDING SITE, designated SEQ ID:43932, to the nucleotide sequence of VGAM2167 RNA, herein designated VGAM RNA, also designated SEQ ID:4878.

[75051] Another function of VGAM2167 is therefore inhibition of LOC220936 (Accession XM_166137). Accordingly, utilities of VGAM2167 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220936. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2168 (VGAM2168) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75052] VGAM2168 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2168 was detected is described hereinabove with reference to Figs. 1-8.

[75053] VGAM2168 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip Yellow Fleck Virus. VGAM2168 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75054] VGAM2168 gene encodes a VGAM2168 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2168 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2168 precursor RNA is designated SEQ ID:2154, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2154 is located at position 4305 relative to the genome of Parsnip Yellow Fleck Virus.

[75055] VGAM2168 precursor RNA folds onto itself, forming VGAM2168 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75056] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2168 folded precursor RNA into VGAM2168 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2168 RNA is designated SEQ ID:4879, and is provided hereinbelow with reference to the sequence listing part.

[75057] VGAM2168 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2168 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2168 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75058] VGAM2168 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2168 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2168 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2168 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2168 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75059] The complementary binding of VGAM2168 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2168 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2168 host target RNA into VGAM2168 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75060] It is appreciated that VGAM2168 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2168 host target genes. The mRNA of each one of this plurality of VGAM2168 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2168 RNA, herein designated VGAM RNA, and which when bound by VGAM2168 RNA causes inhibition of translation of respective one or more VGAM2168 host target proteins.

[75061] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2168 gene, herein designated VGAM GENE, on one or more VGAM2168 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75062] It is yet further appreciated that a function of VGAM2168 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2168 include diagnosis, prevention and treatment of viral infection by Parsnip Yellow Fleck Virus. Specific functions, and accordingly utilities, of VGAM2168 correlate with, and may be deduced from, the identity of the host target genes which VGAM2168 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75063] Nucleotide sequences of the VGAM2168 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2168 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2168 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2168 are further described hereinbelow with reference to Table 1.

[75064] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2168 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2168 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[75065] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2168 gene, herein designated VGAM is inhibition of expression of VGAM2168 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2168 correlate with, and may be deduced from, the identity of the target genes which VGAM2168 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75066] Outer Dense Fiber of Sperm Tails 2 (ODF2, Accession NM_002540) is a VGAM2168 host target gene. ODF2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ODF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ODF2 BINDING SITE, designated SEQ ID:8386, to the nucleotide sequence of VGAM2168 RNA, herein designated VGAM RNA, also designated SEQ ID:4879.

[75067] A function of VGAM2168 is therefore inhibition of Outer Dense Fiber of Sperm Tails 2 (ODF2, Accession NM_002540), a gene which is very strongly similar to rat Odf2 . Accordingly, utilities of VGAM2168 include diagno-

sis, prevention and treatment of diseases and clinical conditions associated with ODF2. The function of ODF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM363.Spinocerebellar Ataxia 7 (olivopontocerebellar atrophy with retinal degeneration) (SCA7, Accession NM_000333) is another VGAM2168 host target gene. SCA7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCA7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCA7 BINDING SITE, designated SEQ ID:5886, to the nucleotide sequence of VGAM2168 RNA, herein designated VGAM RNA, also designated SEQ ID:4879.

[75068] Another function of VGAM2168 is therefore inhibition of Spinocerebellar Ataxia 7 (olivopontocerebellar atrophy with retinal degeneration) (SCA7, Accession NM_000333). Accordingly, utilities of VGAM2168 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCA7. Solute Carrier Family 26, Member 10 (SLC26A10, Accession NM_133489) is another

VGAM2168 host target gene. SLC26A10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC26A10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC26A10 BINDING SITE, designated SEQ ID:28557, to the nucleotide sequence of VGAM2168 RNA, herein designated VGAM RNA, also designated SEQ ID:4879.

[75069] Another function of VGAM2168 is therefore inhibition of Solute Carrier Family 26, Member 10 (SLC26A10, Accession NM_133489). Accordingly, utilities of VGAM2168 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC26A10. LOC158236 (Accession XM_098898) is another VGAM2168 host target gene. LOC158236 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158236, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158236 BINDING SITE, designated SEQ ID:41927, to the nucleotide sequence of VGAM2168 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4879.

[75070] Another function of VGAM2168 is therefore inhibition of LOC158236 (Accession XM_098898). Accordingly, utilities of VGAM2168 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158236. LOC253264 (Accession XM_170639) is another VGAM2168 host target gene. LOC253264 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253264, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253264 BINDING SITE, designated SEQ ID:45417, to the nucleotide sequence of VGAM2168 RNA, herein designated VGAM RNA, also designated SEQ ID:4879.

[75071] Another function of VGAM2168 is therefore inhibition of LOC253264 (Accession XM_170639). Accordingly, utilities of VGAM2168 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253264. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2169 (VGAM2169) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75072] VGAM2169 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2169 was detected is described hereinabove with reference to Figs. 1-8.

[75073] VGAM2169 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2169 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75074] VGAM2169 gene encodes a VGAM2169 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2169 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2169 precursor RNA is designated SEQ ID:2155, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2155 is located at position 183939 relative to the genome of Camelpox Virus.

[75075] VGAM2169 precursor RNA folds onto itself, forming

VGAM2169 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75076] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2169 folded precursor RNA into VGAM2169 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2169 RNA is designated SEQ ID:4880, and is provided hereinbelow with reference to the sequence listing part.

[75077] VGAM2169 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2169 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2169 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75078] VGAM2169 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2169 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2169 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2169 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2169 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75079] The complementary binding of VGAM2169 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2169 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2169 host target RNA into VGAM2169 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75080] It is appreciated that VGAM2169 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2169 host target genes. The mRNA of each one of this plurality of VGAM2169 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2169 RNA, herein designated VGAM RNA, and which when bound by VGAM2169 RNA causes inhibition of translation of respective one or more VGAM2169 host target proteins.

[75081] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2169 gene, herein designated VGAM GENE, on one or more VGAM2169 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75082] It is yet further appreciated that a function of VGAM2169 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2169 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2169 correlate with, and may be deduced from, the identity of the host target genes which VGAM2169 binds and inhibits,

and the function of these host target genes, as elaborated hereinbelow.

[75083] Nucleotide sequences of the VGAM2169 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2169 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2169 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2169 are further described hereinbelow with reference to Table 1.

[75084] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2169 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2169 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75085] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2169 gene, herein designated VGAM is inhibition of expression of VGAM2169 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2169 correlate with, and may be deduced from, the identity of the target genes which VGAM2169 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[75086] D10S170 (Accession NM_005436) is a VGAM2169 host target gene. D10S170 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by D10S170, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of D10S170 BINDING SITE, designated SEQ ID:11918, to the nucleotide sequence of VGAM2169 RNA, herein designated VGAM RNA, also designated SEQ ID:4880.

[75087] A function of VGAM2169 is therefore inhibition of D10S170 (Accession NM_005436), a gene which may provide a structural basis for generation of RET/PTC1 rearrangement . Accordingly, utilities of VGAM2169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with D10S170. The function of D10S170 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM142.Deleted In Azoospermia-like (DAZL, Accession XM_042839) is another VGAM2169 host target gene. DAZL BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by DAZL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAZL BINDING SITE, designated SEQ ID:33798, to the nucleotide sequence of VGAM2169 RNA, herein designated VGAM RNA, also designated SEQ ID:4880.

[75088] Another function of VGAM2169 is therefore inhibition of Deleted In Azoospermia-like (DAZL, Accession XM_042839), a gene which may be essential for gametogenesis. Accordingly, utilities of VGAM2169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAZL. The function of DAZL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Dihydrolipoamide Branched Chain Transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) (DBT, Accession NM_001918) is another VGAM2169 host target gene. DBT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DBT, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DBT BINDING SITE, designated SEQ ID:7632, to the nucleotide sequence of VGAM2169 RNA, herein designated VGAM RNA, also designated SEQ ID:4880.

[75089] Another function of VGAM2169 is therefore inhibition of Dihydrolipoamide Branched Chain Transacylase (E2 component of branched chain keto acid dehydrogenase complex; maple syrup urine disease) (DBT, Accession NM_001918). Accordingly, utilities of VGAM2169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DBT. LOC256277 (Accession XM_170644) is another VGAM2169 host target gene. LOC256277 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256277, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256277 BINDING SITE, designated SEQ ID:45424, to the nucleotide sequence of VGAM2169 RNA, herein designated VGAM RNA, also designated SEQ ID:4880.

[75090] Another function of VGAM2169 is therefore inhibition of

LOC256277 (Accession XM_170644). Accordingly, utilities of VGAM2169 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256277. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2170 (VGAM2170) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75091] VGAM2170 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2170 was detected is described hereinabove with reference to Figs. 1-8.

[75092] VGAM2170 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip Yellow Fleck Virus. VGAM2170 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75093] VGAM2170 gene encodes a VGAM2170 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2170 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2170 precursor RNA is designated SEQ ID:2156, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2156 is located at position 8639 relative to the genome of Parsnip Yellow Fleck Virus.

[75094] VGAM2170 precursor RNA folds onto itself, forming VGAM2170 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75095] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2170 folded precursor RNA into VGAM2170 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide se-

quence of VGAM2170 RNA is designated SEQ ID:4881, and is provided hereinbelow with reference to the sequence listing part.

[75096] VGAM2170 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2170 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2170 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75097] VGAM2170 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2170 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2170 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2170 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2170 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75098] The complementary binding of VGAM2170 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2170 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2170 host target RNA into VGAM2170 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75099] It is appreciated that VGAM2170 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2170 host target genes. The mRNA of each one of this plurality of VGAM2170 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2170 RNA, herein designated VGAM RNA, and which when bound by VGAM2170 RNA causes inhibition of translation of respective one or more VGAM2170 host target proteins.

[75100] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2170 gene, herein designated VGAM GENE, on one or more VGAM2170 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75101] It is yet further appreciated that a function of VGAM2170

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2170 include diagnosis, prevention and treatment of viral infection by Parsnip Yellow Fleck Virus. Specific functions, and accordingly utilities, of VGAM2170 correlate with, and may be deduced from, the identity of the host target genes which VGAM2170 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75102] Nucleotide sequences of the VGAM2170 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2170 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2170 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2170 are further described hereinbelow with reference to Table 1.

[75103] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2170 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2170 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75104] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2170 gene, herein designated VGAM is inhibition of expression of VGAM2170 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2170 correlate with, and may be deduced from, the identity of the target genes which VGAM2170 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75105] Angiopoietin 1 (ANGPT1, Accession NM_001146) is a VGAM2170 host target gene. ANGPT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANGPT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANGPT1 BINDING SITE, designated SEQ ID:6817, to the nucleotide sequence of VGAM2170 RNA, herein designated VGAM RNA, also designated SEQ ID:4881.

[75106] A function of VGAM2170 is therefore inhibition of Angiopoietin 1 (ANGPT1, Accession NM_001146), a gene which binds and activates tie2 receptor by inducing its tyrosine phosphorylation. Accordingly, utilities of VGAM2170 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with ANGPT1. The function of ANGPT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM291.ATPase, Na+/K+ Transporting, Beta 2 Polypeptide (ATP1B2, Accession NM_001678) is another VGAM2170 host target gene. ATP1B2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP1B2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP1B2 BINDING SITE, designated SEQ ID:7397, to the nucleotide sequence of VGAM2170 RNA, herein designated VGAM RNA, also designated SEQ ID:4881.

[75107] Another function of VGAM2170 is therefore inhibition of ATPase, Na+/K+ Transporting, Beta 2 Polypeptide (ATP1B2, Accession NM_001678), a gene which catalyzes the hydrolysis of ATP coupled with the exchange of Na +/K+ ions across the plasma membrane. Accordingly, utilities of VGAM2170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B2. The function of ATP1B2 and its association

with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.Adaptor-related Protein Complex 3, Mu 1 Subunit (AP3M1, Accession NM_012095) is another VGAM2170 host target gene. AP3M1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP3M1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP3M1 BINDING SITE, designated SEQ ID:14397, to the nucleotide sequence of VGAM2170 RNA, herein designated VGAM RNA, also designated SEQ ID:4881.

[75108] Another function of VGAM2170 is therefore inhibition of Adaptor-related Protein Complex 3, Mu 1 Subunit (AP3M1, Accession NM_012095). Accordingly, utilities of VGAM2170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP3M1. BHC80 (Accession NM_016621) is another VGAM2170 host target gene. BHC80 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BHC80, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BHC80 BINDING SITE, designated SEQ ID:18729, to the nucleotide sequence of VGAM2170 RNA, herein designated VGAM RNA, also designated SEQ ID:4881.

[75109] Another function of VGAM2170 is therefore inhibition of BHC80 (Accession NM_016621). Accordingly, utilities of VGAM2170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BHC80. FLJ21916 (Accession NM_023112) is another VGAM2170 host target gene. FLJ21916 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21916, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21916 BINDING SITE, designated SEQ ID:23383, to the nucleotide sequence of VGAM2170 RNA, herein designated VGAM RNA, also designated SEQ ID:4881.

[75110] Another function of VGAM2170 is therefore inhibition of FLJ21916 (Accession NM_023112). Accordingly, utilities of VGAM2170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ21916. KIAA0441 (Accession NM_014797) is another VGAM2170 host target gene. KIAA0441 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0441, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0441 BINDING SITE, designated SEQ ID:16709, to the nucleotide sequence of VGAM2170 RNA, herein designated VGAM RNA, also designated SEQ ID:4881.

[75111] Another function of VGAM2170 is therefore inhibition of KIAA0441 (Accession NM_014797). Accordingly, utilities of VGAM2170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0441. KIAA1157 (Accession XM_051093) is another VGAM2170 host target gene. KIAA1157 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1157, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1157 BINDING SITE, designated SEQ ID:35754, to the nucleotide sequence of VGAM2170 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4881.

[75112] Another function of VGAM2170 is therefore inhibition of KIAA1157 (Accession XM_051093). Accordingly, utilities of VGAM2170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1157. PRO1580 (Accession NM_018502) is another VGAM2170 host target gene. PRO1580 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1580, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1580 BINDING SITE, designated SEQ ID:20567, to the nucleotide sequence of VGAM2170 RNA, herein designated VGAM RNA, also designated SEQ ID:4881.

[75113] Another function of VGAM2170 is therefore inhibition of PRO1580 (Accession NM_018502). Accordingly, utilities of VGAM2170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1580. LOC257484 (Accession XM_114232) is another VGAM2170 host target gene. LOC257484 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257484, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257484 BINDING SITE, designated SEQ ID:42814, to the nucleotide sequence of VGAM2170 RNA, herein designated VGAM RNA, also designated SEQ ID:4881.

[75114] Another function of VGAM2170 is therefore inhibition of LOC257484 (Accession XM_114232). Accordingly, utilities of VGAM2170 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257484. LOC91351 (Accession XM_037817) is another VGAM2170 host target gene. LOC91351 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91351, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91351 BINDING SITE, designated SEQ ID:32698, to the nucleotide sequence of VGAM2170 RNA, herein designated VGAM RNA, also designated SEQ ID:4881.

[75115] Another function of VGAM2170 is therefore inhibition of LOC91351 (Accession XM_037817). Accordingly, utilities of VGAM2170 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC91351. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2171 (VGAM2171) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75116] VGAM2171 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2171 was detected is described hereinabove with reference to Figs. 1-8.

[75117] VGAM2171 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip Yellow Fleck Virus. VGAM2171 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75118] VGAM2171 gene encodes a VGAM2171 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2171 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2171 precursor RNA is desig-

nated SEQ ID:2157, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2157 is located at position 5077 relative to the genome of Parsnip Yellow Fleck Virus.

[75119] VGAM2171 precursor RNA folds onto itself, forming VGAM2171 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75120] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2171 folded precursor RNA into VGAM2171 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2171 RNA is designated SEQ ID:4882, and is provided hereinbelow with reference to the sequence

listing part.

[75121] VGAM2171 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2171 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2171 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75122] VGAM2171 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2171 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2171 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2171 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2171 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75123] The complementary binding of VGAM2171 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2171 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2171 host target RNA into VGAM2171 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75124] It is appreciated that VGAM2171 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2171 host target genes. The mRNA of each one of this plurality of VGAM2171 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2171 RNA, herein designated VGAM

RNA, and which when bound by VGAM2171 RNA causes inhibition of translation of respective one or more VGAM2171 host target proteins.

[75125] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2171 gene, herein designated VGAM GENE, on one or more VGAM2171 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75126] It is yet further appreciated that a function of VGAM2171 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2171 include diagnosis, prevention and treatment of viral infection by Parsnip Yellow Fleck Virus. Specific functions, and accordingly utilities, of VGAM2171 correlate with, and may be deduced from, the identity of the host target genes which VGAM2171 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75127] Nucleotide sequences of the VGAM2171 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2171 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2171 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2171 are further described hereinbelow with reference to Table 1.

[75128] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2171 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2171 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75129] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2171 gene, herein designated VGAM is

inhibition of expression of VGAM2171 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2171 correlate with, and may be deduced from, the identity of the target genes which VGAM2171 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75130] Citron (rho-interacting, serine/threonine kinase 21) (CIT, Accession XM_045786) is a VGAM2171 host target gene. CIT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CIT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CIT BINDING SITE, designated SEQ ID:34559, to the nucleotide sequence of VGAM2171 RNA, herein designated VGAM RNA, also designated SEQ ID:4882.

[75131] A function of VGAM2171 is therefore inhibition of Citron (rho-interacting, serine/threonine kinase 21) (CIT, Accession XM_045786), a gene which is increased several-fold by coexpression of constitutively active Rho . Accordingly, utilities of VGAM2171 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIT. The function of CIT and its association with vari-

ous diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM393.KIAA0475 (Accession NM_014864) is another VGAM2171 host target gene. KIAA0475 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:16944, to the nucleotide sequence of VGAM2171 RNA, herein designated VGAM RNA, also designated SEQ ID:4882.

[75132] Another function of VGAM2171 is therefore inhibition of KIAA0475 (Accession NM_014864). Accordingly, utilities of VGAM2171 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0475. KIAA1649 (Accession NM_032311) is another VGAM2171 host target gene. KIAA1649 BINDING SITE1 and KIAA1649 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1649, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of KIAA1649 BINDING SITE1 and KIAA1649 BINDING SITE2, designated SEQ ID:26100 and SEQ ID:33254 respectively, to the nucleotide sequence of VGAM2171 RNA, herein designated VGAM RNA, also designated SEQ ID:4882.

[75133] Another function of VGAM2171 is therefore inhibition of KIAA1649 (Accession NM_032311). Accordingly, utilities of VGAM2171 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1649. TUSP (Accession NM_020245) is another VGAM2171 host target gene. TUSP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUSP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUSP BINDING SITE, designated SEQ ID:21520, to the nucleotide sequence of VGAM2171 RNA, herein designated VGAM RNA, also designated SEQ ID:4882.

[75134] Another function of VGAM2171 is therefore inhibition of TUSP (Accession NM_020245). Accordingly, utilities of VGAM2171 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUSP.

Zinc Finger Protein 384 (ZNF384, Accession NM_133476) is another VGAM2171 host target gene. ZNF384 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF384, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF384 BINDING SITE, designated SEQ ID:28544, to the nucleotide sequence of VGAM2171 RNA, herein designated VGAM RNA, also designated SEQ ID:4882.

[75135] Another function of VGAM2171 is therefore inhibition of Zinc Finger Protein 384 (ZNF384, Accession NM_133476). Accordingly, utilities of VGAM2171 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF384. LOC221656 (Accession XM_166418) is another VGAM2171 host target gene. LOC221656 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221656, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221656 BINDING SITE, designated SEQ ID:44290, to the nucleotide sequence of

VGAM2171 RNA, herein designated VGAM RNA, also designated SEQ ID:4882.

[75136] Another function of VGAM2171 is therefore inhibition of LOC221656 (Accession XM_166418). Accordingly, utilities of VGAM2171 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221656. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2172 (VGAM2172) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75137] VGAM2172 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2172 was detected is described hereinabove with reference to Figs. 1-8.

[75138] VGAM2172 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip Yellow Fleck Virus. VGAM2172 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75139] VGAM2172 gene encodes a VGAM2172 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2172 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2172 precursor RNA is designated SEQ ID:2158, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2158 is located at position 578 relative to the genome of Parsnip Yellow Fleck Virus.

[75140] VGAM2172 precursor RNA folds onto itself, forming VGAM2172 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75141] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2172 folded precursor RNA into VGAM2172 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2172 RNA is designated SEQ ID:4883, and is provided hereinbelow with reference to the sequence listing part.

[75142] VGAM2172 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2172 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2172 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75143] VGAM2172 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2172 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2172 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2172 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2172 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75144] The complementary binding of VGAM2172 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2172 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2172 host target RNA into VGAM2172 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75145] It is appreciated that VGAM2172 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2172 host target genes. The mRNA of each one of this plurality of VGAM2172 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2172 RNA, herein designated VGAM RNA, and which when bound by VGAM2172 RNA causes inhibition of translation of respective one or more VGAM2172 host target proteins.

[75146] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2172 gene, herein designated VGAM GENE, on one or more VGAM2172 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75147] It is yet further appreciated that a function of VGAM2172 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2172 include diagnosis, prevention and treatment of viral infection by Parsnip Yellow Fleck Virus. Specific functions, and accordingly utilities, of VGAM2172 correlate with, and may be deduced from, the identity of the host target genes which VGAM2172 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75148] Nucleotide sequences of the VGAM2172 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2172 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2172 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2172 are further described hereinbelow with reference to Table 1.

[75149] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2172 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2172 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75150] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2172 gene, herein designated VGAM is inhibition of expression of VGAM2172 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2172 correlate with, and may be deduced from, the identity of the target genes which VGAM2172 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75151] Aldehyde Dehydrogenase 3 Family, Member A2 (ALDH3A2, Accession XM_045060) is a VGAM2172 host target gene. ALDH3A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALDH3A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALDH3A2 BINDING SITE, designated SEQ ID:34338, to the nucleotide sequence of VGAM2172 RNA, herein designated VGAM RNA, also designated SEQ ID:4883.

[75152] A function of VGAM2172 is therefore inhibition of Alde-

hyde Dehydrogenase 3 Family, Member A2 (ALDH3A2, Accession XM_045060). Accordingly, utilities of VGAM2172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH3A2. Fibroblast Growth Factor 2 (basic) (FGF2, Accession NM_002006) is another VGAM2172 host target gene. FGF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF2 BINDING SITE, designated SEQ ID:7730, to the nucleotide sequence of VGAM2172 RNA, herein designated VGAM RNA, also designated SEQ ID:4883.

[75153] Another function of VGAM2172 is therefore inhibition of Fibroblast Growth Factor 2 (basic) (FGF2, Accession NM_002006), a gene which probably involved in nervous system development and function. Accordingly, utilities of VGAM2172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF2. The function of FGF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM51.Heterogeneous Nuclear Ribonucleoprotein K (HNRPK, Accession NM_002140) is another VGAM2172 host target gene. HNRPK BINDING SITE1 and HNRPK BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HNRPK, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNRPK BINDING SITE1 and HNRPK BINDING SITE2, designated SEQ ID:7917 and SEQ ID:25281 respectively, to the nucleotide sequence of VGAM2172 RNA, herein designated VGAM RNA, also designated SEQ ID:4883.

[75154] Another function of VGAM2172 is therefore inhibition of Heterogeneous Nuclear Ribonucleoprotein K (HNRPK, Accession NM_002140), a gene which play a role in the nuclear metabolism of hnrnas, particularly for pre-mrnas that contain cytidine-rich sequence. Accordingly, utilities of VGAM2172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNRPK. The function of HNRPK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM125.Peanut-like 2 (Drosophila)

(PNUTL2, Accession NM_080415) is another VGAM2172 host target gene. PNUTL2 BINDING SITE1 and PNUTL2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PNUTL2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PNUTL2 BINDING SITE1 and PNUTL2 BINDING SITE2, designated SEQ ID:27833 and SEQ ID:23131 respectively, to the nucleotide sequence of VGAM2172 RNA, herein designated VGAM RNA, also designated SEQ ID:4883.

[75155] Another function of VGAM2172 is therefore inhibition of Peanut-like 2 (Drosophila) (PNUTL2, Accession NM_080415), a gene which is involved in cytokinesis. Accordingly, utilities of VGAM2172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNUTL2. The function of PNUTL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM95.KIAA1054 (Accession XM_043493) is another VGAM2172 host target gene. KIAA1054 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by KIAA1054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1054 BINDING SITE, designated SEQ ID:33959, to the nucleotide sequence of VGAM2172 RNA, herein designated VGAM RNA, also designated SEQ ID:4883.

[75156] Another function of VGAM2172 is therefore inhibition of KIAA1054 (Accession XM_043493). Accordingly, utilities of VGAM2172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1054. KIAA1677 (Accession XM_040383) is another VGAM2172 host target gene. KIAA1677 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1677, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1677 BINDING SITE, designated SEQ ID:33292, to the nucleotide sequence of VGAM2172 RNA, herein designated VGAM RNA, also designated SEQ ID:4883.

[75157] Another function of VGAM2172 is therefore inhibition of KIAA1677 (Accession XM_040383). Accordingly, utilities

of VGAM2172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1677. LOC148946 (Accession XM_097557) is another VGAM2172 host target gene. LOC148946 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148946, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148946 BINDING SITE, designated SEQ ID:40935, to the nucleotide sequence of VGAM2172 RNA, herein designated VGAM RNA, also designated SEQ ID:4883.

[75158] Another function of VGAM2172 is therefore inhibition of LOC148946 (Accession XM_097557). Accordingly, utilities of VGAM2172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148946. LOC161829 (Accession XM_091161) is another VGAM2172 host target gene. LOC161829 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC161829, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC161829 BINDING SITE, designated SEQ ID:40039, to the nucleotide sequence of VGAM2172 RNA, herein designated VGAM RNA, also designated SEQ ID:4883.

[75159] Another function of VGAM2172 is therefore inhibition of LOC161829 (Accession XM_091161). Accordingly, utilities of VGAM2172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161829. LOC219333 (Accession XM_167944) is another VGAM2172 host target gene. LOC219333 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219333 BINDING SITE, designated SEQ ID:44935, to the nucleotide sequence of VGAM2172 RNA, herein designated VGAM RNA, also designated SEQ ID:4883.

[75160] Another function of VGAM2172 is therefore inhibition of LOC219333 (Accession XM_167944). Accordingly, utilities of VGAM2172 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219333. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2173 (VGAM2173) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75161] VGAM2173 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2173 was detected is described hereinabove with reference to Figs. 1-8.

[75162] VGAM2173 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Parsnip Yellow Fleck Virus. VGAM2173 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75163] VGAM2173 gene encodes a VGAM2173 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2173 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2173 precursor RNA is designated SEQ ID:2159, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2159 is located at position 3661 relative to the

genome of Parsnip Yellow Fleck Virus.

[75164] VGAM2173 precursor RNA folds onto itself, forming VGAM2173 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75165] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2173 folded precursor RNA into VGAM2173 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 74%) nucleotide sequence of VGAM2173 RNA is designated SEQ ID:4884, and is provided hereinbelow with reference to the sequence listing part.

[75166] VGAM2173 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2173 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2173 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75167] VGAM2173 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2173 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2173 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2173 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2173 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75168] The complementary binding of VGAM2173 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2173 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2173 host target RNA into VGAM2173 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75169] It is appreciated that VGAM2173 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2173 host target genes. The mRNA of each one of this plurality of VGAM2173 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2173 RNA, herein designated VGAM RNA, and which when bound by VGAM2173 RNA causes inhibition of translation of respective one or more VGAM2173 host target proteins.

[75170] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2173 gene, herein designated VGAM GENE, on one or more VGAM2173 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75171] It is yet further appreciated that a function of VGAM2173 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of viral infection by Parsnip Yellow Fleck Virus. Specific functions, and accordingly utilities, of VGAM2173

correlate with, and may be deduced from, the identity of the host target genes which VGAM2173 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75172] Nucleotide sequences of the VGAM2173 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2173 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2173 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2173 are further described hereinbelow with reference to Table 1.

[75173] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2173 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2173 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75174] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2173 gene, herein designated VGAM is inhibition of expression of VGAM2173 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2173 correlate with, and may be deduced

from, the identity of the target genes which VGAM2173 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75175] Calcium Channel, Voltage-dependent, Gamma Subunit 3 (CACNG3, Accession NM_006539) is a VGAM2173 host target gene. CACNG3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CACNG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CACNG3 BINDING SITE, designated SEQ ID:13291, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75176] A function of VGAM2173 is therefore inhibition of Calcium Channel, Voltage-dependent, Gamma Subunit 3 (CACNG3, Accession NM_006539), a gene which is thought to stabilize the calcium channel in an inactivated state. Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNG3. The function of CACNG3 and its association with various diseases and clinical conditions, has been established by previous studies, as described here-

inabove with reference to VGAM1551.Collagen, Type XI, Alpha 2 (COL11A2, Accession NM_080680) is another VGAM2173 host target gene. COL11A2 BINDING SITE1 and COL11A2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by COL11A2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL11A2 BINDING SITE1 and COL11A2 BINDING SITE2, designated SEQ ID:27977 and SEQ ID:27982 respectively, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75177] Another function of VGAM2173 is therefore inhibition of Collagen, Type XI, Alpha 2 (COL11A2, Accession NM_080680). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL11A2. Hypoxia Up-regulated 1 (HYOU1, Accession XM_006464) is another VGAM2173 host target gene. HYOU1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HYOU1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HYOU1 BINDING SITE, designated SEQ ID:30002, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75178] Another function of VGAM2173 is therefore inhibition of Hypoxia Up-regulated 1 (HYOU1, Accession XM_006464). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HYOU1. Megakaryocyte-associated Tyrosine Kinase (MATK, Accession NM_002378) is another VGAM2173 host target gene. MATK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MATK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MATK BINDING SITE, designated SEQ ID:8193, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75179] Another function of VGAM2173 is therefore inhibition of Megakaryocyte-associated Tyrosine Kinase (MATK, Accession NM_002378), a gene which can phosphorylate mem-

bers of the SRC family of PTKs at the regulatory tyrosine residue. Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MATK. The function of MATK has been established by previous studies. In the mouse, Klages et al. (1994) reported the molecular cloning and preliminary functional characterization of a nonreceptor protein tyrosine kinase (PTK) that is related to CSK (OMIM Ref. No. 124095). This PTK, designated Ctk for CSK-type protein-tyrosine kinase, was found to be a 52-kD protein expressed primarily in brain and predicted to be structurally similar to CSK. Klages et al. (1994) found that, like CSK, Ctk can phosphorylate members of the SRC family of PTKs at the regulatory tyrosine residue. Thus, Ctk and CSK define a family of kinases that phosphorylate carboxy-terminal regulatory tyrosine residues. Protein-tyrosine kinases play major roles in signal transduction pathways. Bennett et al. (1994) cloned a novel tyrosine kinase, termed megakaryoctye-associated tyrosine kinase (MATK), from a human megakaryocyte cDNA library using degenerate PCR. The MATK cDNA encodes a 527-amino acid protein that shows 50% amino acid identity to CSK and has the structural features of the CSK subfamily: SRC homol-

ogy SH (2) and SH3 domains, a catalytic domain, a unique N terminus, lack of myristylation signals, lack of a negative regulatory phosphorylation site, and lack of an autophosphorylation site. Bennett et al. (1994) localized the MATK protein to the cytoplasm of megakaryocytic cells using immunofluorescence and immunoblot analysis of subcellular fractions. They showed by Northern blotting that the MATK gene is expressed abundantly in megakaryocytes and at a lower level in adult brain as a 2.3-kb transcript; it was not detectably expressed in any other examined tissue. Bennett et al. (1994) found that MATK expression is upregulated in megakaryocytic cells that are induced to differentiate by phorbol ester. They suggested that MATK functions in signal transduction pathways that are important in megakaryocyte growth and/or differentiation. Avraham et al. (1995) showed that MATK can phosphorylate the SRC (OMIM Ref. No. 176947) protein in vitro. Sakano et al. (1994) cloned the MATK cDNA, named HYL by them, and localized the gene to 19p13.3 using fluorescence in situ hybridization. Avraham et al. (1995) mapped the MATK gene to chromosome 19 using somatic cell hybrids and found that the murine Matk gene maps within a region of synteny on chromosome 10.

Zrihan-Licht et al. (1997) reported that MATK is expressed in human breast cancer but not in the adjacent normal breast tissues, suggesting that MATK might be involved in signaling in some cases of breast cancer. Zrihan-Licht et al. (1997) demonstrated that MATK interacts with ErbB-2 (OMIM Ref. No. 164870) in vivo upon heregulin stimulation and that this interaction occurs via the SH2 domain of MATK.

[75180] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[75181] Klages, S.; Adam, D.; Class, K.; Fargnoli, J.; Bolen, J. B.; Penhallow, R. C. : Ctk: a protein-tyrosine kinase related to Csk that defines an enzyme family. Proc. Nat. Acad. Sci. 91: 2597-2601, 1994. ; and

[75182] Avraham, S.; Jiang, S.; Ota, S.; Fu, Y.; Deng, B.; Dowler, L. L.; White, R. A.; Avraham, H. : Structural and functional studies of the intracellular tyrosine kinase MATK gene and its tra.

[75183] Further studies establishing the function and utilities of MATK are found in John Hopkins OMIM database record ID 600038, and in sited publications numbered 8119-8123 listed in the bibliography section hereinbelow, which are

also hereby incorporated by reference.Paired Box Gene 5 (B-cell lineage specific activator protein) (PAX5, Accession NM_016734) is another VGAM2173 host target gene. PAX5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAX5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAX5 BINDING SITE, designated SEQ ID:18788, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75184] Another function of VGAM2173 is therefore inhibition of Paired Box Gene 5 (B-cell lineage specific activator protein) (PAX5, Accession NM_016734), a gene which plays a role in B-cell differentiation, neural development and spermatogenesis. Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAX5. The function of PAX5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1151.Prokineticin 1 (PROK1, Accession NM_032414) is another VGAM2173 host target gene. PROK1 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PROK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PROK1 BINDING SITE, designated SEQ ID:26196, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75185] Another function of VGAM2173 is therefore inhibition of Prokineticin 1 (PROK1, Accession NM_032414), a gene which induces proliferation, migration and fenestration in capillary endothelial cells derived from endocrine glands. Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROK1. The function of PROK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1000.Transcription Factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) (TCF3, Accession XM_047600) is another VGAM2173 host target gene. TCF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCF3, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF3 BINDING SITE, designated SEQ ID:35004, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75186] Another function of VGAM2173 is therefore inhibition of Transcription Factor 3 (E2A immunoglobulin enhancer binding factors E12/E47) (TCF3, Accession XM_047600), a gene which plays major roles in determining tissue-specific cell fate during embryogenesis. Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF3. The function of TCF3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM144.XT3 (Accession NM_020208) is another VGAM2173 host target gene. XT3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XT3 BINDING SITE, desig-

nated SEQ ID:21437, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75187] Another function of VGAM2173 is therefore inhibition of XT3 (Accession NM_020208), a gene which is a Kidney-specific orphan transporter. Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XT3. The function of XT3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM21.Baculoviral IAP Repeat-containing 1 (BIRC1, Accession NM_004536) is another VGAM2173 host target gene. BIRC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BIRC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIRC1 BINDING SITE, designated SEQ ID:10879, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75188] Another function of VGAM2173 is therefore inhibition of Baculoviral IAP Repeat-containing 1 (BIRC1, Accession

NM_004536). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIRC1. Chemokine (C-C motif) Receptor 5 (CCR5, Accession NM_000579) is another VGAM2173 host target gene. CCR5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CCR5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCR5 BINDING SITE, designated SEQ ID:6181, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75189] Another function of VGAM2173 is therefore inhibition of Chemokine (C-C motif) Receptor 5 (CCR5, Accession NM_000579). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCR5. DKFZP564D166 (Accession NM_030658) is another VGAM2173 host target gene. DKFZP564D166 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564D166, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564D166 BINDING SITE, designated SEQ ID:24988, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75190] Another function of VGAM2173 is therefore inhibition of DKFZP564D166 (Accession NM_030658). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564D166. FLJ20400 (Accession XM_039306) is another VGAM2173 host target gene. FLJ20400 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20400, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20400 BINDING SITE, designated SEQ ID:33043, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75191] Another function of VGAM2173 is therefore inhibition of FLJ20400 (Accession XM_039306). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20400. KIAA0193 (Accession NM_014766) is another VGAM2173 host target gene. KIAA0193 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0193, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0193 BINDING SITE, designated SEQ ID:16537, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75192] Another function of VGAM2173 is therefore inhibition of KIAA0193 (Accession NM_014766). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0193. KIAA0648 (Accession XM_094043) is another VGAM2173 host target gene. KIAA0648 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0648, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0648 BINDING SITE, designated SEQ ID:40218, to the nucleotide sequence of VGAM2173 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4884.

[75193] Another function of VGAM2173 is therefore inhibition of KIAA0648 (Accession XM_094043). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0648. KIAA0903 (Accession XM_049251) is another VGAM2173 host target gene. KIAA0903 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0903, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0903 BINDING SITE, designated SEQ ID:35366, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75194] Another function of VGAM2173 is therefore inhibition of KIAA0903 (Accession XM_049251). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0903. KIAA1037 (Accession NM_015023) is another VGAM2173 host target gene. KIAA1037 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1037, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1037 BINDING SITE, designated SEQ ID:17384, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75195] Another function of VGAM2173 is therefore inhibition of KIAA1037 (Accession NM_015023). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1037. KIAA1786 (Accession XM_038436) is another VGAM2173 host target gene. KIAA1786 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1786 BINDING SITE, designated SEQ ID:32844, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75196] Another function of VGAM2173 is therefore inhibition of KIAA1786 (Accession XM_038436). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1786. NSE1 (Accession NM_145175) is another VGAM2173 host target gene. NSE1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NSE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NSE1 BINDING SITE, designated SEQ ID:29736, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75197] Another function of VGAM2173 is therefore inhibition of NSE1 (Accession NM_145175). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NSE1. P450RAI-2 (Accession NM_019885) is another VGAM2173 host target gene. P450RAI-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P450RAI-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P450RAI-2 BINDING SITE, designated SEQ ID:21269, to the nucleotide se-

quence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75198] Another function of VGAM2173 is therefore inhibition of P450RAI-2 (Accession NM_019885). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P450RAI-2. Protein Serine Kinase H1 (PSKH1, Accession XM_043047) is another VGAM2173 host target gene. PSKH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSKH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSKH1 BINDING SITE, designated SEQ ID:33866, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75199] Another function of VGAM2173 is therefore inhibition of Protein Serine Kinase H1 (PSKH1, Accession XM_043047). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSKH1. RAB40A, Member RAS Oncogene Family (RAB40A, Accession XM_088733) is another

VGAM2173 host target gene. RAB40A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAB40A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB40A BINDING SITE, designated SEQ ID:39927, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75200] Another function of VGAM2173 is therefore inhibition of RAB40A, Member RAS Oncogene Family (RAB40A, Accession XM_088733). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB40A. Rho-related BTB Domain Containing 2 (RHOBTB2, Accession XM_027679) is another VGAM2173 host target gene. RHOBTB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RHOBTB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RHOBTB2 BINDING SITE, designated SEQ ID:30557, to the nucleotide sequence of VGAM2173 RNA,

herein designated VGAM RNA, also designated SEQ ID:4884.

[75201] Another function of VGAM2173 is therefore inhibition of Rho-related BTB Domain Containing 2 (RHOBTB2, Accession XM_027679). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHOBTB2. SEC15B (Accession XM_039570) is another VGAM2173 host target gene. SEC15B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC15B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC15B BINDING SITE, designated SEQ ID:33123, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75202] Another function of VGAM2173 is therefore inhibition of SEC15B (Accession XM_039570). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC15B. WD Repeat Domain 7 (WDR7, Accession NM_015285) is another VGAM2173 host target gene.

WDR7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WDR7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WDR7 BINDING SITE, designated SEQ ID:17607, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75203] Another function of VGAM2173 is therefore inhibition of WD Repeat Domain 7 (WDR7, Accession NM_015285). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WDR7. LOC144558 (Accession XM_096629) is another VGAM2173 host target gene. LOC144558 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144558, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144558 BINDING SITE, designated SEQ ID:40436, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75204] Another function of VGAM2173 is therefore inhibition of LOC144558 (Accession XM_096629). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144558. LOC153196 (Accession XM_098323) is another VGAM2173 host target gene. LOC153196 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153196 BINDING SITE, designated SEQ ID:41584, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75205] Another function of VGAM2173 is therefore inhibition of LOC153196 (Accession XM_098323). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153196. LOC219731 (Accession XM_167596) is another VGAM2173 host target gene. LOC219731 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219731, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219731 BINDING SITE, designated SEQ ID:44714, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75206] Another function of VGAM2173 is therefore inhibition of LOC219731 (Accession XM_167596). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219731. LOC91759 (Accession XM_040467) is another VGAM2173 host target gene. LOC91759 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91759, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91759 BINDING SITE, designated SEQ ID:33302, to the nucleotide sequence of VGAM2173 RNA, herein designated VGAM RNA, also designated SEQ ID:4884.

[75207] Another function of VGAM2173 is therefore inhibition of LOC91759 (Accession XM_040467). Accordingly, utilities of VGAM2173 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC91759. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2174 (VGAM2174) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75208] VGAM2174 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2174 was detected is described hereinabove with reference to Figs. 1-8.

[75209] VGAM2174 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit Fibroma Virus. VGAM2174 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75210] VGAM2174 gene encodes a VGAM2174 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2174 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2174 precursor RNA is designated SEQ ID:2160, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2160 is located at position 17511 relative to the genome of Rabbit Fibroma Virus.

[75211] VGAM2174 precursor RNA folds onto itself, forming VGAM2174 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75212] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2174 folded precursor RNA into VGAM2174 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM2174 RNA is designated SEQ ID:4885, and is provided hereinbelow with reference to the sequence listing part.

[75213] VGAM2174 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2174 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2174 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75214] VGAM2174 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2174 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2174 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2174 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2174 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75215] The complementary binding of VGAM2174 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2174 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2174 host target RNA into VGAM2174 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75216] It is appreciated that VGAM2174 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2174 host target genes. The mRNA of each one of this plurality of VGAM2174 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2174 RNA, herein designated VGAM RNA, and which when bound by VGAM2174 RNA causes

inhibition of translation of respective one or more VGAM2174 host target proteins.

[75217] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2174 gene, herein designated VGAM GENE, on one or more VGAM2174 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75218] It is yet further appreciated that a function of VGAM2174 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2174 include diagnosis, prevention and

treatment of viral infection by Rabbit Fibroma Virus. Specific functions, and accordingly utilities, of VGAM2174 correlate with, and may be deduced from, the identity of the host target genes which VGAM2174 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75219] Nucleotide sequences of the VGAM2174 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2174 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2174 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2174 are further described hereinbelow with reference to Table 1.

[75220] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2174 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2174 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75221] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2174 gene, herein designated VGAM is inhibition of expression of VGAM2174 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2174 correlate with, and may be deduced from, the identity of the target genes which VGAM2174 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75222] UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 5 (B4GALT5, Accession NM_004776) is a VGAM2174 host target gene. B4GALT5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by B4GALT5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B4GALT5 BINDING SITE, designated SEQ ID:11166, to the nucleotide sequence of VGAM2174 RNA, herein designated VGAM RNA, also designated SEQ ID:4885.

[75223] A function of VGAM2174 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 5 (B4GALT5, Accession NM_004776). Accordingly, utilities of VGAM2174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT5. Roundabout, Axon Guidance Receptor, Homolog 1 (Drosophila) (ROBO1, Accession NM_133631) is

another VGAM2174 host target gene. ROBO1 BINDING SITE1 and ROBO1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ROBO1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ROBO1 BINDING SITE1 and ROBO1 BINDING SITE2, designated SEQ ID:28586 and SEQ ID:8850 respectively, to the nucleotide sequence of VGAM2174 RNA, herein designated VGAM RNA, also designated SEQ ID:4885.

[75224] Another function of VGAM2174 is therefore inhibition of Roundabout, Axon Guidance Receptor, Homolog 1 (Drosophila) (ROBO1, Accession NM_133631), a gene which is an axon guidance receptor. Accordingly, utilities of VGAM2174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ROBO1. The function of ROBO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM37.KIAA0276 (Accession XM_048199) is another VGAM2174 host target gene. KIAA0276 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by KIAA0276, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0276 BINDING SITE, designated SEQ ID:35139, to the nucleotide sequence of VGAM2174 RNA, herein designated VGAM RNA, also designated SEQ ID:4885.

[75225] Another function of VGAM2174 is therefore inhibition of KIAA0276 (Accession XM_048199). Accordingly, utilities of VGAM2174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0276. KIAA0976 (Accession NM_014917) is another VGAM2174 host target gene. KIAA0976 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0976, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0976 BINDING SITE, designated SEQ ID:17163, to the nucleotide sequence of VGAM2174 RNA, herein designated VGAM RNA, also designated SEQ ID:4885.

[75226] Another function of VGAM2174 is therefore inhibition of KIAA0976 (Accession NM_014917). Accordingly, utilities

of VGAM2174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0976. PRO0618 (Accession NM_014133) is another VGAM2174 host target gene. PRO0618 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO0618, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0618 BINDING SITE, designated SEQ ID:15399, to the nucleotide sequence of VGAM2174 RNA, herein designated VGAM RNA, also designated SEQ ID:4885.

[75227] Another function of VGAM2174 is therefore inhibition of PRO0618 (Accession NM_014133). Accordingly, utilities of VGAM2174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0618. LOC90092 (Accession XM_028862) is another VGAM2174 host target gene. LOC90092 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC90092 BINDING SITE, designated SEQ ID:30783, to the nucleotide sequence of VGAM2174 RNA, herein designated VGAM RNA, also designated SEQ ID:4885.

[75228] Another function of VGAM2174 is therefore inhibition of LOC90092 (Accession XM_028862). Accordingly, utilities of VGAM2174 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90092. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2175 (VGAM2175) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75229] VGAM2175 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2175 was detected is described hereinabove with reference to Figs. 1-8.

[75230] VGAM2175 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit Fibroma Virus. VGAM2175 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75231] VGAM2175 gene encodes a VGAM2175 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2175 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2175 precursor RNA is designated SEQ ID:2161, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2161 is located at position 10893 relative to the genome of Rabbit Fibroma Virus.

[75232] VGAM2175 precursor RNA folds onto itself, forming VGAM2175 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75233] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2175 folded precursor RNA into VGAM2175 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of VGAM2175 RNA is designated SEQ ID:4886, and is provided hereinbelow with reference to the sequence listing part.

[75234] VGAM2175 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2175 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2175 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75235] VGAM2175 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2175 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2175 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2175 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2175 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75236] The complementary binding of VGAM2175 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2175 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2175 host target RNA into VGAM2175 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75237] It is appreciated that VGAM2175 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2175 host target genes. The mRNA of each one of this plurality of VGAM2175 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2175 RNA, herein designated VGAM RNA, and which when bound by VGAM2175 RNA causes inhibition of translation of respective one or more VGAM2175 host target proteins.

[75238] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2175 gene, herein designated VGAM GENE, on one or more VGAM2175 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75239] It is yet further appreciated that a function of VGAM2175 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2175 include diagnosis, prevention and treatment of viral infection by Rabbit Fibroma Virus. Specific functions, and accordingly utilities, of VGAM2175 correlate with, and may be deduced from, the identity of the host target genes which VGAM2175 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75240] Nucleotide sequences of the VGAM2175 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2175 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2175 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2175 are further described hereinbelow with reference to Table 1.

[75241] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2175 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2175 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75242] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2175 gene, herein designated VGAM is inhibition of expression of VGAM2175 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2175 correlate with, and may be deduced from, the identity of the target genes which VGAM2175 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75243] ATPase, Class VI, Type 11B (ATP11B, Accession XM_087254) is a VGAM2175 host target gene. ATP11B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP11B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP11B BINDING SITE, designated SEQ ID:39142, to the nucleotide sequence of VGAM2175 RNA, herein designated VGAM RNA, also designated SEQ ID:4886.

[75244] A function of VGAM2175 is therefore inhibition of ATPase,

Class VI, Type 11B (ATP11B, Accession XM_087254), a gene which is phosphorylated in their intermediate state, drives uphill transport of ions across membranes. Accordingly, utilities of VGAM2175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP11B. The function of ATP11B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM665.Egl Nine Homolog 3 (C. elegans) (EGLN3, Accession NM_022073) is another VGAM2175 host target gene. EGLN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EGLN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGLN3 BINDING SITE, designated SEQ ID:22616, to the nucleotide sequence of VGAM2175 RNA, herein designated VGAM RNA, also designated SEQ ID:4886.

[75245] Another function of VGAM2175 is therefore inhibition of Egl Nine Homolog 3 (C. elegans) (EGLN3, Accession NM_022073), a gene which is an essential component of the pathway. Accordingly, utilities of VGAM2175 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with EGLN3. The function of EGLN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Phosphodiesterase 4D, CAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D, Accession XM_056815) is another VGAM2175 host target gene. PDE4D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE4D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE4D BINDING SITE, designated SEQ ID:36433, to the nucleotide sequence of VGAM2175 RNA, herein designated VGAM RNA, also designated SEQ ID:4886.

[75246] Another function of VGAM2175 is therefore inhibition of Phosphodiesterase 4D, CAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D, Accession XM_056815), a gene which has similarity to Drosophila dnc, which is the affected protein in learning and memory mutant dunce. Accordingly, utilities of VGAM2175 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4D. The function of PDE4D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM180.Roundabout, Axon Guidance Receptor, Homolog 1 (Drosophila) (ROBO1, Accession NM_133631) is another VGAM2175 host target gene. ROBO1 BINDING SITE1 and ROBO1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ROBO1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ROBO1 BINDING SITE1 and ROBO1 BINDING SITE2, designated SEQ ID:28587 and SEQ ID:8851 respectively, to the nucleotide sequence of VGAM2175 RNA, herein designated VGAM RNA, also designated SEQ ID:4886.

[75247] Another function of VGAM2175 is therefore inhibition of Roundabout, Axon Guidance Receptor, Homolog 1 (Drosophila) (ROBO1, Accession NM_133631), a gene which is an axon guidance receptor. Accordingly, utilities of VGAM2175 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with ROBO1. The function of ROBO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM37.Transcription Termination Factor, RNA Polymerase II (TTF2, Accession NM_003594) is another VGAM2175 host target gene. TTF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TTF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTF2 BINDING SITE, designated SEQ ID:9652, to the nucleotide sequence of VGAM2175 RNA, herein designated VGAM RNA, also designated SEQ ID:4886.

[75248] Another function of VGAM2175 is therefore inhibition of Transcription Termination Factor, RNA Polymerase II (TTF2, Accession NM_003594), a gene which is involved either in promoting the migration process or in repressing differentiation of the TFCs until migration has occurred. Accordingly, utilities of VGAM2175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTF2. The function of TTF2 has been

established by previous studies. Clifton-Bligh et al. (1998) demonstrated that the FKHL15 gene, which is the human homolog of the mouse Titf2 gene, was homozygously mutated in 2 sibs with thyroid agenesis, cleft palate, and choanal atresia, previously reported by Bamforth et al. (1989); see Bamforth-Lazarus syndrome (OMIM Ref. No. 241850). Spiky or curly hair was also a feature, as was bifid epiglottis. Polyhydramnios, which was present in the 2 pregnancies of the brothers and in another reported case of Bamforth-Lazarus syndrome, may have been caused by the choanal atresia. Clifton-Bligh et al. (1998) had found by a database search against the rat TTF2 gene more than 90% homology with FKHL15. The FKHL15 cDNA was encoded by a single-exon gene. A probe specific to the 3-prime UTR of FKHL15 detected a 5.3-kb transcript that was highly expressed in thyroid tissues, and a second 3.2-kb transcript seen in both thyroid and testis. Animal model experiments lend further support to the function of TTF2. Many members of the forkhead/winged-helix transcription factor family are key regulators of embryogenesis (Kaufmann and Knochel, 1996). Thyroid transcription factor-2 (TTF2), a forkhead domain-containing transcription factor, was cloned by Zannini et al. (1997) and the

mouse gene, designated Titf2, was mapped to chromosome 4. De Felice et al. (1998) showed that Titf2-null mutant mice exhibit cleft palate and either a sublingual or completely absent thyroid gland. Thus, the Titf2-/- mutation results in neonatal hypothyroidism that showed similarity to thyroid dysgenesis in humans. Among the 1 in 3,000 or 4,000 newborns in which congenital hypothyroidism is detected, 80% have either an ectopic, small and sublingual thyroid, or have no thyroid tissue (Toublanc, 1992). Most of these cases appear sporadically, although a few cases of recurring familial thyroid dysgenesis (OMIM Ref. No. 218700) have been reported.

[75249] It is appreciated that the abovementioned animal model for TTF2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[75250] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[75251] Clifton-Bligh, R. J.; Wentworth, J. M.; Heinz, P.; Crisp, M. S.; John, R.; Lazarus, J. H.; Ludgate, M.; Chatterjee, V. K. : Mutation of the gene encoding human TTF-2 associated with thyroid agenesis, cleft palate and choanal atresia.

Nature Genet. 19: 399-401, 1998. ; and

[75252] De Felice, M.; Ovitt, C.; Biffali, E.; Rodriguez-Mallon, A.; Arra, C.; Anastassiadis, K.; Macchia, P. E.; Mattei, M.-G.; Mariano, A.; Scholer, H.; Macchia, V.; Di Lauro, R. : A mouse model.

[75253] Further studies establishing the function and utilities of TTF2 are found in John Hopkins OMIM database record ID 602617, and in sited publications numbered 943 and 12372-8462 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Dynactin 4 (p62) (DCTN4, Accession XM_041993) is another VGAM2175 host target gene. DCTN4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCTN4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCTN4 BINDING SITE, designated SEQ ID:33663, to the nucleotide sequence of VGAM2175 RNA, herein designated VGAM RNA, also designated SEQ ID:4886.

[75254] Another function of VGAM2175 is therefore inhibition of Dynactin 4 (p62) (DCTN4, Accession XM_041993). Accordingly, utilities of VGAM2175 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with DCTN4. FLJ00001 (Accession XM_088525) is another VGAM2175 host target gene. FLJ00001 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00001, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00001 BINDING SITE, designated SEQ ID:39773, to the nucleotide sequence of VGAM2175 RNA, herein designated VGAM RNA, also designated SEQ ID:4886.

[75255] Another function of VGAM2175 is therefore inhibition of FLJ00001 (Accession XM_088525). Accordingly, utilities of VGAM2175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00001. LOC131308 (Accession XM_059501) is another VGAM2175 host target gene. LOC131308 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC131308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC131308 BINDING SITE, designated SEQ ID:37012, to

the nucleotide sequence of VGAM2175 RNA, herein designated VGAM RNA, also designated SEQ ID:4886.

[75256] Another function of VGAM2175 is therefore inhibition of LOC131308 (Accession XM_059501). Accordingly, utilities of VGAM2175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC131308. LOC257319 (Accession XM_171049) is another VGAM2175 host target gene. LOC257319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257319, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257319 BINDING SITE, designated SEQ ID:45830, to the nucleotide sequence of VGAM2175 RNA, herein designated VGAM RNA, also designated SEQ ID:4886.

[75257] Another function of VGAM2175 is therefore inhibition of LOC257319 (Accession XM_171049). Accordingly, utilities of VGAM2175 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257319. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2176 (VGAM2176) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75258] VGAM2176 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2176 was detected is described hereinabove with reference to Figs. 1-8.

[75259] VGAM2176 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit Fibroma Virus. VGAM2176 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75260] VGAM2176 gene encodes a VGAM2176 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2176 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2176 precursor RNA is designated SEQ ID:2162, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2162 is located at position 10073 relative to the genome of Rabbit Fibroma Virus.

[75261] VGAM2176 precursor RNA folds onto itself, forming VGAM2176 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75262] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2176 folded precursor RNA into VGAM2176 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2176 RNA is designated SEQ ID:4887, and is provided hereinbelow with reference to the sequence listing part.

[75263] VGAM2176 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2176 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2176 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75264] VGAM2176 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2176 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2176 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2176 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2176 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75265] The complementary binding of VGAM2176 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2176 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2176 host target RNA into VGAM2176 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75266] It is appreciated that VGAM2176 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2176 host target genes. The mRNA of each one of this plurality of VGAM2176 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2176 RNA, herein designated VGAM RNA, and which when bound by VGAM2176 RNA causes inhibition of translation of respective one or more VGAM2176 host target proteins.

[75267] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2176 gene, herein designated VGAM GENE, on one or more VGAM2176 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75268] It is yet further appreciated that a function of VGAM2176 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2176 include diagnosis, prevention and treatment of viral infection by Rabbit Fibroma Virus. Specific functions, and accordingly utilities, of VGAM2176 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2176 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75269] Nucleotide sequences of the VGAM2176 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2176 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2176 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2176 are further described hereinbelow with reference to Table 1.

[75270] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2176 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2176 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75271] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2176 gene, herein designated VGAM is inhibition of expression of VGAM2176 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2176 correlate with, and may be deduced from, the identity of the target genes which VGAM2176

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75272] FLJ00007 (Accession XM_048928) is a VGAM2176 host target gene. FLJ00007 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00007, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00007 BINDING SITE, designated SEQ ID:35315, to the nucleotide sequence of VGAM2176 RNA, herein designated VGAM RNA, also designated SEQ ID:4887.

[75273] A function of VGAM2176 is therefore inhibition of FLJ00007 (Accession XM_048928). Accordingly, utilities of VGAM2176 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00007. FLJ20060 (Accession NM_017645) is another VGAM2176 host target gene. FLJ20060 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20060, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20060

BINDING SITE, designated SEQ ID:19148, to the nucleotide sequence of VGAM2176 RNA, herein designated VGAM RNA, also designated SEQ ID:4887.

[75274] Another function of VGAM2176 is therefore inhibition of FLJ20060 (Accession NM_017645). Accordingly, utilities of VGAM2176 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20060. LOC91250 (Accession XM_037135) is another VGAM2176 host target gene. LOC91250 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91250, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91250 BINDING SITE, designated SEQ ID:32549, to the nucleotide sequence of VGAM2176 RNA, herein designated VGAM RNA, also designated SEQ ID:4887.

[75275] Another function of VGAM2176 is therefore inhibition of LOC91250 (Accession XM_037135). Accordingly, utilities of VGAM2176 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91250. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2177 (VGAM2177) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75276] VGAM2177 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2177 was detected is described hereinabove with reference to Figs. 1-8.

[75277] VGAM2177 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit Fibroma Virus. VGAM2177 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75278] VGAM2177 gene encodes a VGAM2177 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2177 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2177 precursor RNA is designated SEQ ID:2163, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2163 is located at position 14151 relative to the

genome of Rabbit Fibroma Virus.

[75279] VGAM2177 precursor RNA folds onto itself, forming VGAM2177 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75280] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2177 folded precursor RNA into VGAM2177 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2177 RNA is designated SEQ ID:4888, and is provided hereinbelow with reference to the sequence listing part.

[75281] VGAM2177 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2177 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2177 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75282] VGAM2177 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2177 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2177 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2177 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2177 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75283] The complementary binding of VGAM2177 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2177 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2177 host target RNA into VGAM2177 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75284] It is appreciated that VGAM2177 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2177 host target genes. The mRNA of each one of this plurality of VGAM2177 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2177 RNA, herein designated VGAM RNA, and which when bound by VGAM2177 RNA causes inhibition of translation of respective one or more VGAM2177 host target proteins.

[75285] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2177 gene, herein designated VGAM GENE, on one or more VGAM2177 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75286] It is yet further appreciated that a function of VGAM2177 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2177 include diagnosis, prevention and treatment of viral infection by Rabbit Fibroma Virus. Specific functions, and accordingly utilities, of VGAM2177

correlate with, and may be deduced from, the identity of the host target genes which VGAM2177 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75287] Nucleotide sequences of the VGAM2177 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2177 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2177 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2177 are further described hereinbelow with reference to Table 1.

[75288] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2177 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2177 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75289] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2177 gene, herein designated VGAM is inhibition of expression of VGAM2177 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2177 correlate with, and may be deduced

from, the identity of the target genes which VGAM2177 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75290] Inositol 1,4,5-triphosphate Receptor, Type 2 (ITPR2, Accession NM_002223) is a VGAM2177 host target gene. ITPR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITPR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITPR2 BINDING SITE, designated SEQ ID:7990, to the nucleotide sequence of VGAM2177 RNA, herein designated VGAM RNA, also designated SEQ ID:4888.

[75291] A function of VGAM2177 is therefore inhibition of Inositol 1,4,5-triphosphate Receptor, Type 2 (ITPR2, Accession NM_002223). Accordingly, utilities of VGAM2177 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPR2. LOC151878 (Accession XM_087329) is another VGAM2177 host target gene. LOC151878 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151878, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151878 BINDING SITE, designated SEQ ID:39170, to the nucleotide sequence of VGAM2177 RNA, herein designated VGAM RNA, also designated SEQ ID:4888.

[75292] Another function of VGAM2177 is therefore inhibition of LOC151878 (Accession XM_087329). Accordingly, utilities of VGAM2177 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151878. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2178 (VGAM2178) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75293] VGAM2178 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2178 was detected is described hereinabove with reference to Figs. 1-8.

[75294] VGAM2178 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit Fibroma Virus. VGAM2178 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[75295] VGAM2178 gene encodes a VGAM2178 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2178 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2178 precursor RNA is designated SEQ ID:2164, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2164 is located at position 22881 relative to the genome of Rabbit Fibroma Virus.

[75296] VGAM2178 precursor RNA folds onto itself, forming VGAM2178 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75297] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2178 folded precursor RNA into VGAM2178

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2178 RNA is designated SEQ ID:4889, and is provided hereinbelow with reference to the sequence listing part.

[75298] VGAM2178 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2178 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2178 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75299] VGAM2178 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2178 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2178 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2178 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2178 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75300] The complementary binding of VGAM2178 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2178 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2178 host target RNA into VGAM2178 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[75301] It is appreciated that VGAM2178 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2178 host target genes. The mRNA of each one of this plurality of VGAM2178 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2178 RNA, herein designated VGAM RNA, and which when bound by VGAM2178 RNA causes inhibition of translation of respective one or more VGAM2178 host target proteins.

[75302] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2178 gene, herein designated VGAM GENE, on one or more VGAM2178 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75303] It is yet further appreciated that a function of VGAM2178 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2178 include diagnosis, prevention and treatment of viral infection by Rabbit Fibroma Virus. Specific functions, and accordingly utilities, of VGAM2178 correlate with, and may be deduced from, the identity of the host target genes which VGAM2178 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75304] Nucleotide sequences of the VGAM2178 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2178 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2178 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2178 are further described hereinbelow with reference to Table 1.

[75305] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2178 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2178 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75306] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2178 gene, herein designated VGAM is inhibition of expression of VGAM2178 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2178 correlate with, and may be deduced from, the identity of the target genes which VGAM2178 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75307] Retinoblastoma Binding Protein 9 (RBBP9, Accession XM_046553) is a VGAM2178 host target gene. RBBP9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBBP9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBBP9 BINDING SITE, designated SEQ ID:34745, to the nucleotide sequence of VGAM2178 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4889.

[75308] A function of VGAM2178 is therefore inhibition of Retinoblastoma Binding Protein 9 (RBBP9, Accession XM_046553). Accordingly, utilities of VGAM2178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP9. KIAA1056 (Accession NM_014894) is another VGAM2178 host target gene. KIAA1056 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1056, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1056 BINDING SITE, designated SEQ ID:17046, to the nucleotide sequence of VGAM2178 RNA, herein designated VGAM RNA, also designated SEQ ID:4889.

[75309] Another function of VGAM2178 is therefore inhibition of KIAA1056 (Accession NM_014894). Accordingly, utilities of VGAM2178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1056. KIAA1199 (Accession XM_051860) is another VGAM2178 host target gene. KIAA1199 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1199, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1199 BINDING SITE, designated SEQ ID:35898, to the nucleotide sequence of VGAM2178 RNA, herein designated VGAM RNA, also designated SEQ ID:4889.

[75310] Another function of VGAM2178 is therefore inhibition of KIAA1199 (Accession XM_051860). Accordingly, utilities of VGAM2178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1199. KIAA1458 (Accession XM_044434) is another VGAM2178 host target gene. KIAA1458 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1458, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1458 BINDING SITE, designated SEQ ID:34203, to the nucleotide sequence of VGAM2178 RNA, herein designated VGAM RNA, also designated SEQ ID:4889.

[75311] Another function of VGAM2178 is therefore inhibition of KIAA1458 (Accession XM_044434). Accordingly, utilities

of VGAM2178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1458. LOC151234 (Accession XM_087136) is another VGAM2178 host target gene. LOC151234 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151234, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151234 BINDING SITE, designated SEQ ID:39080, to the nucleotide sequence of VGAM2178 RNA, herein designated VGAM RNA, also designated SEQ ID:4889.

[75312] Another function of VGAM2178 is therefore inhibition of LOC151234 (Accession XM_087136). Accordingly, utilities of VGAM2178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151234. LOC257443 (Accession XM_171072) is another VGAM2178 host target gene. LOC257443 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257443, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC257443 BINDING SITE, designated SEQ ID:45872, to the nucleotide sequence of VGAM2178 RNA, herein designated VGAM RNA, also designated SEQ ID:4889.

[75313] Another function of VGAM2178 is therefore inhibition of LOC257443 (Accession XM_171072). Accordingly, utilities of VGAM2178 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257443. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2179 (VGAM2179) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75314] VGAM2179 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2179 was detected is described hereinabove with reference to Figs. 1-8.

[75315] VGAM2179 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rabbit Fibroma Virus. VGAM2179 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75316] VGAM2179 gene encodes a VGAM2179 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2179 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2179 precursor RNA is designated SEQ ID:2165, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2165 is located at position 15205 relative to the genome of Rabbit Fibroma Virus.

[75317] VGAM2179 precursor RNA folds onto itself, forming VGAM2179 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75318] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2179 folded precursor RNA into VGAM2179 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2179 RNA is designated SEQ ID:4890, and is provided hereinbelow with reference to the sequence listing part.

[75319] VGAM2179 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2179 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2179 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75320] VGAM2179 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2179 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2179 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2179 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2179 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75321] The complementary binding of VGAM2179 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2179 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2179 host target RNA into VGAM2179 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75322] It is appreciated that VGAM2179 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2179 host target genes. The mRNA of each one of this plurality of VGAM2179 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2179 RNA, herein designated VGAM RNA, and which when bound by VGAM2179 RNA causes inhibition of translation of respective one or more VGAM2179 host target proteins.

[75323] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2179 gene, herein designated VGAM GENE, on one or more VGAM2179 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75324] It is yet further appreciated that a function of VGAM2179 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2179 include diagnosis, prevention and treatment of viral infection by Rabbit Fibroma Virus. Specific functions, and accordingly utilities, of VGAM2179 correlate with, and may be deduced from, the identity of the host target genes which VGAM2179 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75325] Nucleotide sequences of the VGAM2179 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2179 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2179 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2179 are further described hereinbelow with reference to Table 1.

[75326] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2179 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2179 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75327] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2179 gene, herein designated VGAM is inhibition of expression of VGAM2179 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2179 correlate with, and may be deduced from, the identity of the target genes which VGAM2179 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75328] LOC158865 (Accession XM_099000) is a VGAM2179 host target gene. LOC158865 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158865, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158865 BINDING SITE, designated SEQ ID:42037, to the nucleotide sequence of VGAM2179 RNA, herein designated VGAM RNA, also designated SEQ ID:4890.

[75329] A function of VGAM2179 is therefore inhibition of

LOC158865 (Accession XM_099000). Accordingly, utilities of VGAM2179 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158865. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2180 (VGAM2180) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75330] VGAM2180 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2180 was detected is described hereinabove with reference to Figs. 1-8.

[75331] VGAM2180 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like Disease Virus. VGAM2180 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75332] VGAM2180 gene encodes a VGAM2180 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2180 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2180 precursor RNA is designated SEQ ID:2166, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2166 is located at position 128284 relative to the genome of Yaba-like Disease Virus.

[75333] VGAM2180 precursor RNA folds onto itself, forming VGAM2180 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75334] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2180 folded precursor RNA into VGAM2180 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide se-

quence of VGAM2180 RNA is designated SEQ ID:4891, and is provided hereinbelow with reference to the sequence listing part.

[75335] VGAM2180 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2180 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2180 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75336] VGAM2180 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2180 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2180 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2180 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2180 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75337] The complementary binding of VGAM2180 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2180 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2180 host target RNA into VGAM2180 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75338] It is appreciated that VGAM2180 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2180 host target genes. The mRNA of each one of this plurality of VGAM2180 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2180 RNA, herein designated VGAM RNA, and which when bound by VGAM2180 RNA causes inhibition of translation of respective one or more VGAM2180 host target proteins.

[75339] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2180 gene, herein designated VGAM GENE, on one or more VGAM2180 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75340] It is yet further appreciated that a function of VGAM2180

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2180 include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGAM2180 correlate with, and may be deduced from, the identity of the host target genes which VGAM2180 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75341] Nucleotide sequences of the VGAM2180 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2180 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2180 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2180 are further described hereinbelow with reference to Table 1.

[75342] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2180 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2180 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75343] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2180 gene, herein designated VGAM is inhibition of expression of VGAM2180 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2180 correlate with, and may be deduced from, the identity of the target genes which VGAM2180 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75344] Zinc Finger Protein 387 (ZNF387, Accession NM_014682) is a VGAM2180 host target gene. ZNF387 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF387, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF387 BINDING SITE, designated SEQ ID:16178, to the nucleotide sequence of VGAM2180 RNA, herein designated VGAM RNA, also designated SEQ ID:4891.

[75345] A function of VGAM2180 is therefore inhibition of Zinc Finger Protein 387 (ZNF387, Accession NM_014682). Accordingly, utilities of VGAM2180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF387. LOC157507 (Accession

XM_088312) is another VGAM2180 host target gene. LOC157507 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157507, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157507 BINDING SITE, designated SEQ ID:39603, to the nucleotide sequence of VGAM2180 RNA, herein designated VGAM RNA, also designated SEQ ID:4891.

[75346] Another function of VGAM2180 is therefore inhibition of LOC157507 (Accession XM_088312). Accordingly, utilities of VGAM2180 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157507. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2181 (VGAM2181) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75347] VGAM2181 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2181 was detected is described hereinabove with reference to Figs. 1-8.

[75348] VGAM2181 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like Disease Virus. VGAM2181 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75349] VGAM2181 gene encodes a VGAM2181 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2181 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2181 precursor RNA is designated SEQ ID:2167, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2167 is located at position 125843 relative to the genome of Yaba-like Disease Virus.

[75350] VGAM2181 precursor RNA folds onto itself, forming VGAM2181 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75351] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2181 folded precursor RNA into VGAM2181 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 75%) nucleotide sequence of VGAM2181 RNA is designated SEQ ID:4892, and is provided hereinbelow with reference to the sequence listing part.

[75352] VGAM2181 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2181 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2181 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75353] VGAM2181 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2181 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2181 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2181 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2181 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75354] The complementary binding of VGAM2181 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2181 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2181 host target RNA into VGAM2181 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75355] It is appreciated that VGAM2181 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2181 host target genes. The mRNA of each one of this plurality of VGAM2181 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2181 RNA, herein designated VGAM RNA, and which when bound by VGAM2181 RNA causes inhibition of translation of respective one or more VGAM2181 host target proteins.

[75356] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2181 gene, herein designated VGAM GENE, on one or more VGAM2181 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75357] It is yet further appreciated that a function of VGAM2181 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGAM2181 correlate with, and may be deduced from, the identity of the host target genes which VGAM2181 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75358] Nucleotide sequences of the VGAM2181 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2181 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2181 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2181 are further described hereinbelow with reference to Table 1.

[75359] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2181 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2181 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75360] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2181 gene, herein designated VGAM is inhibition of expression of VGAM2181 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2181 correlate with, and may be deduced from, the identity of the target genes which VGAM2181 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75361] Integrin, Alpha 1 (ITGA1, Accession XM_032902) is a VGAM2181 host target gene. ITGA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGA1, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA1 BINDING SITE, designated SEQ ID:31790, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75362] A function of VGAM2181 is therefore inhibition of Integrin, Alpha 1 (ITGA1, Accession XM_032902). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA1. Pyruvate Dehydrogenase Kinase, Isoenzyme 4 (PDK4, Accession XM_173198) is another VGAM2181 host target gene. PDK4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDK4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDK4 BINDING SITE, designated SEQ ID:46440, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75363] Another function of VGAM2181 is therefore inhibition of Pyruvate Dehydrogenase Kinase, Isoenzyme 4 (PDK4, Ac-

cession XM_173198). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDK4. Podocalyxin-like (PODXL, Accession NM_005397) is another VGAM2181 host target gene. PODXL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PODXL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PODXL BINDING SITE, designated SEQ ID:11875, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75364] Another function of VGAM2181 is therefore inhibition of Podocalyxin-like (PODXL, Accession NM_005397), a gene which is an antiadhesin. Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PODXL. The function of PODXL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM247.Dual Specificity Phosphatase 10 (DUSP10, Accession NM_144729) is another VGAM2181 host target

gene. DUSP10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DUSP10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DUSP10 BINDING SITE, designated SEQ ID:29556, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75365] Another function of VGAM2181 is therefore inhibition of Dual Specificity Phosphatase 10 (DUSP10, Accession NM_144729). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP10. FLJ10342 (Accession NM_018064) is another VGAM2181 host target gene. FLJ10342 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10342, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10342 BINDING SITE, designated SEQ ID:19836, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ

ID:4892.

[75366] Another function of VGAM2181 is therefore inhibition of FLJ10342 (Accession NM_018064). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10342. FLJ11267 (Accession NM_019607) is another VGAM2181 host target gene. FLJ11267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11267 BINDING SITE, designated SEQ ID:21224, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75367] Another function of VGAM2181 is therefore inhibition of FLJ11267 (Accession NM_019607). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11267. FLJ13340 (Accession NM_057175) is another VGAM2181 host target gene. FLJ13340 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13340, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13340 BINDING SITE, designated SEQ ID:27706, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75368] Another function of VGAM2181 is therefore inhibition of FLJ13340 (Accession NM_057175). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13340. FLJ21777 (Accession NM_032209) is another VGAM2181 host target gene. FLJ21777 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ21777, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21777 BINDING SITE, designated SEQ ID:25923, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75369] Another function of VGAM2181 is therefore inhibition of FLJ21777 (Accession NM_032209). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ21777. FLJ23153 (Accession NM_024636) is another VGAM2181 host target gene. FLJ23153 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23153, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23153 BINDING SITE, designated SEQ ID:23907, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75370] Another function of VGAM2181 is therefore inhibition of FLJ23153 (Accession NM_024636). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23153. FLJ31978 (Accession NM_144669) is another VGAM2181 host target gene. FLJ31978 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ31978, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ31978 BINDING SITE, designated SEQ ID:29488, to the nucleotide

sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75371] Another function of VGAM2181 is therefore inhibition of FLJ31978 (Accession NM_144669). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31978. Heat Shock 90kDa Protein 1, Alpha-like 3 (HSPCAL3, Accession XM_084514) is another VGAM2181 host target gene. HSPCAL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSPCAL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPCAL3 BINDING SITE, designated SEQ ID:37615, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75372] Another function of VGAM2181 is therefore inhibition of Heat Shock 90kDa Protein 1, Alpha-like 3 (HSPCAL3, Accession XM_084514). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPCAL3. KIAA0276 (Accession XM_048199) is another VGAM2181

host target gene. KIAA0276 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0276, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0276 BINDING SITE, designated SEQ ID:35133, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75373] Another function of VGAM2181 is therefore inhibition of KIAA0276 (Accession XM_048199). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0276. TBDN100 (Accession NM_025085) is another VGAM2181 host target gene. TBDN100 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBDN100, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBDN100 BINDING SITE, designated SEQ ID:24697, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75374] Another function of VGAM2181 is therefore inhibition of TBDN100 (Accession NM_025085). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBDN100. Thioesterase, Adipose Associated (THEA, Accession XM_038922) is another VGAM2181 host target gene. THEA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by THEA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of THEA BINDING SITE, designated SEQ ID:32944, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75375] Another function of VGAM2181 is therefore inhibition of Thioesterase, Adipose Associated (THEA, Accession XM_038922). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THEA. TUSP (Accession NM_020245) is another VGAM2181 host target gene. TUSP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TUSP, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUSP BINDING SITE, designated SEQ ID:21519, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75376] Another function of VGAM2181 is therefore inhibition of TUSP (Accession NM_020245). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUSP. UBCE7IP5 (Accession NM_014948) is another VGAM2181 host target gene. UBCE7IP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UBCE7IP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBCE7IP5 BINDING SITE, designated SEQ ID:17269, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75377] Another function of VGAM2181 is therefore inhibition of UBCE7IP5 (Accession NM_014948). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

UBCE7IP5. LOC143196 (Accession XM_096389) is another VGAM2181 host target gene. LOC143196 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143196 BINDING SITE, designated SEQ ID:40329, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75378] Another function of VGAM2181 is therefore inhibition of LOC143196 (Accession XM_096389). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143196. LOC147837 (Accession XM_085915) is another VGAM2181 host target gene. LOC147837 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147837, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147837 BINDING SITE, designated SEQ ID:38391, to the nucleotide sequence of VGAM2181 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4892.

[75379] Another function of VGAM2181 is therefore inhibition of LOC147837 (Accession XM_085915). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147837. LOC149111 (Accession XM_086429) is another VGAM2181 host target gene. LOC149111 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149111, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149111 BINDING SITE, designated SEQ ID:38646, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75380] Another function of VGAM2181 is therefore inhibition of LOC149111 (Accession XM_086429). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149111. LOC149420 (Accession XM_086530) is another VGAM2181 host target gene. LOC149420 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149420, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149420 BINDING SITE, designated SEQ ID:38746, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75381] Another function of VGAM2181 is therefore inhibition of LOC149420 (Accession XM_086530). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149420. LOC151414 (Accession XM_087197) is another VGAM2181 host target gene. LOC151414 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151414, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151414 BINDING SITE, designated SEQ ID:39110, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75382] Another function of VGAM2181 is therefore inhibition of LOC151414 (Accession XM_087197). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC151414. LOC87769 (Accession XM_049058) is another VGAM2181 host target gene. LOC87769 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC87769, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC87769 BINDING SITE, designated SEQ ID:35335, to the nucleotide sequence of VGAM2181 RNA, herein designated VGAM RNA, also designated SEQ ID:4892.

[75383] Another function of VGAM2181 is therefore inhibition of LOC87769 (Accession XM_049058). Accordingly, utilities of VGAM2181 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC87769. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2182 (VGAM2182) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75384] VGAM2182 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2182 was detected is described hereinabove with reference to Figs. 1-8.

[75385] VGAM2182 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like Disease Virus. VGAM2182 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75386] VGAM2182 gene encodes a VGAM2182 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2182 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2182 precursor RNA is designated SEQ ID:2168, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2168 is located at position 132254 relative to the genome of Yaba-like Disease Virus.

[75387] VGAM2182 precursor RNA folds onto itself, forming VGAM2182 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75388] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2182 folded precursor RNA into VGAM2182 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2182 RNA is designated SEQ ID:4893, and is provided hereinbelow with reference to the sequence listing part.

[75389] VGAM2182 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2182 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2182 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75390] VGAM2182 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2182 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2182 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2182 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2182 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75391] The complementary binding of VGAM2182 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2182 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2182 host target RNA into VGAM2182 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75392] It is appreciated that VGAM2182 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2182 host target genes. The mRNA of each one of this plurality of VGAM2182 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2182 RNA, herein designated VGAM RNA, and which when bound by VGAM2182 RNA causes inhibition of translation of respective one or more VGAM2182 host target proteins.

[75393] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2182 gene, herein designated VGAM GENE, on one or more VGAM2182 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75394] It is yet further appreciated that a function of VGAM2182 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2182 include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGAM2182 correlate with, and may be deduced from, the identity of the host target genes which VGAM2182 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75395] Nucleotide sequences of the VGAM2182 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2182 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2182 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2182 are further described hereinbelow with reference to Table 1.

[75396] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2182 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2182 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75397] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2182 gene, herein designated VGAM is inhibition of expression of VGAM2182 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2182 correlate with, and may be deduced from, the identity of the target genes which VGAM2182 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75398] Kelch-like 1 (Drosophila) (KLHL1, Accession NM_020866) is a VGAM2182 host target gene. KLHL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KLHL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLHL1 BINDING SITE, designated SEQ ID:21920, to the nucleotide sequence of VGAM2182 RNA, herein designated VGAM RNA, also designated SEQ ID:4893.

[75399] A function of VGAM2182 is therefore inhibition of Kelch-like 1 (Drosophila) (KLHL1, Accession NM_020866). Accordingly, utilities of VGAM2182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLHL1. Baculoviral IAP Repeat-containing 1 (BIRC1, Accession NM_004536) is another VGAM2182 host target gene. BIRC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BIRC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIRC1 BINDING SITE, designated SEQ ID:10882, to the nucleotide sequence of VGAM2182 RNA, herein designated VGAM RNA, also designated SEQ ID:4893.

[75400] Another function of VGAM2182 is therefore inhibition of

Baculoviral IAP Repeat-containing 1 (BIRC1, Accession NM_004536). Accordingly, utilities of VGAM2182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIRC1. Chromosome 20 Open Reading Frame 103 (C20orf103, Accession NM_012261) is another VGAM2182 host target gene. C20orf103 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf103, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf103 BINDING SITE, designated SEQ ID:14569, to the nucleotide sequence of VGAM2182 RNA, herein designated VGAM RNA, also designated SEQ ID:4893.

[75401] Another function of VGAM2182 is therefore inhibition of Chromosome 20 Open Reading Frame 103 (C20orf103, Accession NM_012261). Accordingly, utilities of VGAM2182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf103. KIAA1404 (Accession XM_030494) is another VGAM2182 host target gene. KIAA1404 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1404, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1404 BINDING SITE, designated SEQ ID:31048, to the nucleotide sequence of VGAM2182 RNA, herein designated VGAM RNA, also designated SEQ ID:4893.

[75402] Another function of VGAM2182 is therefore inhibition of KIAA1404 (Accession XM_030494). Accordingly, utilities of VGAM2182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1404. Serine/threonine Kinase 38 Like (STK38L, Accession XM_044823) is another VGAM2182 host target gene. STK38L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STK38L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STK38L BINDING SITE, designated SEQ ID:34287, to the nucleotide sequence of VGAM2182 RNA, herein designated VGAM RNA, also designated SEQ ID:4893.

[75403] Another function of VGAM2182 is therefore inhibition of

Serine/threonine Kinase 38 Like (STK38L, Accession XM_044823). Accordingly, utilities of VGAM2182 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK38L. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2183 (VGAM2183) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75404] VGAM2183 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2183 was detected is described hereinabove with reference to Figs. 1-8.

[75405] VGAM2183 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like Disease Virus. VGAM2183 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75406] VGAM2183 gene encodes a VGAM2183 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2183 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2183 precursor RNA is designated SEQ ID:2169, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2169 is located at position 135497 relative to the genome of Yaba-like Disease Virus.

[75407] VGAM2183 precursor RNA folds onto itself, forming VGAM2183 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75408] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2183 folded precursor RNA into VGAM2183 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2183 RNA is designated SEQ ID:4894, and is provided hereinbelow with reference to the sequence listing part.

[75409] VGAM2183 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2183 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2183 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75410] VGAM2183 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2183 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2183 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2183 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2183 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75411] The complementary binding of VGAM2183 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2183 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2183 host target RNA into VGAM2183 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75412] It is appreciated that VGAM2183 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2183 host target genes. The mRNA of each one of this plurality of VGAM2183 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2183 RNA, herein designated VGAM RNA, and which when bound by VGAM2183 RNA causes inhibition of translation of respective one or more VGAM2183 host target proteins.

[75413] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2183 gene, herein designated VGAM GENE, on one or more VGAM2183 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75414] It is yet further appreciated that a function of VGAM2183

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2183 include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGAM2183 correlate with, and may be deduced from, the identity of the host target genes which VGAM2183 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75415] Nucleotide sequences of the VGAM2183 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2183 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2183 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2183 are further described hereinbelow with reference to Table 1.

[75416] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2183 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2183 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75417] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2183 gene, herein designated VGAM is inhibition of expression of VGAM2183 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2183 correlate with, and may be deduced from, the identity of the target genes which VGAM2183 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75418] A Disintegrin and Metalloproteinase Domain 12 (meltrin alpha) (ADAM12, Accession NM_003474) is a VGAM2183 host target gene. ADAM12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADAM12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAM12 BINDING SITE, designated SEQ ID:9545, to the nucleotide sequence of VGAM2183 RNA, herein designated VGAM RNA, also designated SEQ ID:4894.

[75419] A function of VGAM2183 is therefore inhibition of A Disintegrin and Metalloproteinase Domain 12 (meltrin alpha) (ADAM12, Accession NM_003474), a gene which involved in skeletal muscle regeneration, specifically at the onset of

cell fusion. Accordingly, utilities of VGAM2183 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAM12. The function of ADAM12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM675.Caldesmon 1 (CALD1, Accession NM_033138) is another VGAM2183 host target gene. CALD1 BINDING SITE1 and CALD1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CALD1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CALD1 BINDING SITE1 and CALD1 BINDING SITE2, designated SEQ ID:26990 and SEQ ID:27008 respectively, to the nucleotide sequence of VGAM2183 RNA, herein designated VGAM RNA, also designated SEQ ID:4894.

[75420] Another function of VGAM2183 is therefore inhibition of Caldesmon 1 (CALD1, Accession NM_033138), a gene which is implicated in the regulation of actomyosin interactions in smooth muscle and nonmuscle cells. Accordingly, utilities of VGAM2183 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with CALD1. The function of CALD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1960.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2184 (VGAM2184) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75421] VGAM2184 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2184 was detected is described hereinabove with reference to Figs. 1-8.

[75422] VGAM2184 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2184 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75423] VGAM2184 gene encodes a VGAM2184 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2184 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2184 precursor RNA is designated SEQ ID:2170, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2170 is located at position 187541 relative to the genome of Monkeypox Virus.

[75424] VGAM2184 precursor RNA folds onto itself, forming VGAM2184 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[75425] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2184 folded precursor RNA into VGAM2184 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2184 RNA is designated SEQ ID:4895, and is provided hereinbelow with reference to the sequence listing part.

[75426] VGAM2184 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2184 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2184 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75427] VGAM2184 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2184 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2184 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2184 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2184 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75428] The complementary binding of VGAM2184 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2184 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2184 host target RNA into VGAM2184 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75429] It is appreciated that VGAM2184 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2184 host target genes. The mRNA of each one of this plurality of VGAM2184 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2184 RNA, herein designated VGAM RNA, and which when bound by VGAM2184 RNA causes inhibition of translation of respective one or more VGAM2184 host target proteins.

[75430] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2184 gene, herein designated VGAM GENE, on one or more VGAM2184 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75431] It is yet further appreciated that a function of VGAM2184 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2184 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2184 correlate with, and may be deduced from, the identity of the host target genes which VGAM2184 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75432] Nucleotide sequences of the VGAM2184 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2184 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2184 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2184 are further described hereinbelow with reference to Table 1.

[75433] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2184 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2184 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75434] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2184 gene, herein designated VGAM is inhibition of expression of VGAM2184 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2184 correlate with, and may be deduced from, the identity of the target genes which VGAM2184 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75435] Angiopoietin 1 (ANGPT1, Accession NM_001146) is a VGAM2184 host target gene. ANGPT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANGPT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of ANGPT1 BINDING SITE, designated SEQ ID:6813, to the nucleotide sequence of VGAM2184 RNA, herein designated VGAM RNA, also designated SEQ ID:4895.

[75436] A function of VGAM2184 is therefore inhibition of Angiopoietin 1 (ANGPT1, Accession NM_001146), a gene which binds and activates tie2 receptor by inducing its tyrosine phosphorylation. Accordingly, utilities of VGAM2184 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANGPT1. The function of ANGPT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM291.FLJ10970 (Accession NM_018286) is another VGAM2184 host target gene. FLJ10970 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10970, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10970 BINDING SITE, designated SEQ ID:20279, to the nucleotide sequence of VGAM2184 RNA, herein designated VGAM RNA, also designated SEQ ID:4895.

[75437] Another function of VGAM2184 is therefore inhibition of FLJ10970 (Accession NM_018286). Accordingly, utilities of VGAM2184 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10970. KIAA0976 (Accession NM_014917) is another VGAM2184 host target gene. KIAA0976 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0976, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0976 BINDING SITE, designated SEQ ID:17168, to the nucleotide sequence of VGAM2184 RNA, herein designated VGAM RNA, also designated SEQ ID:4895.

[75438] Another function of VGAM2184 is therefore inhibition of KIAA0976 (Accession NM_014917). Accordingly, utilities of VGAM2184 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0976. LOC118491 (Accession XM_058324) is another VGAM2184 host target gene. LOC118491 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC118491, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC118491 BINDING SITE, designated SEQ ID:36595, to the nucleotide sequence of VGAM2184 RNA, herein designated VGAM RNA, also designated SEQ ID:4895.

[75439] Another function of VGAM2184 is therefore inhibition of LOC118491 (Accession XM_058324). Accordingly, utilities of VGAM2184 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118491. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2185 (VGAM2185) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75440] VGAM2185 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2185 was detected is described hereinabove with reference to Figs. 1-8.

[75441] VGAM2185 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2185 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[75442] VGAM2185 gene encodes a VGAM2185 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2185 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2185 precursor RNA is designated SEQ ID:2171, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2171 is located at position 195252 relative to the genome of Camelpox Virus.

[75443] VGAM2185 precursor RNA folds onto itself, forming VGAM2185 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75444] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2185 folded precursor RNA into VGAM2185

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2185 RNA is designated SEQ ID:4896, and is provided hereinbelow with reference to the sequence listing part.

[75445] VGAM2185 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2185 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2185 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75446] VGAM2185 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2185 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2185 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2185 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2185 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75447] The complementary binding of VGAM2185 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2185 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2185 host target RNA into VGAM2185 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[75448] It is appreciated that VGAM2185 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2185 host target genes. The mRNA of each one of this plurality of VGAM2185 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2185 RNA, herein designated VGAM RNA, and which when bound by VGAM2185 RNA causes inhibition of translation of respective one or more VGAM2185 host target proteins.

[75449] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2185 gene, herein designated VGAM GENE, on one or more VGAM2185 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75450] It is yet further appreciated that a function of VGAM2185 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2185 correlate with, and may be deduced from, the identity of the host target genes which VGAM2185 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75451] Nucleotide sequences of the VGAM2185 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2185 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2185 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2185 are further described hereinbelow with reference to Table 1.

[75452] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2185 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2185 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75453] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2185 gene, herein designated VGAM is inhibition of expression of VGAM2185 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2185 correlate with, and may be deduced from, the identity of the target genes which VGAM2185 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75454] Estrogen-related Receptor Gamma (ESRRG, Accession XM_039053) is a VGAM2185 host target gene. ESRRG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ESRRG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESRRG BINDING SITE, designated SEQ ID:32999, to the nucleotide sequence of VGAM2185 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4896.

[75455] A function of VGAM2185 is therefore inhibition of Estrogen-related Receptor Gamma (ESRRG, Accession XM_039053), a gene which Estrogen-related receptor gamma. Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESRRG. The function of ESRRG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM359.Integrin, Alpha L (antigen CD11A (p180), Lymphocyte Function-associated Antigen 1; Alpha Polypeptide) (ITGAL, Accession NM_002209) is another VGAM2185 host target gene. ITGAL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGAL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGAL BINDING SITE, designated SEQ ID:7972, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75456] Another function of VGAM2185 is therefore inhibition of Integrin, Alpha L (antigen CD11A (p180), Lymphocyte

Function-associated Antigen 1; Alpha Polypeptide) (ITGAL, Accession NM_002209), a gene which s a receptor for icam1, icam2, icam3 and icam4. it is involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, cytotoxic t-cell mediated killing, and antibody dependent killing by granulocytes and monocytes. Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAL. The function of ITGAL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Nuclear Fragile X Mental Retardation Protein Interacting Protein 1 (NUFIP1, Accession NM_012345) is another VGAM2185 host target gene. NUFIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUFIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUFIP1 BINDING SITE, designated SEQ ID:14737, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75457] Another function of VGAM2185 is therefore inhibition of Nuclear Fragile X Mental Retardation Protein Interacting Protein 1 (NUFIP1, Accession NM_012345), a gene which binds and colocalizes with nuclear fragile X mental retardation protein. Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUFIP1. The function of NUFIP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM733.POU Domain, Class 2, Associating Factor 1 (POU2AF1, Accession NM_006235) is another VGAM2185 host target gene. POU2AF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POU2AF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POU2AF1 BINDING SITE, designated SEQ ID:12892, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75458] Another function of VGAM2185 is therefore inhibition of POU Domain, Class 2, Associating Factor 1 (POU2AF1, Ac-

cession NM_006235), a gene which is a transcriptional coactivator that specifically associates with either oct1 or oct2. Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POU2AF1. The function of POU2AF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM171.Recombination Activating Gene 2 (RAG2, Accession XM_089839) is another VGAM2185 host target gene. RAG2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAG2 BINDING SITE, designated SEQ ID:39985, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75459] Another function of VGAM2185 is therefore inhibition of Recombination Activating Gene 2 (RAG2, Accession XM_089839). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAG2. Tensin (TNS, Acces-

sion NM_022648) is another VGAM2185 host target gene. TNS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNS BINDING SITE, designated SEQ ID:22903, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75460] Another function of VGAM2185 is therefore inhibition of Tensin (TNS, Accession NM_022648). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNS. DKFZP434I092 (Accession XM_042042) is another VGAM2185 host target gene. DKFZP434I092 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434I092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434I092 BINDING SITE, designated SEQ ID:33673, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75461] Another function of VGAM2185 is therefore inhibition of DKFZP434I092 (Accession XM_042042). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434I092. FLJ10656 (Accession NM_018170) is another VGAM2185 host target gene. FLJ10656 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10656, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10656 BINDING SITE, designated SEQ ID:19988, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75462] Another function of VGAM2185 is therefore inhibition of FLJ10656 (Accession NM_018170). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10656. GABA(A) Receptor-associated Protein Like 1 (GABARAPL1, Accession NM_031412) is another VGAM2185 host target gene. GABARAPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL1, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABARAPL1 BINDING SITE, designated SEQ ID:25392, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75463] Another function of VGAM2185 is therefore inhibition of GABA(A) Receptor-associated Protein Like 1 (GABARAPL1, Accession NM_031412). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL1. GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568) is another VGAM2185 host target gene. GABARAPL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABARAPL3 BINDING SITE, designated SEQ ID:26300, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75464] Another function of VGAM2185 is therefore inhibition of

GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL3. HT002 (Accession NM_014066) is another VGAM2185 host target gene. HT002 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HT002, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HT002 BINDING SITE, designated SEQ ID:15281, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75465] Another function of VGAM2185 is therefore inhibition of HT002 (Accession NM_014066). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HT002. KIAA0475 (Accession NM_014864) is another VGAM2185 host target gene. KIAA0475 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:16949, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75466] Another function of VGAM2185 is therefore inhibition of KIAA0475 (Accession NM_014864). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0475. KIAA0712 (Accession NM_014715) is another VGAM2185 host target gene. KIAA0712 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0712, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0712 BINDING SITE, designated SEQ ID:16262, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75467] Another function of VGAM2185 is therefore inhibition of KIAA0712 (Accession NM_014715). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0712. KIAA1301 (Accession XM_038999) is another VGAM2185 host target gene. KIAA1301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1301 BINDING SITE, designated SEQ ID:32978, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75468] Another function of VGAM2185 is therefore inhibition of KIAA1301 (Accession XM_038999). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1301. Seizure Related 6 Homolog (mouse) (SEZ6, Accession XM_058869) is another VGAM2185 host target gene. SEZ6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEZ6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEZ6 BINDING SITE, designated SEQ ID:36774, to the nucleotide sequence of VGAM2185 RNA, herein

designated VGAM RNA, also designated SEQ ID:4896.

[75469] Another function of VGAM2185 is therefore inhibition of Seizure Related 6 Homolog (mouse) (SEZ6, Accession XM_058869). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEZ6. VMP1 (Accession NM_030938) is another VGAM2185 host target gene. VMP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VMP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VMP1 BINDING SITE, designated SEQ ID:25204, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75470] Another function of VGAM2185 is therefore inhibition of VMP1 (Accession NM_030938). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VMP1. LOC115110 (Accession XM_049825) is another VGAM2185 host target gene. LOC115110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115110, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115110 BINDING SITE, designated SEQ ID:35503, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75471] Another function of VGAM2185 is therefore inhibition of LOC115110 (Accession XM_049825). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115110. LOC132235 (Accession XM_072302) is another VGAM2185 host target gene. LOC132235 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC132235, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132235 BINDING SITE, designated SEQ ID:37483, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75472] Another function of VGAM2185 is therefore inhibition of LOC132235 (Accession XM_072302). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC132235. LOC142941 (Accession XM_096363) is another VGAM2185 host target gene. LOC142941 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC142941, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC142941 BINDING SITE, designated SEQ ID:40322, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75473] Another function of VGAM2185 is therefore inhibition of LOC142941 (Accession XM_096363). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142941. LOC158549 (Accession XM_098963) is another VGAM2185 host target gene. LOC158549 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158549, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158549 BINDING SITE, designated SEQ ID:42007, to

the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75474] Another function of VGAM2185 is therefore inhibition of LOC158549 (Accession XM_098963). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158549. LOC221882 (Accession XM_166507) is another VGAM2185 host target gene. LOC221882 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221882, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221882 BINDING SITE, designated SEQ ID:44434, to the nucleotide sequence of VGAM2185 RNA, herein designated VGAM RNA, also designated SEQ ID:4896.

[75475] Another function of VGAM2185 is therefore inhibition of LOC221882 (Accession XM_166507). Accordingly, utilities of VGAM2185 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221882. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2186 (VGAM2186) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75476] VGAM2186 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2186 was detected is described hereinabove with reference to Figs. 1-8.

[75477] VGAM2186 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2186 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75478] VGAM2186 gene encodes a VGAM2186 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2186 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2186 precursor RNA is designated SEQ ID:2172, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2172 is located at position 184211 relative to the genome of Monkeypox Virus.

[75479] VGAM2186 precursor RNA folds onto itself, forming VGAM2186 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75480] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2186 folded precursor RNA into VGAM2186 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM2186 RNA is designated SEQ ID:4897, and is provided hereinbelow with reference to the sequence listing part.

[75481] VGAM2186 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2186 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2186 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75482] VGAM2186 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2186 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2186 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2186 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2186 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75483] The complementary binding of VGAM2186 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2186 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2186 host target RNA into VGAM2186 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75484] It is appreciated that VGAM2186 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2186 host target genes. The mRNA of each one of this plurality of VGAM2186 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2186 RNA, herein designated VGAM RNA, and which when bound by VGAM2186 RNA causes inhibition of translation of respective one or more VGAM2186 host target proteins.

[75485] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2186 gene, herein designated VGAM GENE, on one or more VGAM2186 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75486] It is yet further appreciated that a function of VGAM2186 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2186 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2186 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75487] Nucleotide sequences of the VGAM2186 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2186 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2186 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2186 are further described hereinbelow with reference to Table 1.

[75488] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2186 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2186 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75489] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2186 gene, herein designated VGAM is inhibition of expression of VGAM2186 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2186 correlate with, and may be deduced from, the identity of the target genes which VGAM2186

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75490] Glycoprotein M6A (GPM6A, Accession NM_005277) is a VGAM2186 host target gene. GPM6A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPM6A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPM6A BINDING SITE, designated SEQ ID:11778, to the nucleotide sequence of VGAM2186 RNA, herein designated VGAM RNA, also designated SEQ ID:4897.

[75491] A function of VGAM2186 is therefore inhibition of Glycoprotein M6A (GPM6A, Accession NM_005277), a gene which may play a role in neuronal development. Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPM6A. The function of GPM6A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM326.Membrane-spanning 4-domains, Subfamily A, Member 1 (MS4A1, Accession NM_000139) is another VGAM2186 host target gene.

MS4A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MS4A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MS4A1 BINDING SITE, designated SEQ ID:5633, to the nucleotide sequence of VGAM2186 RNA, herein designated VGAM RNA, also designated SEQ ID:4897.

[75492] Another function of VGAM2186 is therefore inhibition of Membrane-spanning 4-domains, Subfamily A, Member 1 (MS4A1, Accession NM_000139), a gene which may be involved in the regulation of b-cell activation and proliferation. Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MS4A1. The function of MS4A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM362.Nuclear Receptor Subfamily 3, Group C, Member 1 (glucocorticoid receptor) (NR3C1, Accession NM_000176) is another VGAM2186 host target gene. NR3C1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by NR3C1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR3C1 BINDING SITE, designated SEQ ID:5684, to the nucleotide sequence of VGAM2186 RNA, herein designated VGAM RNA, also designated SEQ ID:4897.

[75493] Another function of VGAM2186 is therefore inhibition of Nuclear Receptor Subfamily 3, Group C, Member 1 (glucocorticoid receptor) (NR3C1, Accession NM_000176). Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR3C1. Smcx Homolog, X Chromosome (mouse) (SMCX, Accession NM_004187) is another VGAM2186 host target gene. SMCX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMCX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMCX BINDING SITE, designated SEQ ID:10396, to the nucleotide sequence of VGAM2186 RNA, herein designated VGAM RNA, also designated SEQ ID:4897.

[75494] Another function of VGAM2186 is therefore inhibition of Smcx Homolog, X Chromosome (mouse) (SMCX, Accession NM_004187), a gene which escapes X inactivation. Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMCX. The function of SMCX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM60.Calcyphosphine 2 (CAPS2, Accession XM_047354) is another VGAM2186 host target gene. CAPS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAPS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAPS2 BINDING SITE, designated SEQ ID:34954, to the nucleotide sequence of VGAM2186 RNA, herein designated VGAM RNA, also designated SEQ ID:4897.

[75495] Another function of VGAM2186 is therefore inhibition of Calcyphosphine 2 (CAPS2, Accession XM_047354). Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with CAPS2. DKFZP434I092 (Accession XM_042042) is another VGAM2186 host target gene. DKFZP434I092 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434I092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434I092 BINDING SITE, designated SEQ ID:33672, to the nucleotide sequence of VGAM2186 RNA, herein designated VGAM RNA, also designated SEQ ID:4897.

[75496] Another function of VGAM2186 is therefore inhibition of DKFZP434I092 (Accession XM_042042). Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434I092. ICK (Accession NM_014920) is another VGAM2186 host target gene. ICK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:17192, to the nucleotide sequence of

VGAM2186 RNA, herein designated VGAM RNA, also designated SEQ ID:4897.

[75497] Another function of VGAM2186 is therefore inhibition of ICK (Accession NM_014920). Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICK. KIAA0746 (Accession XM_045277) is another VGAM2186 host target gene. KIAA0746 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0746, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0746 BINDING SITE, designated SEQ ID:34417, to the nucleotide sequence of VGAM2186 RNA, herein designated VGAM RNA, also designated SEQ ID:4897.

[75498] Another function of VGAM2186 is therefore inhibition of KIAA0746 (Accession XM_045277). Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0746. Monocyte to Macrophage Differentiation-associated (MMD, Accession XM_008269) is another VGAM2186 host target gene. MMD BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by MMD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MMD BINDING SITE, designated SEQ ID:30075, to the nucleotide sequence of VGAM2186 RNA, herein designated VGAM RNA, also designated SEQ ID:4897.

[75499] Another function of VGAM2186 is therefore inhibition of Monocyte to Macrophage Differentiation-associated (MMD, Accession XM_008269). Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMD. VIT1 (Accession NM_018693) is another VGAM2186 host target gene. VIT1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by VIT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VIT1 BINDING SITE, designated SEQ ID:20767, to the nucleotide sequence of VGAM2186 RNA, herein designated VGAM RNA, also designated SEQ ID:4897.

[75500] Another function of VGAM2186 is therefore inhibition of VIT1 (Accession NM_018693). Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIT1. LOC150311 (Accession XM_086858) is another VGAM2186 host target gene. LOC150311 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150311, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150311 BINDING SITE, designated SEQ ID:38925, to the nucleotide sequence of VGAM2186 RNA, herein designated VGAM RNA, also designated SEQ ID:4897.

[75501] Another function of VGAM2186 is therefore inhibition of LOC150311 (Accession XM_086858). Accordingly, utilities of VGAM2186 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150311. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2187 (VGAM2187) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[75502] VGAM2187 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2187 was detected is described hereinabove with reference to Figs. 1-8.

[75503] VGAM2187 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2187 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75504] VGAM2187 gene encodes a VGAM2187 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2187 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2187 precursor RNA is designated SEQ ID:2173, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2173 is located at position 186422 relative to the genome of Monkeypox Virus.

[75505] VGAM2187 precursor RNA folds onto itself, forming VGAM2187 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75506] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2187 folded precursor RNA into VGAM2187 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2187 RNA is designated SEQ ID:4898, and is provided hereinbelow with reference to the sequence listing part.

[75507] VGAM2187 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2187 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2187 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75508] VGAM2187 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2187 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2187 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2187 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2187 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75509] The complementary binding of VGAM2187 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2187 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2187 host target RNA into VGAM2187 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75510] It is appreciated that VGAM2187 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2187 host target genes. The mRNA of each one of this plurality of VGAM2187 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2187 RNA, herein designated VGAM RNA, and which when bound by VGAM2187 RNA causes inhibition of translation of respective one or more VGAM2187 host target proteins.

[75511] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2187 gene, herein designated VGAM GENE, on one or more VGAM2187 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75512] It is yet further appreciated that a function of VGAM2187 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2187 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2187 correlate with, and may be deduced from, the identity of the host target genes which VGAM2187 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[75513] Nucleotide sequences of the VGAM2187 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2187 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2187 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2187 are further described hereinbelow with reference to Table 1.

[75514] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2187 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2187 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75515] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2187 gene, herein designated VGAM is inhibition of expression of VGAM2187 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2187 correlate with, and may be deduced from, the identity of the target genes which VGAM2187 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75516] Gap Junction Protein, Alpha 1, 43kDa (connexin 43) (GJA1, Accession NM_000165) is a VGAM2187 host target gene. GJA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GJA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GJA1 BINDING SITE, designated SEQ ID:5677, to the nucleotide sequence of VGAM2187 RNA, herein designated VGAM RNA, also designated SEQ ID:4898.

[75517] A function of VGAM2187 is therefore inhibition of Gap Junction Protein, Alpha 1, 43kDa (connexin 43) (GJA1, Accession NM_000165), a gene which may act in synchronizing heart contraction and embryonic development. Accordingly, utilities of VGAM2187 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GJA1. The function of GJA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM341.Protocadherin 11 X-linked (PCDH11X, Accession NM_032968) is another VGAM2187 host target gene. PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2 are HOST TARGET binding sites

found in untranslated regions of mRNA encoded by PCDH11X, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2, designated SEQ ID:26783 and SEQ ID:26798 respectively, to the nucleotide sequence of VGAM2187 RNA, herein designated VGAM RNA, also designated SEQ ID:4898.

[75518] Another function of VGAM2187 is therefore inhibition of Protocadherin 11 X-linked (PCDH11X, Accession NM_032968), a gene which is thought to play a fundamental role in cell-cell recognition essential for the segmental development and function of the central nervous system. Accordingly, utilities of VGAM2187 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11X. The function of PCDH11X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.FLJ20184 (Accession NM_017700) is another VGAM2187 host target gene. FLJ20184 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ20184, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20184 BINDING SITE, designated SEQ ID:19273, to the nucleotide sequence of VGAM2187 RNA, herein designated VGAM RNA, also designated SEQ ID:4898.

[75519] Another function of VGAM2187 is therefore inhibition of FLJ20184 (Accession NM_017700). Accordingly, utilities of VGAM2187 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20184. Syntaxin 3A (STX3A, Accession NM_004177) is another VGAM2187 host target gene. STX3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STX3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STX3A BINDING SITE, designated SEQ ID:10386, to the nucleotide sequence of VGAM2187 RNA, herein designated VGAM RNA, also designated SEQ ID:4898.

[75520] Another function of VGAM2187 is therefore inhibition of Syntaxin 3A (STX3A, Accession NM_004177). Accordingly,

utilities of VGAM2187 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STX3A. Zinc Finger Protein 313 (ZNF313, Accession NM_018683) is another VGAM2187 host target gene. ZNF313 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF313, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF313 BINDING SITE, designated SEQ ID:20754, to the nucleotide sequence of VGAM2187 RNA, herein designated VGAM RNA, also designated SEQ ID:4898.

[75521] Another function of VGAM2187 is therefore inhibition of Zinc Finger Protein 313 (ZNF313, Accession NM_018683). Accordingly, utilities of VGAM2187 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF313. LOC130026 (Accession NM_138468) is another VGAM2187 host target gene. LOC130026 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130026, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130026 BINDING SITE, designated SEQ ID:28819, to the nucleotide sequence of VGAM2187 RNA, herein designated VGAM RNA, also designated SEQ ID:4898.

[75522] Another function of VGAM2187 is therefore inhibition of LOC130026 (Accession NM_138468). Accordingly, utilities of VGAM2187 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130026. LOC144438 (Accession XM_084860) is another VGAM2187 host target gene. LOC144438 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144438, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144438 BINDING SITE, designated SEQ ID:37737, to the nucleotide sequence of VGAM2187 RNA, herein designated VGAM RNA, also designated SEQ ID:4898.

[75523] Another function of VGAM2187 is therefore inhibition of LOC144438 (Accession XM_084860). Accordingly, utilities of VGAM2187 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC144438. LOC149722 (Accession XM_097709) is another VGAM2187 host target gene. LOC149722 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149722, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149722 BINDING SITE, designated SEQ ID:41042, to the nucleotide sequence of VGAM2187 RNA, herein designated VGAM RNA, also designated SEQ ID:4898.

[75524] Another function of VGAM2187 is therefore inhibition of LOC149722 (Accession XM_097709). Accordingly, utilities of VGAM2187 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149722. LOC220988 (Accession XM_165561) is another VGAM2187 host target gene. LOC220988 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220988, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220988 BINDING SITE, designated SEQ ID:43681, to the nucleotide sequence of VGAM2187 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4898.

[75525] Another function of VGAM2187 is therefore inhibition of LOC220988 (Accession XM_165561). Accordingly, utilities of VGAM2187 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220988. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2188 (VGAM2188) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75526] VGAM2188 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2188 was detected is described hereinabove with reference to Figs. 1-8.

[75527] VGAM2188 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2188 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75528] VGAM2188 gene encodes a VGAM2188 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2188 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2188 precursor RNA is designated SEQ ID:2174, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2174 is located at position 185906 relative to the genome of Monkeypox Virus.

[75529] VGAM2188 precursor RNA folds onto itself, forming VGAM2188 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75530] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2188 folded precursor RNA into VGAM2188 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2188 RNA is designated SEQ ID:4899, and is provided hereinbelow with reference to the sequence listing part.

[75531] VGAM2188 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2188 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2188 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75532] VGAM2188 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2188 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2188 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2188 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2188 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75533] The complementary binding of VGAM2188 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2188 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2188 host target RNA into VGAM2188 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75534] It is appreciated that VGAM2188 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2188 host target genes. The mRNA of

each one of this plurality of VGAM2188 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2188 RNA, herein designated VGAM RNA, and which when bound by VGAM2188 RNA causes inhibition of translation of respective one or more VGAM2188 host target proteins.

[75535] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2188 gene, herein designated VGAM GENE, on one or more VGAM2188 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[75536] It is yet further appreciated that a function of VGAM2188 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2188 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2188 correlate with, and may be deduced from, the identity of the host target genes which VGAM2188 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75537] Nucleotide sequences of the VGAM2188 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2188 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2188 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2188 are further described hereinbelow with reference to Table 1.

[75538] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2188 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2188 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75539] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2188 gene, herein designated VGAM is inhibition of expression of VGAM2188 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2188 correlate with, and may be deduced from, the identity of the target genes which VGAM2188 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75540] Calcitonin Receptor-like (CALCRL, Accession NM_005795) is a VGAM2188 host target gene. CALCRL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CALCRL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CALCRL BINDING SITE, designated SEQ ID:12377, to the nucleotide sequence of VGAM2188 RNA, herein designated VGAM RNA, also designated SEQ ID:4899.

[75541] A function of VGAM2188 is therefore inhibition of Calcitonin Receptor-like (CALCRL, Accession NM_005795), a gene which is a receptor for calcitonin gene-related pep-

tide type 1. Accordingly, utilities of VGAM2188 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CALCRL. The function of CALCRL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM995.Desmocollin 1 (DSC1, Accession NM_004948) is another VGAM2188 host target gene. DSC1 BINDING SITE1 and DSC1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DSC1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DSC1 BINDING SITE1 and DSC1 BINDING SITE2, designated SEQ ID:11389 and SEQ ID:23659 respectively, to the nucleotide sequence of VGAM2188 RNA, herein designated VGAM RNA, also designated SEQ ID:4899.

[75542] Another function of VGAM2188 is therefore inhibition of Desmocollin 1 (DSC1, Accession NM_004948), a gene which is a component of intercellular desmosome junctions. Accordingly, utilities of VGAM2188 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DSC1. The function of DSC1 and

its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1502.Runt-related Transcription Factor 3 (RUNX3, Accession NM_004350) is another VGAM2188 host target gene. RUNX3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RUNX3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RUNX3 BINDING SITE, designated SEQ ID:10551, to the nucleotide sequence of VGAM2188 RNA, herein designated VGAM RNA, also designated SEQ ID:4899.

[75543] Another function of VGAM2188 is therefore inhibition of Runt-related Transcription Factor 3 (RUNX3, Accession NM_004350), a gene which binds to the core site, 5'-pygpyggt-3', of a number of enhancers and promoters. Accordingly, utilities of VGAM2188 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RUNX3. The function of RUNX3 and its association with various diseases and clinical conditions, has been established by previous studies, as de-

scribed hereinabove with reference to VGAM1151.KIAA0731 (Accession XM_039975) is another VGAM2188 host target gene. KIAA0731 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0731, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0731 BINDING SITE, designated SEQ ID:33242, to the nucleotide sequence of VGAM2188 RNA, herein designated VGAM RNA, also designated SEQ ID:4899.

[75544] Another function of VGAM2188 is therefore inhibition of KIAA0731 (Accession XM_039975). Accordingly, utilities of VGAM2188 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0731. Kruppel-like Factor 5 (intestinal) (KLF5, Accession NM_001730) is another VGAM2188 host target gene. KLF5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLF5 BINDING SITE, designated SEQ ID:7459,

to the nucleotide sequence of VGAM2188 RNA, herein designated VGAM RNA, also designated SEQ ID:4899.

[75545] Another function of VGAM2188 is therefore inhibition of Kruppel-like Factor 5 (intestinal) (KLF5, Accession NM_001730). Accordingly, utilities of VGAM2188 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF5. LOC149773 (Accession XM_086628) is another VGAM2188 host target gene. LOC149773 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149773, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149773 BINDING SITE, designated SEQ ID:38799, to the nucleotide sequence of VGAM2188 RNA, herein designated VGAM RNA, also designated SEQ ID:4899.

[75546] Another function of VGAM2188 is therefore inhibition of LOC149773 (Accession XM_086628). Accordingly, utilities of VGAM2188 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149773. LOC153387 (Accession XM_098369) is another VGAM2188 host target gene. LOC153387 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153387, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153387 BINDING SITE, designated SEQ ID:41634, to the nucleotide sequence of VGAM2188 RNA, herein designated VGAM RNA, also designated SEQ ID:4899.

[75547] Another function of VGAM2188 is therefore inhibition of LOC153387 (Accession XM_098369). Accordingly, utilities of VGAM2188 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153387. LOC51157 (Accession NM_016202) is another VGAM2188 host target gene. LOC51157 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51157, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51157 BINDING SITE, designated SEQ ID:18296, to the nucleotide sequence of VGAM2188 RNA, herein designated VGAM RNA, also designated SEQ ID:4899.

[75548] Another function of VGAM2188 is therefore inhibition of

LOC51157 (Accession NM_016202). Accordingly, utilities of VGAM2188 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51157. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2189 (VGAM2189) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75549] VGAM2189 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2189 was detected is described hereinabove with reference to Figs. 1-8.

[75550] VGAM2189 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2189 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75551] VGAM2189 gene encodes a VGAM2189 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2189 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2189 precursor RNA is designated SEQ ID:2175, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2175 is located at position 189835 relative to the genome of Monkeypox Virus.

[75552] VGAM2189 precursor RNA folds onto itself, forming VGAM2189 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75553] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2189 folded precursor RNA into VGAM2189 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2189 RNA is designated SEQ ID:4900, and is provided hereinbelow with reference to the sequence listing part.

[75554] VGAM2189 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2189 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2189 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75555] VGAM2189 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2189 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2189 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2189 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2189 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75556] The complementary binding of VGAM2189 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2189 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2189 host target RNA into VGAM2189 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75557] It is appreciated that VGAM2189 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2189 host target genes. The mRNA of each one of this plurality of VGAM2189 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2189 RNA, herein designated VGAM RNA, and which when bound by VGAM2189 RNA causes inhibition of translation of respective one or more VGAM2189 host target proteins.

[75558] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2189 gene, herein designated VGAM GENE, on one or more VGAM2189 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75559] It is yet further appreciated that a function of VGAM2189

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2189 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2189 correlate with, and may be deduced from, the identity of the host target genes which VGAM2189 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75560] Nucleotide sequences of the VGAM2189 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2189 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2189 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2189 are further described hereinbelow with reference to Table 1.

[75561] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2189 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2189 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75562] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2189 gene, herein designated VGAM is inhibition of expression of VGAM2189 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2189 correlate with, and may be deduced from, the identity of the target genes which VGAM2189 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75563] Coagulation Factor III (thromboplastin, tissue factor) (F3, Accession XM_040465) is a VGAM2189 host target gene. F3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by F3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of F3 BINDING SITE, designated SEQ ID:33298, to the nucleotide sequence of VGAM2189 RNA, herein designated VGAM RNA, also designated SEQ ID:4900.

[75564] A function of VGAM2189 is therefore inhibition of Coagulation Factor III (thromboplastin, tissue factor) (F3, Accession XM_040465), a gene which functions in normal hemostasis. Accordingly, utilities of VGAM2189 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with F3. The function of F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM817.Chromosome 1 Open Reading Frame 24 (C1orf24, Accession NM_052966) is another VGAM2189 host target gene. C1orf24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:27528, to the nucleotide sequence of VGAM2189 RNA, herein designated VGAM RNA, also designated SEQ ID:4900.

[75565] Another function of VGAM2189 is therefore inhibition of Chromosome 1 Open Reading Frame 24 (C1orf24, Accession NM_052966). Accordingly, utilities of VGAM2189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24. Epsin 2 (EPN2, Accession NM_014964) is another VGAM2189 host target gene. EPN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

EPN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPN2 BINDING SITE, designated SEQ ID:17345, to the nucleotide sequence of VGAM2189 RNA, herein designated VGAM RNA, also designated SEQ ID:4900.

[75566] Another function of VGAM2189 is therefore inhibition of Epsin 2 (EPN2, Accession NM_014964). Accordingly, utilities of VGAM2189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPN2. STAF65(gamma) (Accession NM_014860) is another VGAM2189 host target gene. STAF65(gamma) BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STAF65(gamma), corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAF65(gamma) BINDING SITE, designated SEQ ID:16922, to the nucleotide sequence of VGAM2189 RNA, herein designated VGAM RNA, also designated SEQ ID:4900.

[75567] Another function of VGAM2189 is therefore inhibition of STAF65(gamma) (Accession NM_014860). Accordingly,

utilities of VGAM2189 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAF65(gamma). Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2190 (VGAM2190) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75568] VGAM2190 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2190 was detected is described hereinabove with reference to Figs. 1-8.

[75569] VGAM2190 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2190 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75570] VGAM2190 gene encodes a VGAM2190 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2190 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2190 precursor RNA is designated SEQ ID:2176, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2176 is located at position 181733 relative to the genome of Monkeypox Virus.

[75571] VGAM2190 precursor RNA folds onto itself, forming VGAM2190 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75572] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2190 folded precursor RNA into VGAM2190 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2190 RNA is designated SEQ ID:4901, and

is provided hereinbelow with reference to the sequence listing part.

[75573] VGAM2190 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2190 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2190 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75574] VGAM2190 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2190 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2190 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2190 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2190 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75575] The complementary binding of VGAM2190 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2190 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2190 host target RNA into VGAM2190 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75576] It is appreciated that VGAM2190 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2190 host target genes. The mRNA of each one of this plurality of VGAM2190 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2190 RNA, herein designated VGAM RNA, and which when bound by VGAM2190 RNA causes inhibition of translation of respective one or more VGAM2190 host target proteins.

[75577] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2190 gene, herein designated VGAM GENE, on one or more VGAM2190 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75578] It is yet further appreciated that a function of VGAM2190 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2190 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2190 correlate with, and may be deduced from, the identity of the host target genes which VGAM2190 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75579] Nucleotide sequences of the VGAM2190 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2190 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2190 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2190 are further described hereinbelow with reference to Table 1.

[75580] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2190 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2190 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75581] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2190 gene, herein designated VGAM is inhibition of expression of VGAM2190 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2190 correlate with, and may be deduced from, the identity of the target genes which VGAM2190 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75582] Ribonucleotide Reductase M2 Polypeptide (RRM2, Accession NM_001034) is a VGAM2190 host target gene. RRM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RRM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RRM2 BINDING SITE, designated SEQ ID:6699, to the nucleotide sequence of VGAM2190 RNA, herein designated VGAM RNA, also designated SEQ ID:4901.

[75583] A function of VGAM2190 is therefore inhibition of Ribonucleotide Reductase M2 Polypeptide (RRM2, Accession NM_001034). Accordingly, utilities of VGAM2190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RRM2. KIAA1762 (Accession XM_033370) is another VGAM2190 host target

gene. KIAA1762 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1762, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1762 BINDING SITE, designated SEQ ID:31910, to the nucleotide sequence of VGAM2190 RNA, herein designated VGAM RNA, also designated SEQ ID:4901.

[75584] Another function of VGAM2190 is therefore inhibition of KIAA1762 (Accession XM_033370). Accordingly, utilities of VGAM2190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1762. LOC157623 (Accession XM_088346) is another VGAM2190 host target gene. LOC157623 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157623, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157623 BINDING SITE, designated SEQ ID:39614, to the nucleotide sequence of VGAM2190 RNA, herein designated VGAM RNA, also designated SEQ ID:4901.

[75585] Another function of VGAM2190 is therefore inhibition of LOC157623 (Accession XM_088346). Accordingly, utilities of VGAM2190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157623. LOC91759 (Accession XM_040467) is another VGAM2190 host target gene. LOC91759 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91759, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91759 BINDING SITE, designated SEQ ID:33299, to the nucleotide sequence of VGAM2190 RNA, herein designated VGAM RNA, also designated SEQ ID:4901.

[75586] Another function of VGAM2190 is therefore inhibition of LOC91759 (Accession XM_040467). Accordingly, utilities of VGAM2190 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91759. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2191 (VGAM2191) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[75587] VGAM2191 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2191 was detected is described hereinabove with reference to Figs. 1-8.

[75588] VGAM2191 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2191 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75589] VGAM2191 gene encodes a VGAM2191 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2191 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2191 precursor RNA is designated SEQ ID:2177, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2177 is located at position 812 relative to the genome of Monkeypox Virus.

[75590] VGAM2191 precursor RNA folds onto itself, forming VGAM2191 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75591] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2191 folded precursor RNA into VGAM2191 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2191 RNA is designated SEQ ID:4902, and is provided hereinbelow with reference to the sequence listing part.

[75592] VGAM2191 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2191 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2191 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75593] VGAM2191 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2191 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2191 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2191 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2191 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75594] The complementary binding of VGAM2191 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2191 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2191 host target RNA into VGAM2191 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75595] It is appreciated that VGAM2191 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2191 host target genes. The mRNA of each one of this plurality of VGAM2191 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2191 RNA, herein designated VGAM RNA, and which when bound by VGAM2191 RNA causes inhibition of translation of respective one or more VGAM2191 host target proteins.

[75596] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2191 gene, herein designated VGAM GENE, on one or more VGAM2191 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75597] It is yet further appreciated that a function of VGAM2191 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2191 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2191 correlate with, and may be deduced from, the identity of the host target genes which VGAM2191 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[75598] Nucleotide sequences of the VGAM2191 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2191 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2191 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2191 are further described hereinbelow with reference to Table 1.

[75599] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2191 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2191 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75600] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2191 gene, herein designated VGAM is inhibition of expression of VGAM2191 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2191 correlate with, and may be deduced from, the identity of the target genes which VGAM2191 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75601] EFG1 (Accession XM_170611) is a VGAM2191 host target gene. EFG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EFG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFG1 BINDING SITE, designated SEQ ID:45397, to the nucleotide sequence of VGAM2191 RNA, herein designated VGAM RNA, also designated SEQ ID:4902.

[75602] A function of VGAM2191 is therefore inhibition of EFG1 (Accession XM_170611), a gene which promotes the gtp-dependent translocation of the nascent protein chain from the a-site to the p-site of the ribosome in the mitochondria. Accordingly, utilities of VGAM2191 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFG1. The function of EFG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1753.Solute Carrier Family 6 (neurotransmitter transporter, dopamine), Member 3 (SLC6A3, Accession NM_001044) is another VGAM2191 host target gene. SLC6A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by SLC6A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC6A3 BINDING SITE, designated SEQ ID:6713, to the nucleotide sequence of VGAM2191 RNA, herein designated VGAM RNA, also designated SEQ ID:4902.

[75603] Another function of VGAM2191 is therefore inhibition of Solute Carrier Family 6 (neurotransmitter transporter, dopamine), Member 3 (SLC6A3, Accession NM_001044), a gene which terminates the action of dopamine by its high affinity sodium-dependent reuptake into presynaptic terminals. Accordingly, utilities of VGAM2191 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A3. The function of SLC6A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1753.H2AV (Accession NM_138635) is another VGAM2191 host target gene. H2AV BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by H2AV, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H2AV BINDING SITE, designated SEQ ID:28912, to the nucleotide sequence of VGAM2191 RNA, herein designated VGAM RNA, also designated SEQ ID:4902.

[75604] Another function of VGAM2191 is therefore inhibition of H2AV (Accession NM_138635). Accordingly, utilities of VGAM2191 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H2AV. HMP19 (Accession XM_113455) is another VGAM2191 host target gene. HMP19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HMP19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMP19 BINDING SITE, designated SEQ ID:42273, to the nucleotide sequence of VGAM2191 RNA, herein designated VGAM RNA, also designated SEQ ID:4902.

[75605] Another function of VGAM2191 is therefore inhibition of HMP19 (Accession XM_113455). Accordingly, utilities of VGAM2191 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMP19.

Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2192 (VGAM2192) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75606] VGAM2192 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2192 was detected is described hereinabove with reference to Figs. 1-8.

[75607] VGAM2192 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2192 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75608] VGAM2192 gene encodes a VGAM2192 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2192 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2192 precursor RNA is designated SEQ ID:2178, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2178 is located at position 2502 relative to the genome of Monkeypox Virus.

[75609] VGAM2192 precursor RNA folds onto itself, forming VGAM2192 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75610] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2192 folded precursor RNA into VGAM2192 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2192 RNA is designated SEQ ID:4903, and is provided hereinbelow with reference to the sequence listing part.

[75611] VGAM2192 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2192 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2192 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75612] VGAM2192 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2192 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2192 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2192 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2192 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75613] The complementary binding of VGAM2192 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2192 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2192 host target RNA into VGAM2192 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75614] It is appreciated that VGAM2192 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2192 host target genes. The mRNA of each one of this plurality of VGAM2192 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2192 RNA, herein designated VGAM RNA, and which when bound by VGAM2192 RNA causes inhibition of translation of respective one or more

VGAM2192 host target proteins.

[75615] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2192 gene, herein designated VGAM GENE, on one or more VGAM2192 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75616] It is yet further appreciated that a function of VGAM2192 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2192 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific

functions, and accordingly utilities, of VGAM2192 correlate with, and may be deduced from, the identity of the host target genes which VGAM2192 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75617] Nucleotide sequences of the VGAM2192 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2192 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2192 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2192 are further described hereinbelow with reference to Table 1.

[75618] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2192 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2192 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75619] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2192 gene, herein designated VGAM is inhibition of expression of VGAM2192 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2192 correlate with, and may be deduced from, the identity of the target genes which VGAM2192 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75620] BTB and CNC Homology 1, Basic Leucine Zipper Transcription Factor 1 (BACH1, Accession NM_001186) is a VGAM2192 host target gene. BACH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BACH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BACH1 BINDING SITE, designated SEQ ID:6855, to the nucleotide sequence of VGAM2192 RNA, herein designated VGAM RNA, also designated SEQ ID:4903.

[75621] A function of VGAM2192 is therefore inhibition of BTB and CNC Homology 1, Basic Leucine Zipper Transcription Factor 1 (BACH1, Accession NM_001186), a gene which acts as repressor or activator, binds to nf-e2 binding sites. Accordingly, utilities of VGAM2192 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BACH1. The function of BACH1 and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to VGAM724.Estrogen Receptor 1 (ESR1, Accession NM_000125) is another VGAM2192 host target gene. ESR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ESR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESR1 BINDING SITE, designated SEQ ID:5597, to the nucleotide sequence of VGAM2192 RNA, herein designated VGAM RNA, also designated SEQ ID:4903.

[75622] Another function of VGAM2192 is therefore inhibition of Estrogen Receptor 1 (ESR1, Accession NM_000125), a gene which involved in hormone-mediated inhibition of gene expression. Accordingly, utilities of VGAM2192 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESR1. The function of ESR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM695.IDI2 (Accession NM_033261) is another VGAM2192 host target gene. IDI2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

IDI2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IDI2 BINDING SITE, designated SEQ ID:27089, to the nucleotide sequence of VGAM2192 RNA, herein designated VGAM RNA, also designated SEQ ID:4903.

[75623] Another function of VGAM2192 is therefore inhibition of IDI2 (Accession NM_033261). Accordingly, utilities of VGAM2192 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IDI2. KIAA1979 (Accession XM_113984) is another VGAM2192 host target gene. KIAA1979 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1979, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1979 BINDING SITE, designated SEQ ID:42587, to the nucleotide sequence of VGAM2192 RNA, herein designated VGAM RNA, also designated SEQ ID:4903.

[75624] Another function of VGAM2192 is therefore inhibition of KIAA1979 (Accession XM_113984). Accordingly, utilities of VGAM2192 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1979. LBP-9 (Accession NM_014553) is another VGAM2192 host target gene. LBP-9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LBP-9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LBP-9 BINDING SITE, designated SEQ ID:15880, to the nucleotide sequence of VGAM2192 RNA, herein designated VGAM RNA, also designated SEQ ID:4903.

[75625] Another function of VGAM2192 is therefore inhibition of LBP-9 (Accession NM_014553). Accordingly, utilities of VGAM2192 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LBP-9. Lipoma HMGIC Fusion Partner-like 2 (LHFPL2, Accession XM_046054) is another VGAM2192 host target gene. LHFPL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LHFPL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LHFPL2 BINDING SITE, designated SEQ

ID:34656, to the nucleotide sequence of VGAM2192 RNA, herein designated VGAM RNA, also designated SEQ ID:4903.

[75626] Another function of VGAM2192 is therefore inhibition of Lipoma HMGIC Fusion Partner-like 2 (LHFPL2, Accession XM_046054). Accordingly, utilities of VGAM2192 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHFPL2. Serologically Defined Colon Cancer Antigen 43 (SDCCAG43, Accession XM_046834) is another VGAM2192 host target gene. SDCCAG43 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SDCCAG43, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDCCAG43 BINDING SITE, designated SEQ ID:34844, to the nucleotide sequence of VGAM2192 RNA, herein designated VGAM RNA, also designated SEQ ID:4903.

[75627] Another function of VGAM2192 is therefore inhibition of Serologically Defined Colon Cancer Antigen 43 (SDCCAG43, Accession XM_046834). Accordingly, utilities of VGAM2192 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with SDCCAG43. TRAD (Accession NM_007064) is another VGAM2192 host target gene. TRAD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRAD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRAD BINDING SITE, designated SEQ ID:13928, to the nucleotide sequence of VGAM2192 RNA, herein designated VGAM RNA, also designated SEQ ID:4903.

[75628] Another function of VGAM2192 is therefore inhibition of TRAD (Accession NM_007064). Accordingly, utilities of VGAM2192 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAD. LOC135293 (Accession XM_072402) is another VGAM2192 host target gene. LOC135293 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC135293, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC135293 BINDING SITE, designated SEQ ID:37495, to

the nucleotide sequence of VGAM2192 RNA, herein designated VGAM RNA, also designated SEQ ID:4903.

[75629] Another function of VGAM2192 is therefore inhibition of LOC135293 (Accession XM_072402). Accordingly, utilities of VGAM2192 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135293. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2193 (VGAM2193) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75630] VGAM2193 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2193 was detected is described hereinabove with reference to Figs. 1-8.

[75631] VGAM2193 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus.
VGAM2193 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75632] VGAM2193 gene encodes a VGAM2193 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2193 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2193 precursor RNA is designated SEQ ID:2179, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2179 is located at position 18641 relative to the genome of Cowpox Virus.

[75633] VGAM2193 precursor RNA folds onto itself, forming VGAM2193 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75634] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2193 folded precursor RNA into VGAM2193 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2193 RNA is designated SEQ ID:4904, and is provided hereinbelow with reference to the sequence listing part.

[75635] VGAM2193 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2193 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2193 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75636] VGAM2193 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2193 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2193 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2193 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2193 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75637] The complementary binding of VGAM2193 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2193 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2193 host target RNA into VGAM2193 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75638] It is appreciated that VGAM2193 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2193 host target genes. The mRNA of each one of this plurality of VGAM2193 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2193 RNA, herein designated VGAM RNA, and which when bound by VGAM2193 RNA causes inhibition of translation of respective one or more VGAM2193 host target proteins.

[75639] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2193 gene, herein designated VGAM GENE, on one or more VGAM2193 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75640] It is yet further appreciated that a function of VGAM2193 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2193 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2193 correlate with, and may be deduced from, the identity of the host target genes which VGAM2193 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75641] Nucleotide sequences of the VGAM2193 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2193 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2193 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2193 are further described hereinbelow with reference to Table 1.

[75642] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2193 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2193 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75643] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2193 gene, herein designated VGAM is inhibition of expression of VGAM2193 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2193 correlate with, and may be deduced from, the identity of the target genes which VGAM2193 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75644] Nuclear Receptor Coactivator 3 (NCOA3, Accession NM_006534) is a VGAM2193 host target gene. NCOA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NCOA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOA3 BINDING SITE, designated SEQ ID:13286, to the nucleotide sequence of VGAM2193 RNA, herein designated VGAM RNA, also designated SEQ ID:4904.

[75645] A function of VGAM2193 is therefore inhibition of Nuclear Receptor Coactivator 3 (NCOA3, Accession NM_006534), a

gene which directly binds nuclear receptors and stimulates the transcriptional activities in hormone-dependent fashion. Accordingly, utilities of VGAM2193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA3. The function of NCOA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM215.Phenylalanine Hydroxylase (PAH, Accession NM_000277) is another VGAM2193 host target gene. PAH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAH BINDING SITE, designated SEQ ID:5823, to the nucleotide sequence of VGAM2193 RNA, herein designated VGAM RNA, also designated SEQ ID:4904.

[75646] Another function of VGAM2193 is therefore inhibition of Phenylalanine Hydroxylase (PAH, Accession NM_000277). Accordingly, utilities of VGAM2193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAH. Sialyltransferase 9

(CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9, Accession NM_003896) is another VGAM2193 host target gene. SIAT9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIAT9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIAT9 BINDING SITE, designated SEQ ID:9977, to the nucleotide sequence of VGAM2193 RNA, herein designated VGAM RNA, also designated SEQ ID:4904.

[75647] Another function of VGAM2193 is therefore inhibition of Sialyltransferase 9 (CMP-NeuAc:lactosylceramide alpha-2,3-sialyltransferase; GM3 synthase) (SIAT9, Accession NM_003896). Accordingly, utilities of VGAM2193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIAT9. LOC51075 (Accession NM_015959) is another VGAM2193 host target gene. LOC51075 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51075, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of LOC51075 BINDING SITE, designated SEQ ID:18068, to the nucleotide sequence of VGAM2193 RNA, herein designated VGAM RNA, also designated SEQ ID:4904.

[75648] Another function of VGAM2193 is therefore inhibition of LOC51075 (Accession NM_015959). Accordingly, utilities of VGAM2193 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51075. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2194 (VGAM2194) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75649] VGAM2194 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2194 was detected is described hereinabove with reference to Figs. 1-8.

[75650] VGAM2194 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Monkeypox Virus. VGAM2194 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[75651] VGAM2194 gene encodes a VGAM2194 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2194 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2194 precursor RNA is designated SEQ ID:2180, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2180 is located at position 269 relative to the genome of Monkeypox Virus.

[75652] VGAM2194 precursor RNA folds onto itself, forming VGAM2194 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75653] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2194 folded precursor RNA into VGAM2194 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2194 RNA is designated SEQ ID:4905, and is provided hereinbelow with reference to the sequence listing part.

[75654] VGAM2194 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2194 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2194 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75655] VGAM2194 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2194 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2194 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2194 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2194 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75656] The complementary binding of VGAM2194 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2194 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2194 host target RNA into VGAM2194 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75657] It is appreciated that VGAM2194 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2194 host target genes. The mRNA of each one of this plurality of VGAM2194 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2194 RNA, herein designated VGAM RNA, and which when bound by VGAM2194 RNA causes inhibition of translation of respective one or more VGAM2194 host target proteins.

[75658] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2194 gene, herein designated VGAM GENE, on one or more VGAM2194 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75659] It is yet further appreciated that a function of VGAM2194 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2194 include diagnosis, prevention and treatment of viral infection by Monkeypox Virus. Specific functions, and accordingly utilities, of VGAM2194 correlate with, and may be deduced from, the identity of the host target genes which VGAM2194 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75660] Nucleotide sequences of the VGAM2194 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2194 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2194 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2194 are further described hereinbelow with reference to Table 1.

[75661] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2194 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2194 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75662] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2194 gene, herein designated VGAM is inhibition of expression of VGAM2194 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2194 correlate with, and may be deduced from, the identity of the target genes which VGAM2194 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75663] A Disintegrin and Metalloproteinase Domain 12 (meltrin alpha) (ADAM12, Accession NM_003474) is a VGAM2194 host target gene. ADAM12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADAM12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAM12 BINDING SITE, designated SEQ ID:9546, to the nucleotide sequence of VGAM2194 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4905.

[75664] A function of VGAM2194 is therefore inhibition of A Disintegrin and Metalloproteinase Domain 12 (meltrin alpha) (ADAM12, Accession NM_003474), a gene which involved in skeletal muscle regeneration, specifically at the onset of cell fusion. Accordingly, utilities of VGAM2194 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAM12. The function of ADAM12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM675.Adducin 3 (gamma) (ADD3, Accession NM_016824) is another VGAM2194 host target gene. ADD3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADD3 BINDING SITE, designated SEQ ID:18817, to the nucleotide sequence of VGAM2194 RNA, herein designated VGAM RNA, also designated SEQ ID:4905.

[75665] Another function of VGAM2194 is therefore inhibition of Adducin 3 (gamma) (ADD3, Accession NM_016824), a

gene which membrane-cytoskeleton-associated protein that promotes the assembly of the spectrin-actin network. Accordingly, utilities of VGAM2194 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADD3. The function of ADD3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM579.Chromosome 9 Open Reading Frame 12 (C9orf12, Accession NM_022755) is another VGAM2194 host target gene. C9orf12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C9orf12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C9orf12 BINDING SITE, designated SEQ ID:22989, to the nucleotide sequence of VGAM2194 RNA, herein designated VGAM RNA, also designated SEQ ID:4905.

[75666] Another function of VGAM2194 is therefore inhibition of Chromosome 9 Open Reading Frame 12 (C9orf12, Accession NM_022755). Accordingly, utilities of VGAM2194 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf12. KIAA1813

(Accession XM_046743) is another VGAM2194 host target gene. KIAA1813 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1813, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1813 BINDING SITE, designated SEQ ID:34807, to the nucleotide sequence of VGAM2194 RNA, herein designated VGAM RNA, also designated SEQ ID:4905.

[75667] Another function of VGAM2194 is therefore inhibition of KIAA1813 (Accession XM_046743). Accordingly, utilities of VGAM2194 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1813. Ornithine Decarboxylase Antizyme Inhibitor (OAZIN, Accession NM_015878) is another VGAM2194 host target gene. OAZIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OAZIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OAZIN BINDING SITE, designated SEQ ID:18023, to the nucleotide sequence of

VGAM2194 RNA, herein designated VGAM RNA, also designated SEQ ID:4905.

[75668] Another function of VGAM2194 is therefore inhibition of Ornithine Decarboxylase Antizyme Inhibitor (OAZIN, Accession NM_015878). Accordingly, utilities of VGAM2194 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OAZIN. Oncostatin M Receptor (OSMR, Accession NM_003999) is another VGAM2194 host target gene. OSMR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSMR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSMR BINDING SITE, designated SEQ ID:10149, to the nucleotide sequence of VGAM2194 RNA, herein designated VGAM RNA, also designated SEQ ID:4905.

[75669] Another function of VGAM2194 is therefore inhibition of Oncostatin M Receptor (OSMR, Accession NM_003999). Accordingly, utilities of VGAM2194 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSMR. TSPAN-2 (Accession NM_005725) is another VGAM2194 host target gene.

TSPAN-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TSPAN-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TSPAN-2 BINDING SITE, designated SEQ ID:12281, to the nucleotide sequence of VGAM2194 RNA, herein designated VGAM RNA, also designated SEQ ID:4905.

[75670] Another function of VGAM2194 is therefore inhibition of TSPAN-2 (Accession NM_005725). Accordingly, utilities of VGAM2194 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSPAN-2. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2195 (VGAM2195) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75671] VGAM2195 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2195 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[75672] VGAM2195 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like Disease Virus. VGAM2195 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75673] VGAM2195 gene encodes a VGAM2195 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2195 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2195 precursor RNA is designated SEQ ID:2181, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2181 is located at position 9471 relative to the genome of Yaba-like Disease Virus.

[75674] VGAM2195 precursor RNA folds onto itself, forming VGAM2195 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75675] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2195 folded precursor RNA into VGAM2195 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2195 RNA is designated SEQ ID:4906, and is provided hereinbelow with reference to the sequence listing part.

[75676] VGAM2195 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2195 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2195 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75677] VGAM2195 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2195 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2195 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2195 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2195 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75678] The complementary binding of VGAM2195 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2195 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2195 host target RNA into VGAM2195 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75679] It is appreciated that VGAM2195 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2195 host target genes. The mRNA of each one of this plurality of VGAM2195 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2195 RNA, herein designated VGAM RNA, and which when bound by VGAM2195 RNA causes inhibition of translation of respective one or more VGAM2195 host target proteins.

[75680] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2195 gene, herein designated VGAM GENE, on one or more VGAM2195 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75681] It is yet further appreciated that a function of VGAM2195 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2195 include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGAM2195 correlate with, and may be deduced from, the identity of the host target genes which VGAM2195 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75682] Nucleotide sequences of the VGAM2195 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2195 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2195 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2195 are further described hereinbelow with reference to Table 1.

[75683] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2195 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2195 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75684] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2195 gene, herein designated VGAM is inhibition of expression of VGAM2195 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2195 correlate with, and may be deduced from, the identity of the target genes which VGAM2195 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75685] LOC256846 (Accession XM_170921) is a VGAM2195 host target gene. LOC256846 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256846, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256846 BINDING SITE, designated SEQ ID:45695, to the nucleotide sequence of VGAM2195 RNA, herein designated VGAM RNA, also designated SEQ ID:4906.

[75686] A function of VGAM2195 is therefore inhibition of LOC256846 (Accession XM_170921). Accordingly, utilities of VGAM2195 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256846. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2196 (VGAM2196) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75687] VGAM2196 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2196 was detected is described hereinabove with reference to Figs. 1-8.

[75688] VGAM2196 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like Disease Virus. VGAM2196 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[75689] VGAM2196 gene encodes a VGAM2196 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2196 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2196 precursor RNA is designated SEQ ID:2182, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2182 is located at position 11842 relative to the genome of Yaba-like Disease Virus.

[75690] VGAM2196 precursor RNA folds onto itself, forming VGAM2196 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75691] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2196 folded precursor RNA into VGAM2196

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2196 RNA is designated SEQ ID:4907, and is provided hereinbelow with reference to the sequence listing part.

[75692] VGAM2196 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2196 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2196 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75693] VGAM2196 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2196 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2196 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2196 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2196 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75694] The complementary binding of VGAM2196 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2196 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2196 host target RNA into VGAM2196 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[75695] It is appreciated that VGAM2196 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2196 host target genes. The mRNA of each one of this plurality of VGAM2196 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2196 RNA, herein designated VGAM RNA, and which when bound by VGAM2196 RNA causes inhibition of translation of respective one or more VGAM2196 host target proteins.

[75696] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2196 gene, herein designated VGAM GENE, on one or more VGAM2196 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75697] It is yet further appreciated that a function of VGAM2196 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2196 include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGAM2196 correlate with, and may be deduced from, the identity of the host target genes which VGAM2196 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75698] Nucleotide sequences of the VGAM2196 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2196 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2196 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2196 are further described hereinbelow with reference to Table 1.

[75699] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2196 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2196 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75700] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2196 gene, herein designated VGAM is inhibition of expression of VGAM2196 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2196 correlate with, and may be deduced from, the identity of the target genes which VGAM2196 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75701] Tripartite Motif-containing 34 (TRIM34, Accession NM_021616) is a VGAM2196 host target gene. TRIM34 BINDING SITE1 and TRIM34 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TRIM34, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM34 BINDING SITE1 and TRIM34 BINDING SITE2, designated SEQ ID:22248 and SEQ

ID:28172 respectively, to the nucleotide sequence of VGAM2196 RNA, herein designated VGAM RNA, also designated SEQ ID:4907.

[75702] A function of VGAM2196 is therefore inhibition of Tripartite Motif-containing 34 (TRIM34, Accession NM_021616). Accordingly, utilities of VGAM2196 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM34. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2197 (VGAM2197) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75703] VGAM2197 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2197 was detected is described hereinabove with reference to Figs. 1-8.

[75704] VGAM2197 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like Disease Virus. VGAM2197 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75705] VGAM2197 gene encodes a VGAM2197 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2197 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2197 precursor RNA is designated SEQ ID:2183, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2183 is located at position 6543 relative to the genome of Yaba-like Disease Virus.

[75706] VGAM2197 precursor RNA folds onto itself, forming VGAM2197 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75707] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2197 folded precursor RNA into VGAM2197 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2197 RNA is designated SEQ ID:4908, and is provided hereinbelow with reference to the sequence listing part.

[75708] VGAM2197 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2197 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2197 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75709] VGAM2197 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2197 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2197 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2197 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2197 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75710] The complementary binding of VGAM2197 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2197 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2197 host target RNA into VGAM2197 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75711] It is appreciated that VGAM2197 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2197 host target genes. The mRNA of each one of this plurality of VGAM2197 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2197 RNA, herein designated VGAM RNA, and which when bound by VGAM2197 RNA causes inhibition of translation of respective one or more VGAM2197 host target proteins.

[75712] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2197 gene, herein designated VGAM GENE, on one or more VGAM2197 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75713] It is yet further appreciated that a function of VGAM2197 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGAM2197 correlate with, and may be deduced from, the identity of the host target genes which VGAM2197 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75714] Nucleotide sequences of the VGAM2197 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2197 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2197 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2197 are further described hereinbelow with reference to Table 1.

[75715] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2197 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2197 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75716] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2197 gene, herein designated VGAM is inhibition of expression of VGAM2197 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2197 correlate with, and may be deduced from, the identity of the target genes which VGAM2197 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75717] Caspase Recruitment Domain Family, Member 4 (CARD4, Accession NM_006092) is a VGAM2197 host target gene. CARD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CARD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CARD4 BINDING SITE, designated SEQ ID:12742, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75718] A function of VGAM2197 is therefore inhibition of Caspase Recruitment Domain Family, Member 4 (CARD4, Accession NM_006092), a gene which Activates CASP9 to induce apoptosis, regulates activation of NF-kappaB. Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD4. The function of CARD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM492.Chemokine (C-X-C motif) Receptor 6 (CXCR6, Accession NM_006564) is another VGAM2197 host target gene. CXCR6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CXCR6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CXCR6 BINDING SITE, designated SEQ ID:13334, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75719] Another function of VGAM2197 is therefore inhibition of Chemokine (C-X-C motif) Receptor 6 (CXCR6, Accession NM_006564), a gene which probably interacts between

dendritic cells and T cells and regulates T-cell migration. Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCR6. The function of CXCR6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2144.Phosphoribosyl Pyrophosphate Synthetase-associated Protein 1 (PRPSAP1, Accession NM_002766) is another VGAM2197 host target gene. PRPSAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRPSAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRPSAP1 BINDING SITE, designated SEQ ID:8659, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75720] Another function of VGAM2197 is therefore inhibition of Phosphoribosyl Pyrophosphate Synthetase-associated Protein 1 (PRPSAP1, Accession NM_002766), a gene which catalyzes the formation of PRPP from ATP and ribose 5-phosphate. Accordingly, utilities of VGAM2197 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with PRPSAP1. The function of PRPSAP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM914.SH3 and Multiple Ankyrin Repeat Domains 2 (SHANK2, Accession NM_012309) is another VGAM2197 host target gene. SHANK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SHANK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SHANK2 BINDING SITE, designated SEQ ID:14683, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75721] Another function of VGAM2197 is therefore inhibition of SH3 and Multiple Ankyrin Repeat Domains 2 (SHANK2, Accession NM_012309). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHANK2. SMURF1 (Accession XM_166483) is another VGAM2197 host target gene. SMURF1 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by SMURF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMURF1 BINDING SITE, designated SEQ ID:44417, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75722] Another function of VGAM2197 is therefore inhibition of SMURF1 (Accession XM_166483). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMURF1. TEM6 (Accession NM_022748) is another VGAM2197 host target gene. TEM6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEM6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEM6 BINDING SITE, designated SEQ ID:22962, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75723] Another function of VGAM2197 is therefore inhibition of

TEM6 (Accession NM_022748), a gene which displayes elevated expression during tumor angiogenesis. Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEM6. The function of TEM6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM175.Chromosome 1 Open Reading Frame 9 (C1orf9, Accession NM_016227) is another VGAM2197 host target gene. C1orf9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf9 BINDING SITE, designated SEQ ID:18340, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75724] Another function of VGAM2197 is therefore inhibition of Chromosome 1 Open Reading Frame 9 (C1orf9, Accession NM_016227). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf9. Chromosome 20

Open Reading Frame 4 (C20orf4, Accession NM_015511) is another VGAM2197 host target gene. C20orf4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf4 BINDING SITE, designated SEQ ID:17773, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75725] Another function of VGAM2197 is therefore inhibition of Chromosome 20 Open Reading Frame 4 (C20orf4, Accession NM_015511). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf4. Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_000793) is another VGAM2197 host target gene. DIO2 BINDING SITE1 and DIO2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DIO2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DIO2 BINDING SITE1 and DIO2 BINDING SITE2,

designated SEQ ID:6463 and SEQ ID:15174 respectively, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75726] Another function of VGAM2197 is therefore inhibition of Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_000793). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIO2. HSH2 (Accession NM_032855) is another VGAM2197 host target gene. HSH2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSH2 BINDING SITE, designated SEQ ID:26655, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75727] Another function of VGAM2197 is therefore inhibition of HSH2 (Accession NM_032855). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSH2. KIAA0322 (Accession XM_166591) is another VGAM2197 host target gene. KIAA0322 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by KIAA0322, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0322 BINDING SITE, designated SEQ ID:44561, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75728] Another function of VGAM2197 is therefore inhibition of KIAA0322 (Accession XM_166591). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0322. KIAA0700 (Accession XM_050561) is another VGAM2197 host target gene. KIAA0700 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0700, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0700 BINDING SITE, designated SEQ ID:35661, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75729] Another function of VGAM2197 is therefore inhibition of

KIAA0700 (Accession XM_050561). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0700. KIAA1045 (Accession XM_048592) is another VGAM2197 host target gene. KIAA1045 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1045, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1045 BINDING SITE, designated SEQ ID:35197, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75730] Another function of VGAM2197 is therefore inhibition of KIAA1045 (Accession XM_048592). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1045. KIAA1163 (Accession XM_086231) is another VGAM2197 host target gene. KIAA1163 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1163, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1163 BINDING SITE, designated SEQ ID:38558, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75731] Another function of VGAM2197 is therefore inhibition of KIAA1163 (Accession XM_086231). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1163. KIAA1673 (Accession XM_047672) is another VGAM2197 host target gene. KIAA1673 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1673, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1673 BINDING SITE, designated SEQ ID:35028, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75732] Another function of VGAM2197 is therefore inhibition of KIAA1673 (Accession XM_047672). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1673. MGC4172 (Accession NM_024308) is another

VGAM2197 host target gene. MGC4172 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4172, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4172 BINDING SITE, designated SEQ ID:23602, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75733] Another function of VGAM2197 is therefore inhibition of MGC4172 (Accession NM_024308). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4172. LOC132332 (Accession XM_072306) is another VGAM2197 host target gene. LOC132332 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC132332, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132332 BINDING SITE, designated SEQ ID:37489, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75734] Another function of VGAM2197 is therefore inhibition of LOC132332 (Accession XM_072306). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132332. LOC138654 (Accession XM_071015) is another VGAM2197 host target gene. LOC138654 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC138654, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC138654 BINDING SITE, designated SEQ ID:37398, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75735] Another function of VGAM2197 is therefore inhibition of LOC138654 (Accession XM_071015). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC138654. LOC149670 (Accession XM_086647) is another VGAM2197 host target gene. LOC149670 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149670, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149670 BINDING SITE, designated SEQ ID:38807, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75736] Another function of VGAM2197 is therefore inhibition of LOC149670 (Accession XM_086647). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149670. LOC157695 (Accession XM_098811) is another VGAM2197 host target gene. LOC157695 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157695, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157695 BINDING SITE, designated SEQ ID:41831, to the nucleotide sequence of VGAM2197 RNA, herein designated VGAM RNA, also designated SEQ ID:4908.

[75737] Another function of VGAM2197 is therefore inhibition of LOC157695 (Accession XM_098811). Accordingly, utilities of VGAM2197 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC157695. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2198 (VGAM2198) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75738] VGAM2198 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2198 was detected is described hereinabove with reference to Figs. 1-8.

[75739] VGAM2198 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like Disease Virus. VGAM2198 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75740] VGAM2198 gene encodes a VGAM2198 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2198 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2198 precursor RNA is designated SEQ ID:2184, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2184 is located at position 22309 relative to the genome of Yaba-like Disease Virus.

[75741] VGAM2198 precursor RNA folds onto itself, forming VGAM2198 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75742] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2198 folded precursor RNA into VGAM2198 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2198 RNA is designated SEQ ID:4909, and is provided hereinbelow with reference to the sequence listing part.

[75743] VGAM2198 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2198 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2198 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75744] VGAM2198 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2198 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2198 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2198 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2198 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75745] The complementary binding of VGAM2198 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2198 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2198 host target RNA into VGAM2198 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75746] It is appreciated that VGAM2198 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2198 host target genes. The mRNA of each one of this plurality of VGAM2198 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2198 RNA, herein designated VGAM RNA, and which when bound by VGAM2198 RNA causes

inhibition of translation of respective one or more VGAM2198 host target proteins.

[75747] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2198 gene, herein designated VGAM GENE, on one or more VGAM2198 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75748] It is yet further appreciated that a function of VGAM2198 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2198 include diagnosis, prevention and

treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGAM2198 correlate with, and may be deduced from, the identity of the host target genes which VGAM2198 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75749] Nucleotide sequences of the VGAM2198 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2198 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2198 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2198 are further described hereinbelow with reference to Table 1.

[75750] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2198 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2198 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75751] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2198 gene, herein designated VGAM is inhibition of expression of VGAM2198 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2198 correlate with, and may be deduced from, the identity of the target genes which VGAM2198 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75752] Collagen, Type IV, Alpha 5 (Alport syndrome) (COL4A5, Accession NM_000495) is a VGAM2198 host target gene. COL4A5 BINDING SITE1 through COL4A5 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by COL4A5, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL4A5 BINDING SITE1 through COL4A5 BINDING SITE3, designated SEQ ID:6108, SEQ ID:27211 and SEQ ID:27214 respectively, to the nucleotide sequence of VGAM2198 RNA, herein designated VGAM RNA, also designated SEQ ID:4909.

[75753] A function of VGAM2198 is therefore inhibition of Collagen, Type IV, Alpha 5 (Alport syndrome) (COL4A5, Accession NM_000495). Accordingly, utilities of VGAM2198 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A5. MGC10646

(Accession NM_032693) is another VGAM2198 host target gene. MGC10646 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC10646, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10646 BINDING SITE, designated SEQ ID:26413, to the nucleotide sequence of VGAM2198 RNA, herein designated VGAM RNA, also designated SEQ ID:4909.

[75754] Another function of VGAM2198 is therefore inhibition of MGC10646 (Accession NM_032693). Accordingly, utilities of VGAM2198 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10646. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2199 (VGAM2199) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75755] VGAM2199 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2199 was detected is described hereinabove with reference to Figs. 1-8.

[75756] VGAM2199 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Yaba-like Disease Virus. VGAM2199 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75757] VGAM2199 gene encodes a VGAM2199 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2199 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2199 precursor RNA is designated SEQ ID:2185, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2185 is located at position 3375 relative to the genome of Yaba-like Disease Virus.

[75758] VGAM2199 precursor RNA folds onto itself, forming VGAM2199 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75759] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2199 folded precursor RNA into VGAM2199 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2199 RNA is designated SEQ ID:4910, and is provided hereinbelow with reference to the sequence listing part.

[75760] VGAM2199 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2199 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2199 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75761] VGAM2199 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2199 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2199 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2199 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2199 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75762] The complementary binding of VGAM2199 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2199 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2199 host target RNA into VGAM2199 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75763] It is appreciated that VGAM2199 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2199 host target genes. The mRNA of each one of this plurality of VGAM2199 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2199 RNA, herein designated VGAM RNA, and which when bound by VGAM2199 RNA causes inhibition of translation of respective one or more VGAM2199 host target proteins.

[75764] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2199 gene, herein designated VGAM GENE, on one or more VGAM2199 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75765] It is yet further appreciated that a function of VGAM2199 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2199 include diagnosis, prevention and treatment of viral infection by Yaba-like Disease Virus. Specific functions, and accordingly utilities, of VGAM2199 correlate with, and may be deduced from, the identity of the host target genes which VGAM2199 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75766] Nucleotide sequences of the VGAM2199 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2199 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2199 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2199 are further described hereinbelow with reference to Table 1.

[75767] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2199 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2199 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75768] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2199 gene, herein designated VGAM is inhibition of expression of VGAM2199 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2199 correlate with, and may be deduced from, the identity of the target genes which VGAM2199 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75769] LOC219672 (Accession XM_166111) is a VGAM2199 host target gene. LOC219672 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219672, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219672 BINDING SITE, designated SEQ ID:43888, to the nucleotide sequence of VGAM2199 RNA, herein designated VGAM RNA, also designated SEQ ID:4910.

[75770] A function of VGAM2199 is therefore inhibition of LOC219672 (Accession XM_166111). Accordingly, utilities of VGAM2199 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219672. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2200 (VGAM2200) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75771] VGAM2200 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2200 was detected is described hereinabove with reference to Figs. 1-8.

[75772] VGAM2200 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus.

VGAM2200 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75773] VGAM2200 gene encodes a VGAM2200 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2200 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2200 precursor RNA is designated SEQ ID:2186, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2186 is located at position 184637 relative to the genome of Cowpox Virus.

[75774] VGAM2200 precursor RNA folds onto itself, forming VGAM2200 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75775] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2200 folded precursor RNA into VGAM2200 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2200 RNA is designated SEQ ID:4911, and is provided hereinbelow with reference to the sequence listing part.

[75776] VGAM2200 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2200 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2200 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75777] VGAM2200 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2200 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2200 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2200 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2200 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75778] The complementary binding of VGAM2200 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2200 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2200 host target RNA into VGAM2200 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75779] It is appreciated that VGAM2200 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2200 host target genes. The mRNA of each one of this plurality of VGAM2200 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2200 RNA, herein designated VGAM RNA, and which when bound by VGAM2200 RNA causes inhibition of translation of respective one or more VGAM2200 host target proteins.

[75780] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2200 gene, herein designated VGAM GENE, on one or more VGAM2200 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75781] It is yet further appreciated that a function of VGAM2200 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2200 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2200 correlate with, and may be deduced from, the identity of the host target genes which VGAM2200 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75782] Nucleotide sequences of the VGAM2200 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2200 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2200 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2200 are further described hereinbelow with reference to Table 1.

[75783] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2200 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2200 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75784] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2200 gene, herein designated VGAM is inhibition of expression of VGAM2200 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2200 correlate with, and may be deduced from, the identity of the target genes which VGAM2200 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75785] ENDOFIN (Accession NM_014733) is a VGAM2200 host target gene. ENDOFIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ENDOFIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ENDOFIN BINDING SITE, designated SEQ ID:16368, to the nucleotide sequence of

VGAM2200 RNA, herein designated VGAM RNA, also designated SEQ ID:4911.

[75786] A function of VGAM2200 is therefore inhibition of ENDOFIN (Accession NM_014733). Accordingly, utilities of VGAM2200 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENDOFIN. FLJ10498 (Accession NM_018115) is another VGAM2200 host target gene. FLJ10498 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10498, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10498 BINDING SITE, designated SEQ ID:19886, to the nucleotide sequence of VGAM2200 RNA, herein designated VGAM RNA, also designated SEQ ID:4911.

[75787] Another function of VGAM2200 is therefore inhibition of FLJ10498 (Accession NM_018115). Accordingly, utilities of VGAM2200 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10498. KIAA0534 (Accession XM_049349) is another VGAM2200 host target gene. KIAA0534 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA0534, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0534 BINDING SITE, designated SEQ ID:35381, to the nucleotide sequence of VGAM2200 RNA, herein designated VGAM RNA, also designated SEQ ID:4911.

[75788] Another function of VGAM2200 is therefore inhibition of KIAA0534 (Accession XM_049349). Accordingly, utilities of VGAM2200 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0534. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2201 (VGAM2201) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75789] VGAM2201 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2201 was detected is described hereinabove with reference to Figs. 1-8.

[75790] VGAM2201 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Cowpox Virus. VGAM2201 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75791] VGAM2201 gene encodes a VGAM2201 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2201 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2201 precursor RNA is designated SEQ ID:2187, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2187 is located at position 185848 relative to the genome of Cowpox Virus.

[75792] VGAM2201 precursor RNA folds onto itself, forming VGAM2201 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75793] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2201 folded precursor RNA into VGAM2201 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2201 RNA is designated SEQ ID:4912, and is provided hereinbelow with reference to the sequence listing part.

[75794] VGAM2201 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2201 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2201 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75795] VGAM2201 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2201 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2201 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2201 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2201 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75796] The complementary binding of VGAM2201 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2201 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2201

host target RNA into VGAM2201 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75797] It is appreciated that VGAM2201 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2201 host target genes. The mRNA of each one of this plurality of VGAM2201 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2201 RNA, herein designated VGAM RNA, and which when bound by VGAM2201 RNA causes inhibition of translation of respective one or more VGAM2201 host target proteins.

[75798] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2201 gene, herein designated VGAM GENE, on one or more VGAM2201 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75799] It is yet further appreciated that a function of VGAM2201 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2201 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2201 correlate with, and may be deduced from, the identity of the host target genes which VGAM2201 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75800] Nucleotide sequences of the VGAM2201 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2201 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2201 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2201 are further

described hereinbelow with reference to Table 1.

[75801] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2201 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2201 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75802] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2201 gene, herein designated VGAM is inhibition of expression of VGAM2201 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2201 correlate with, and may be deduced from, the identity of the target genes which VGAM2201 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75803] Alpha-methylacyl-CoA Racemase (AMACR, Accession XM_043771) is a VGAM2201 host target gene. AMACR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AMACR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of AMACR BINDING SITE, designated SEQ ID:34016, to the nucleotide sequence of VGAM2201 RNA, herein designated VGAM RNA, also designated SEQ ID:4912.

[75804] A function of VGAM2201 is therefore inhibition of Alpha-methylacyl-CoA Racemase (AMACR, Accession XM_043771). Accordingly, utilities of VGAM2201 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMACR. ATPase, H+ Transporting, Lysosomal 13kDa, V1 Subunit G Isoform 2 (ATP6V1G2, Accession NM_130463) is another VGAM2201 host target gene. ATP6V1G2 BINDING SITE1 and ATP6V1G2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ATP6V1G2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP6V1G2 BINDING SITE1 and ATP6V1G2 BINDING SITE2, designated SEQ ID:28222 and SEQ ID:28696 respectively, to the nucleotide sequence of VGAM2201 RNA, herein designated VGAM RNA, also designated SEQ ID:4912.

[75805] Another function of VGAM2201 is therefore inhibition of ATPase, H+ Transporting, Lysosomal 13kDa, V1 Subunit G

Isoform 2 (ATP6V1G2, Accession NM_130463). Accordingly, utilities of VGAM2201 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP6V1G2. FLJ00007 (Accession XM_048928) is another VGAM2201 host target gene. FLJ00007 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00007, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00007 BINDING SITE, designated SEQ ID:35309, to the nucleotide sequence of VGAM2201 RNA, herein designated VGAM RNA, also designated SEQ ID:4912.

[75806] Another function of VGAM2201 is therefore inhibition of FLJ00007 (Accession XM_048928). Accordingly, utilities of VGAM2201 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00007. FLJ13105 (Accession NM_025001) is another VGAM2201 host target gene. FLJ13105 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13105, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ13105 BINDING SITE, designated SEQ ID:24570, to the nucleotide sequence of VGAM2201 RNA, herein designated VGAM RNA, also designated SEQ ID:4912.

[75807] Another function of VGAM2201 is therefore inhibition of FLJ13105 (Accession NM_025001). Accordingly, utilities of VGAM2201 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13105. Protein Tyrosine Phosphatase, Receptor Type, R (PTPRR, Accession NM_130846) is another VGAM2201 host target gene. PTPRR BINDING SITE1 and PTPRR BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTPRR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRR BINDING SITE1 and PTPRR BINDING SITE2, designated SEQ ID:28381 and SEQ ID:8742 respectively, to the nucleotide sequence of VGAM2201 RNA, herein designated VGAM RNA, also designated SEQ ID:4912.

[75808] Another function of VGAM2201 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, R (PTPRR, Accession NM_130846). Accordingly, utilities of

VGAM2201 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRR. LOC150213 (Accession XM_059324) is another VGAM2201 host target gene. LOC150213 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150213, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150213 BINDING SITE, designated SEQ ID:36958, to the nucleotide sequence of VGAM2201 RNA, herein designated VGAM RNA, also designated SEQ ID:4912.

[75809] Another function of VGAM2201 is therefore inhibition of LOC150213 (Accession XM_059324). Accordingly, utilities of VGAM2201 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150213. LOC151742 (Accession NM_139245) is another VGAM2201 host target gene. LOC151742 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151742, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC151742 BINDING SITE, designated SEQ ID:29240, to the nucleotide sequence of VGAM2201 RNA, herein designated VGAM RNA, also designated SEQ ID:4912.

[75810] Another function of VGAM2201 is therefore inhibition of LOC151742 (Accession NM_139245). Accordingly, utilities of VGAM2201 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151742. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2202 (VGAM2202) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75811] VGAM2202 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2202 was detected is described hereinabove with reference to Figs. 1-8.

[75812] VGAM2202 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2202 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75813] VGAM2202 gene encodes a VGAM2202 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2202 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2202 precursor RNA is designated SEQ ID:2188, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2188 is located at position 162506 relative to the genome of Camelpox Virus.

[75814] VGAM2202 precursor RNA folds onto itself, forming VGAM2202 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75815] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2202 folded precursor RNA into VGAM2202 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2202 RNA is designated SEQ ID:4913, and is provided hereinbelow with reference to the sequence listing part.

[75816] VGAM2202 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2202 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2202 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75817] VGAM2202 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2202 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2202 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2202 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2202 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75818] The complementary binding of VGAM2202 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2202 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2202 host target RNA into VGAM2202 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75819] It is appreciated that VGAM2202 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2202 host target genes. The mRNA of each one of this plurality of VGAM2202 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2202 RNA, herein designated VGAM RNA, and which when bound by VGAM2202 RNA causes inhibition of translation of respective one or more VGAM2202 host target proteins.

[75820] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2202 gene, herein designated VGAM GENE, on one or more VGAM2202 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75821] It is yet further appreciated that a function of VGAM2202 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2202 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2202 correlate with, and may be deduced from, the identity of the host target genes which VGAM2202 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75822] Nucleotide sequences of the VGAM2202 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2202 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2202 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2202 are further described hereinbelow with reference to Table 1.

[75823] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2202 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2202 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75824] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2202 gene, herein designated VGAM is inhibition of expression of VGAM2202 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2202 correlate with, and may be deduced from, the identity of the target genes which VGAM2202 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75825] Actinin, Alpha 2 (ACTN2, Accession NM_001103) is a VGAM2202 host target gene. ACTN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ACTN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACTN2 BINDING SITE, designated SEQ ID:6754, to the nucleotide sequence of VGAM2202 RNA, herein designated VGAM RNA, also designated SEQ ID:4913.

[75826] A function of VGAM2202 is therefore inhibition of Actinin,

Alpha 2 (ACTN2, Accession NM_001103), a gene which an actin-binding protein with multiple roles in different cell types. Accordingly, utilities of VGAM2202 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACTN2. The function of ACTN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM88.Synaptotagmin I (SYT1, Accession NM_005639) is another VGAM2202 host target gene. SYT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYT1 BINDING SITE, designated SEQ ID:12168, to the nucleotide sequence of VGAM2202 RNA, herein designated VGAM RNA, also designated SEQ ID:4913.

[75827] Another function of VGAM2202 is therefore inhibition of Synaptotagmin I (SYT1, Accession NM_005639), a gene which may have a regulatory role in the membrane interactions during trafficking of synaptic vesicles at the active zone of the synapse. Accordingly, utilities of VGAM2202

include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT1. The function of SYT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM739.FLJ22173 (Accession NM_025041) is another VGAM2202 host target gene. FLJ22173 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22173, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22173 BINDING SITE, designated SEQ ID:24635, to the nucleotide sequence of VGAM2202 RNA, herein designated VGAM RNA, also designated SEQ ID:4913.

[75828] Another function of VGAM2202 is therefore inhibition of FLJ22173 (Accession NM_025041). Accordingly, utilities of VGAM2202 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22173. SH3 Domain Binding Glutamic Acid-rich Protein Like 2 (SH3BGRL2, Accession NM_031469) is another VGAM2202 host target gene. SH3BGRL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by SH3BGRL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3BGRL2 BINDING SITE, designated SEQ ID:25524, to the nucleotide sequence of VGAM2202 RNA, herein designated VGAM RNA, also designated SEQ ID:4913.

[75829] Another function of VGAM2202 is therefore inhibition of SH3 Domain Binding Glutamic Acid-rich Protein Like 2 (SH3BGRL2, Accession NM_031469). Accordingly, utilities of VGAM2202 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BGRL2. LOC146823 (Accession XM_097105) is another VGAM2202 host target gene. LOC146823 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146823, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146823 BINDING SITE, designated SEQ ID:40745, to the nucleotide sequence of VGAM2202 RNA, herein designated VGAM RNA, also designated SEQ ID:4913.

[75830] Another function of VGAM2202 is therefore inhibition of

LOC146823 (Accession XM_097105). Accordingly, utilities of VGAM2202 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146823. LOC255231 (Accession XM_170908) is another VGAM2202 host target gene. LOC255231 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255231 BINDING SITE, designated SEQ ID:45671, to the nucleotide sequence of VGAM2202 RNA, herein designated VGAM RNA, also designated SEQ ID:4913.

[75831] Another function of VGAM2202 is therefore inhibition of LOC255231 (Accession XM_170908). Accordingly, utilities of VGAM2202 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255231. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2203 (VGAM2203) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[75832] VGAM2203 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2203 was detected is described hereinabove with reference to Figs. 1-8.

[75833] VGAM2203 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2203 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75834] VGAM2203 gene encodes a VGAM2203 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2203 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2203 precursor RNA is designated SEQ ID:2189, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2189 is located at position 173794 relative to the genome of Cowpox Virus.

[75835] VGAM2203 precursor RNA folds onto itself, forming VGAM2203 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75836] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2203 folded precursor RNA into VGAM2203 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2203 RNA is designated SEQ ID:4914, and is provided hereinbelow with reference to the sequence listing part.

[75837] VGAM2203 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2203 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2203 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75838] VGAM2203 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2203 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2203 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2203 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2203 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[75839] The complementary binding of VGAM2203 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2203 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2203 host target RNA into VGAM2203 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75840] It is appreciated that VGAM2203 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2203 host target genes. The mRNA of each one of this plurality of VGAM2203 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2203 RNA, herein designated VGAM RNA, and which when bound by VGAM2203 RNA causes inhibition of translation of respective one or more VGAM2203 host target proteins.

[75841] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2203 gene, herein designated VGAM GENE, on one

or more VGAM2203 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75842] It is yet further appreciated that a function of VGAM2203 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2203 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2203 correlate with, and may be deduced from, the identity of the host target genes which VGAM2203 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75843] Nucleotide sequences of the VGAM2203 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2203 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2203 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2203 are further described hereinbelow with reference to Table 1.

[75844] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2203 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2203 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75845] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2203 gene, herein designated VGAM is inhibition of expression of VGAM2203 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2203 correlate with, and may be deduced from, the identity of the target genes which VGAM2203 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75846] Espin (ESPN, Accession NM_031475) is a VGAM2203 host

target gene. ESPN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ESPN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ESPN BINDING SITE, designated SEQ ID:25548, to the nucleotide sequence of VGAM2203 RNA, herein designated VGAM RNA, also designated SEQ ID:4914.

[75847] A function of VGAM2203 is therefore inhibition of Espin (ESPN, Accession NM_031475), a gene which a membrane-cytoskeletal assemblages . Accordingly, utilities of VGAM2203 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ESPN. The function of ESPN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1006.Glucocorticoid Receptor DNA Binding Factor 1 (GRLF1, Accession XM_085943) is another VGAM2203 host target gene. GRLF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRLF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRLF1 BINDING SITE, designated SEQ ID:38407, to the nucleotide sequence of VGAM2203 RNA, herein designated VGAM RNA, also designated SEQ ID:4914.

[75848] Another function of VGAM2203 is therefore inhibition of Glucocorticoid Receptor DNA Binding Factor 1 (GRLF1, Accession XM_085943), a gene which inhibits transcription of the glucocorticoid receptor gene. Accordingly, utilities of VGAM2203 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRLF1. The function of GRLF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Integrin, Alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) (ITGA2, Accession NM_002203) is another VGAM2203 host target gene. ITGA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA2 BINDING SITE, designated SEQ ID:7962,

to the nucleotide sequence of VGAM2203 RNA, herein designated VGAM RNA, also designated SEQ ID:4914.

[75849] Another function of VGAM2203 is therefore inhibition of Integrin, Alpha 2 (CD49B, alpha 2 subunit of VLA-2 receptor) (ITGA2, Accession NM_002203), a gene which has roles in blood clotting and angiogenesis, acts as a collagen and laminin receptor. Accordingly, utilities of VGAM2203 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA2. The function of ITGA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM827.Wilms Tumor 1 (WT1, Accession NM_024425) is another VGAM2203 host target gene. WT1 BINDING SITE1 through WT1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WT1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WT1 BINDING SITE1 through WT1 BINDING SITE4, designated SEQ ID:23671, SEQ ID:23675, SEQ ID:23667 and SEQ ID:5951 respectively, to the nucleotide sequence of VGAM2203 RNA, herein designated

VGAM RNA, also designated SEQ ID:4914.

[75850] Another function of VGAM2203 is therefore inhibition of Wilms Tumor 1 (WT1, Accession NM_024425). Accordingly, utilities of VGAM2203 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WT1. KIAA0993 (Accession XM_034413) is another VGAM2203 host target gene. KIAA0993 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0993, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0993 BINDING SITE, designated SEQ ID:32083, to the nucleotide sequence of VGAM2203 RNA, herein designated VGAM RNA, also designated SEQ ID:4914.

[75851] Another function of VGAM2203 is therefore inhibition of KIAA0993 (Accession XM_034413). Accordingly, utilities of VGAM2203 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0993. KIAA1416 (Accession XM_098762) is another VGAM2203 host target gene. KIAA1416 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1416, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1416 BINDING SITE, designated SEQ ID:41797, to the nucleotide sequence of VGAM2203 RNA, herein designated VGAM RNA, also designated SEQ ID:4914.

[75852] Another function of VGAM2203 is therefore inhibition of KIAA1416 (Accession XM_098762). Accordingly, utilities of VGAM2203 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1416. My015 (Accession XM_039512) is another VGAM2203 host target gene. My015 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by My015, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of My015 BINDING SITE, designated SEQ ID:33103, to the nucleotide sequence of VGAM2203 RNA, herein designated VGAM RNA, also designated SEQ ID:4914.

[75853] Another function of VGAM2203 is therefore inhibition of My015 (Accession XM_039512). Accordingly, utilities of VGAM2203 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with My015. Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2, Accession NM_014737) is another VGAM2203 host target gene. RASSF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RASSF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RASSF2 BINDING SITE, designated SEQ ID:16388, to the nucleotide sequence of VGAM2203 RNA, herein designated VGAM RNA, also designated SEQ ID:4914.

[75854] Another function of VGAM2203 is therefore inhibition of Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2, Accession NM_014737). Accordingly, utilities of VGAM2203 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2. Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession NM_033285) is another VGAM2203 host target gene. TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TP53INP1, corresponding to HOST TARGET binding sites such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2, designated SEQ ID:27101 and SEQ ID:36112 respectively, to the nucleotide sequence of VGAM2203 RNA, herein designated VGAM RNA, also designated SEQ ID:4914.

[75855] Another function of VGAM2203 is therefore inhibition of Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession NM_033285). Accordingly, utilities of VGAM2203 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53INP1. LOC157503 (Accession XM_098767) is another VGAM2203 host target gene. LOC157503 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157503, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157503 BINDING SITE, designated SEQ ID:41815, to the nucleotide sequence of VGAM2203 RNA, herein designated VGAM RNA, also designated SEQ ID:4914.

[75856] Another function of VGAM2203 is therefore inhibition of LOC157503 (Accession XM_098767). Accordingly, utilities

of VGAM2203 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157503. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2204 (VGAM2204) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75857] VGAM2204 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2204 was detected is described hereinabove with reference to Figs. 1-8.

[75858] VGAM2204 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2204 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75859] VGAM2204 gene encodes a VGAM2204 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2204 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2204 precursor RNA is designated SEQ ID:2190, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2190 is located at position 183474 relative to the genome of Cowpox Virus.

[75860] VGAM2204 precursor RNA folds onto itself, forming VGAM2204 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75861] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2204 folded precursor RNA into VGAM2204 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2204 RNA is designated SEQ ID:4915, and

is provided hereinbelow with reference to the sequence listing part.

[75862] VGAM2204 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2204 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2204 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75863] VGAM2204 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2204 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2204 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2204 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2204 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75864] The complementary binding of VGAM2204 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2204 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2204 host target RNA into VGAM2204 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75865] It is appreciated that VGAM2204 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2204 host target genes. The mRNA of each one of this plurality of VGAM2204 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2204 RNA, herein designated VGAM RNA, and which when bound by VGAM2204 RNA causes inhibition of translation of respective one or more VGAM2204 host target proteins.

[75866] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2204 gene, herein designated VGAM GENE, on one or more VGAM2204 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75867] It is yet further appreciated that a function of VGAM2204 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2204 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2204 correlate with, and may be deduced from, the identity of the host target genes which VGAM2204 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75868] Nucleotide sequences of the VGAM2204 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2204 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2204 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2204 are further described hereinbelow with reference to Table 1.

[75869] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2204 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2204 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75870] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2204 gene, herein designated VGAM is inhibition of expression of VGAM2204 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2204 correlate with, and may be deduced from, the identity of the target genes which VGAM2204 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75871] FLJ20094 (Accession NM_017665) is a VGAM2204 host target gene. FLJ20094 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20094, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20094 BINDING SITE, designated SEQ ID:19207, to the nucleotide sequence of VGAM2204 RNA, herein designated VGAM RNA, also designated SEQ ID:4915.

[75872] A function of VGAM2204 is therefore inhibition of FLJ20094 (Accession NM_017665). Accordingly, utilities of VGAM2204 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20094. Tankyrase, TRF1-interacting Ankyrin-related ADP-ribose Polymerase 2 (TNKS2, Accession NM_025235)

is another VGAM2204 host target gene. TNKS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNKS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNKS2 BINDING SITE, designated SEQ ID:24913, to the nucleotide sequence of VGAM2204 RNA, herein designated VGAM RNA, also designated SEQ ID:4915.

[75873] Another function of VGAM2204 is therefore inhibition of Tankyrase, TRF1-interacting Ankyrin-related ADP-ribose Polymerase 2 (TNKS2, Accession NM_025235). Accordingly, utilities of VGAM2204 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNKS2. LOC202025 (Accession XM_117353) is another VGAM2204 host target gene. LOC202025 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202025, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202025 BINDING SITE, designated SEQ ID:43400, to the nucleotide sequence of VGAM2204 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4915.

[75874] Another function of VGAM2204 is therefore inhibition of LOC202025 (Accession XM_117353). Accordingly, utilities of VGAM2204 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202025. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2205 (VGAM2205) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75875] VGAM2205 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2205 was detected is described hereinabove with reference to Figs. 1-8.

[75876] VGAM2205 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2205 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75877] VGAM2205 gene encodes a VGAM2205 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2205 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2205 precursor RNA is designated SEQ ID:2191, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2191 is located at position 188975 relative to the genome of Cowpox Virus.

[75878] VGAM2205 precursor RNA folds onto itself, forming VGAM2205 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75879] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2205 folded precursor RNA into VGAM2205 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2205 RNA is designated SEQ ID:4916, and is provided hereinbelow with reference to the sequence listing part.

[75880] VGAM2205 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2205 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2205 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75881] VGAM2205 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2205 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2205 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2205 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2205 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75882] The complementary binding of VGAM2205 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2205 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2205 host target RNA into VGAM2205 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75883] It is appreciated that VGAM2205 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2205 host target genes. The mRNA of

each one of this plurality of VGAM2205 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2205 RNA, herein designated VGAM RNA, and which when bound by VGAM2205 RNA causes inhibition of translation of respective one or more VGAM2205 host target proteins.

[75884] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2205 gene, herein designated VGAM GENE, on one or more VGAM2205 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[75885] It is yet further appreciated that a function of VGAM2205 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific functions, and accordingly utilities, of VGAM2205 correlate with, and may be deduced from, the identity of the host target genes which VGAM2205 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75886] Nucleotide sequences of the VGAM2205 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2205 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2205 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2205 are further described hereinbelow with reference to Table 1.

[75887] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2205 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2205 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75888] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2205 gene, herein designated VGAM is inhibition of expression of VGAM2205 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2205 correlate with, and may be deduced from, the identity of the target genes which VGAM2205 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75889] Ankyrin 3, Node of Ranvier (ankyrin G) (ANK3, Accession NM_020987) is a VGAM2205 host target gene. ANK3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANK3 BINDING SITE, designated SEQ ID:21984, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75890] A function of VGAM2205 is therefore inhibition of Ankyrin 3, Node of Ranvier (ankyrin G) (ANK3, Accession NM_020987), a gene which plays key roles in activities

such as cell motility, activation, proliferation. Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANK3. The function of ANK3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1527.CD2-associated Protein (CD2AP, Accession NM_012120) is another VGAM2205 host target gene. CD2AP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD2AP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD2AP BINDING SITE, designated SEQ ID:14433, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75891] Another function of VGAM2205 is therefore inhibition of CD2-associated Protein (CD2AP, Accession NM_012120), a gene which binds CAS ligand and may therefor involves in its growth regulatory pathway. Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD2AP.

The function of CD2AP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM95.Cadherin 6, Type 2, K-cadherin (fetal kidney) (CDH6, Accession NM_004932) is another VGAM2205 host target gene. CDH6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDH6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDH6 BINDING SITE, designated SEQ ID:11378, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75892] Another function of VGAM2205 is therefore inhibition of Cadherin 6, Type 2, K-cadherin (fetal kidney) (CDH6, Accession NM_004932), a gene which is a calcium dependent cell adhesion protein. Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH6. The function of CDH6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM60.Mitogen-activated Protein Kinase Kinase Kinase 7 (MAP3K7, Accession NM_003188) is another VGAM2205 host target gene. MAP3K7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K7 BINDING SITE, designated SEQ ID:9165, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75893] Another function of VGAM2205 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 7 (MAP3K7, Accession NM_003188), a gene which can phosphorylate and activate yet undefined mapkks. mediator of tgf-beta signal transduction. stimulates nf-kappa b activation. Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K7. The function of MAP3K7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1968.PSA (Accession NM_021154) is another

VGAM2205 host target gene. PSA BINDING SITE1 and PSA BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PSA, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSA BINDING SITE1 and PSA BINDING SITE2, designated SEQ ID:22131 and SEQ ID:27740 respectively, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75894] Another function of VGAM2205 is therefore inhibition of PSA (Accession NM_021154), a gene which is puromycin-sensitive aminopeptidase and has metallopeptidase activity. Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSA. The function of PSA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM65.Transforming Growth Factor, Beta Receptor III (betaglycan, 300kDa) (TGFBR3, Accession NM_003243) is another VGAM2205 host target gene. TGFBR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

TGFBR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TGFBR3 BINDING SITE, designated SEQ ID:9253, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75895] Another function of VGAM2205 is therefore inhibition of Transforming Growth Factor, Beta Receptor III (betaglycan, 300kDa) (TGFBR3, Accession NM_003243), a gene which involves in capturing and retaining TGF-beta for presentation to the signaling receptors. Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGFBR3. The function of TGFBR3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM139.FLJ20136 (Accession NM_017684) is another VGAM2205 host target gene. FLJ20136 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20136, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of FLJ20136 BINDING SITE, designated SEQ ID:19231, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75896] Another function of VGAM2205 is therefore inhibition of FLJ20136 (Accession NM_017684). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20136. IL-23R (Accession NM_144701) is another VGAM2205 host target gene. IL-23R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL-23R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL-23R BINDING SITE, designated SEQ ID:29526, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75897] Another function of VGAM2205 is therefore inhibition of IL-23R (Accession NM_144701). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL-23R. KIAA0007 (Accession XM_087089) is another VGAM2205

host target gene. KIAA0007 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0007, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0007 BINDING SITE, designated SEQ ID:39047, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75898] Another function of VGAM2205 is therefore inhibition of KIAA0007 (Accession XM_087089). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0007. MGC5576 (Accession NM_024056) is another VGAM2205 host target gene. MGC5576 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC5576, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5576 BINDING SITE, designated SEQ ID:23494, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75899] Another function of VGAM2205 is therefore inhibition of MGC5576 (Accession NM_024056). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5576. Oxysterol Binding Protein-like 5 (OSBPL5, Accession XM_052567) is another VGAM2205 host target gene. OSBPL5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL5 BINDING SITE, designated SEQ ID:35993, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75900] Another function of VGAM2205 is therefore inhibition of Oxysterol Binding Protein-like 5 (OSBPL5, Accession XM_052567). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL5. PEGASUS (Accession NM_022466) is another VGAM2205 host target gene. PEGASUS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

PEGASUS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEGASUS BINDING SITE, designated SEQ ID:22816, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75901] Another function of VGAM2205 is therefore inhibition of PEGASUS (Accession NM_022466). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEGASUS. PURG (Accession NM_013357) is another VGAM2205 host target gene. PURG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PURG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PURG BINDING SITE, designated SEQ ID:15007, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75902] Another function of VGAM2205 is therefore inhibition of PURG (Accession NM_013357). Accordingly, utilities of

VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PURG. SMOC2 (Accession XM_051452) is another VGAM2205 host target gene. SMOC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMOC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMOC2 BINDING SITE, designated SEQ ID:35838, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75903] Another function of VGAM2205 is therefore inhibition of SMOC2 (Accession XM_051452). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMOC2. LOC122773 (Accession XM_058665) is another VGAM2205 host target gene. LOC122773 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC122773, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC122773 BINDING SITE, designated SEQ ID:36712, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75904] Another function of VGAM2205 is therefore inhibition of LOC122773 (Accession XM_058665). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122773. LOC144305 (Accession XM_096572) is another VGAM2205 host target gene. LOC144305 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144305, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144305 BINDING SITE, designated SEQ ID:40402, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75905] Another function of VGAM2205 is therefore inhibition of LOC144305 (Accession XM_096572). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144305. LOC145845 (Accession XM_096884) is another VGAM2205 host target gene. LOC145845 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145845, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145845 BINDING SITE, designated SEQ ID:40617, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75906] Another function of VGAM2205 is therefore inhibition of LOC145845 (Accession XM_096884). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145845. LOC152185 (Accession NM_144718) is another VGAM2205 host target gene. LOC152185 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152185, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152185 BINDING SITE, designated SEQ ID:29540, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75907] Another function of VGAM2205 is therefore inhibition of

LOC152185 (Accession NM_144718). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152185. LOC153688 (Accession XM_098416) is another VGAM2205 host target gene. LOC153688 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153688, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153688 BINDING SITE, designated SEQ ID:41663, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75908] Another function of VGAM2205 is therefore inhibition of LOC153688 (Accession XM_098416). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153688. LOC196527 (Accession XM_113743) is another VGAM2205 host target gene. LOC196527 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196527, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC196527 BINDING SITE, designated SEQ ID:42402, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75909] Another function of VGAM2205 is therefore inhibition of LOC196527 (Accession XM_113743). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196527. LOC221271 (Accession XM_166307) is another VGAM2205 host target gene. LOC221271 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221271 BINDING SITE, designated SEQ ID:44128, to the nucleotide sequence of VGAM2205 RNA, herein designated VGAM RNA, also designated SEQ ID:4916.

[75910] Another function of VGAM2205 is therefore inhibition of LOC221271 (Accession XM_166307). Accordingly, utilities of VGAM2205 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221271. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2206 (VGAM2206) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75911] VGAM2206 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2206 was detected is described hereinabove with reference to Figs. 1-8.

[75912] VGAM2206 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Cowpox Virus. VGAM2206 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75913] VGAM2206 gene encodes a VGAM2206 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2206 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2206 precursor RNA is designated SEQ ID:2192, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2192 is located at position 178296 relative to the genome of Cowpox Virus.

[75914] VGAM2206 precursor RNA folds onto itself, forming VGAM2206 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75915] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2206 folded precursor RNA into VGAM2206 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2206 RNA is designated SEQ ID:4917, and is provided hereinbelow with reference to the sequence listing part.

[75916] VGAM2206 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2206 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2206 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75917] VGAM2206 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2206 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2206 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2206 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2206 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75918] The complementary binding of VGAM2206 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2206 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2206 host target RNA into VGAM2206 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75919] It is appreciated that VGAM2206 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2206 host target genes. The mRNA of each one of this plurality of VGAM2206 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2206 RNA, herein designated VGAM RNA, and which when bound by VGAM2206 RNA causes inhibition of translation of respective one or more

VGAM2206 host target proteins.

[75920] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2206 gene, herein designated VGAM GENE, on one or more VGAM2206 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75921] It is yet further appreciated that a function of VGAM2206 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2206 include diagnosis, prevention and treatment of viral infection by Cowpox Virus. Specific

functions, and accordingly utilities, of VGAM2206 correlate with, and may be deduced from, the identity of the host target genes which VGAM2206 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75922] Nucleotide sequences of the VGAM2206 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2206 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2206 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2206 are further described hereinbelow with reference to Table 1.

[75923] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2206 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2206 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75924] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2206 gene, herein designated VGAM is inhibition of expression of VGAM2206 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2206 correlate with, and may be deduced from, the identity of the target genes which VGAM2206 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75925] DKFZp434G179 (Accession XM_087065) is a VGAM2206 host target gene. DKFZp434G179 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434G179, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434G179 BINDING SITE, designated SEQ ID:39039, to the nucleotide sequence of VGAM2206 RNA, herein designated VGAM RNA, also designated SEQ ID:4917.

[75926] A function of VGAM2206 is therefore inhibition of DKFZp434G179 (Accession XM_087065). Accordingly, utilities of VGAM2206 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434G179. ORM1-like 2 (S. cerevisiae) (ORMDL2, Accession NM_014182) is another VGAM2206 host target gene. ORMDL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ORMDL2, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ORMDL2 BINDING SITE, designated SEQ ID:15466, to the nucleotide sequence of VGAM2206 RNA, herein designated VGAM RNA, also designated SEQ ID:4917.

[75927] Another function of VGAM2206 is therefore inhibition of ORM1-like 2 (S. cerevisiae) (ORMDL2, Accession NM_014182). Accordingly, utilities of VGAM2206 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ORMDL2. Tubby Homolog (mouse) (TUB, Accession NM_003320) is another VGAM2206 host target gene. TUB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUB BINDING SITE, designated SEQ ID:9321, to the nucleotide sequence of VGAM2206 RNA, herein designated VGAM RNA, also designated SEQ ID:4917.

[75928] Another function of VGAM2206 is therefore inhibition of Tubby Homolog (mouse) (TUB, Accession NM_003320).

Accordingly, utilities of VGAM2206 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUB. LOC115265 (Accession XM_055596) is another VGAM2206 host target gene. LOC115265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115265 BINDING SITE, designated SEQ ID:36307, to the nucleotide sequence of VGAM2206 RNA, herein designated VGAM RNA, also designated SEQ ID:4917.

[75929] Another function of VGAM2206 is therefore inhibition of LOC115265 (Accession XM_055596). Accordingly, utilities of VGAM2206 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115265. LOC157657 (Accession XM_088352) is another VGAM2206 host target gene. LOC157657 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157657, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC157657 BINDING SITE, designated SEQ ID:39624, to the nucleotide sequence of VGAM2206 RNA, herein designated VGAM RNA, also designated SEQ ID:4917.

[75930] Another function of VGAM2206 is therefore inhibition of LOC157657 (Accession XM_088352). Accordingly, utilities of VGAM2206 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157657. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2207 (VGAM2207) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75931] VGAM2207 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2207 was detected is described hereinabove with reference to Figs. 1-8.

[75932] VGAM2207 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma Virus. VGAM2207 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[75933] VGAM2207 gene encodes a VGAM2207 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2207 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2207 precursor RNA is designated SEQ ID:2193, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2193 is located at position 11555 relative to the genome of Myxoma Virus.

[75934] VGAM2207 precursor RNA folds onto itself, forming VGAM2207 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75935] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2207 folded precursor RNA into VGAM2207 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2207 RNA is designated SEQ ID:4918, and is provided hereinbelow with reference to the sequence listing part.

[75936] VGAM2207 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2207 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2207 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75937] VGAM2207 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2207 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2207 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2207 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2207 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75938] The complementary binding of VGAM2207 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2207 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2207 host target RNA into VGAM2207 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75939] It is appreciated that VGAM2207 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2207 host target genes. The mRNA of each one of this plurality of VGAM2207 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2207 RNA, herein designated VGAM RNA, and which when bound by VGAM2207 RNA causes inhibition of translation of respective one or more VGAM2207 host target proteins.

[75940] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2207 gene, herein designated VGAM GENE, on one or more VGAM2207 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75941] It is yet further appreciated that a function of VGAM2207 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2207 include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific functions, and accordingly utilities, of VGAM2207 correlate with, and may be deduced from, the identity of the host target genes which VGAM2207 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75942] Nucleotide sequences of the VGAM2207 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2207 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2207 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2207 are further described hereinbelow with reference to Table 1.

[75943] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2207 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2207 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75944] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2207 gene, herein designated VGAM is inhibition of expression of VGAM2207 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2207 correlate with, and may be deduced from, the identity of the target genes which VGAM2207 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75945] Poly (ADP-ribose) Glycohydrolase (PARG, Accession NM_003631) is a VGAM2207 host target gene. PARG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PARG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PARG BINDING SITE, designated SEQ ID:9693, to the nucleotide sequence of VGAM2207 RNA, herein designated VGAM RNA, also designated SEQ ID:4918.

[75946] A function of VGAM2207 is therefore inhibition of Poly (ADP-ribose) Glycohydrolase (PARG, Accession NM_003631), a gene which is found in many tissues and may be subject to proteolysis generating smaller, active products. Accordingly, utilities of VGAM2207 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PARG. The function of PARG has been established by previous studies. The synthesis and rapid turnover of ADP-ribose polymers is an immediate cellular response to DNA damage. Once synthesized by PARP (OMIM Ref. No. 173870), polymers are rapidly turned over and converted to free ADP-ribose by the action of poly(ADP-ribose) glycohydrolase (PARG). By PCR with degenerate primers based on the partial protein sequence of bovine PARG, Lin et al. (1997) isolated bovine PARG cDNAs. The protein had a calculated molecular mass of 111 kD, nearly twice the size of the 59-kD enzymatically active PARG isolated from bovine thymus. Using an activity gel assay of extracts from bacteria expressing PARG, the authors determined that cDNA encoded proteins of approximately 115 and 59 kD. The larger protein was sensitive to proteolysis, yielding a protein of approximately 59 kD. The enzymatically active 59-kD PARG cor-

responded to the C-terminal portion of the protein. The authors suggested that proteolysis explains the presence of PARG activity with a molecular mass of approximately 74 and 59 kD in bovine thymus preparations, and previous reports of a 74-kD PARG in guinea pig liver and human placenta. Using the sequence of the bovine cDNA, they searched sequence databases and identified human and rat PARG cDNAs. By fluorescence in situ hybridization, Ame et al. (1999) mapped the PARG gene to human chromosome 10q11.23 and mouse chromosome 14B.

[75947] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[75948] Lin, W.; Ame, J.-C.; Aboul-Ela, N.; Jacobson, E. L.; Jacobson, M. K. : Isolation and characterization of the cDNA encoding bovine poly(ADP-ribose) glycohydrolase. J. Biol. Chem. 272: 11895-11901, 1997. ; and

[75949] Ame, J.-C.; Apiou, F.; Jacobson, E. L.; Jacobson, M. K. : Assignment of the poly(ADP-ribose) glycohydrolase gene (PARG) to human chromosome 10q11.23 and mouse chromosome 14B by in situ.

[75950] Further studies establishing the function and utilities of PARG are found in John Hopkins OMIM database record ID

603501, and in sited publications numbered 7988-7989 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Suppression of Tumorigenicity 7 (ST7, Accession NM_021908) is another VGAM2207 host target gene. ST7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ST7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ST7 BINDING SITE, designated SEQ ID:22433, to the nucleotide sequence of VGAM2207 RNA, herein designated VGAM RNA, also designated SEQ ID:4918.

[75951] Another function of VGAM2207 is therefore inhibition of Suppression of Tumorigenicity 7 (ST7, Accession NM_021908), a gene which has a role in regulating cell-environment or cell-cell interactions. Accordingly, utilities of VGAM2207 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ST7. The function of ST7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM107.BMF (Accession NM_033503) is another

VGAM2207 host target gene. BMF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BMF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BMF BINDING SITE, designated SEQ ID:27284, to the nucleotide sequence of VGAM2207 RNA, herein designated VGAM RNA, also designated SEQ ID:4918.

[75952] Another function of VGAM2207 is therefore inhibition of BMF (Accession NM_033503). Accordingly, utilities of VGAM2207 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BMF. FLJ11274 (Accession NM_018375) is another VGAM2207 host target gene. FLJ11274 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11274, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11274 BINDING SITE, designated SEQ ID:20402, to the nucleotide sequence of VGAM2207 RNA, herein designated VGAM RNA, also designated SEQ ID:4918.

[75953] Another function of VGAM2207 is therefore inhibition of FLJ11274 (Accession NM_018375). Accordingly, utilities of VGAM2207 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11274. FLJ20457 (Accession NM_017832) is another VGAM2207 host target gene. FLJ20457 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20457, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20457 BINDING SITE, designated SEQ ID:19498, to the nucleotide sequence of VGAM2207 RNA, herein designated VGAM RNA, also designated SEQ ID:4918.

[75954] Another function of VGAM2207 is therefore inhibition of FLJ20457 (Accession NM_017832). Accordingly, utilities of VGAM2207 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20457. KIAA1165 (Accession XM_041162) is another VGAM2207 host target gene. KIAA1165 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1165, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1165 BINDING SITE, designated SEQ ID:33479, to the nucleotide sequence of VGAM2207 RNA, herein designated VGAM RNA, also designated SEQ ID:4918.

[75955] Another function of VGAM2207 is therefore inhibition of KIAA1165 (Accession XM_041162). Accordingly, utilities of VGAM2207 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1165. Mitochondrial Ribosomal Protein L13 (MRPL13, Accession NM_014078) is another VGAM2207 host target gene. MRPL13 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MRPL13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPL13 BINDING SITE, designated SEQ ID:15305, to the nucleotide sequence of VGAM2207 RNA, herein designated VGAM RNA, also designated SEQ ID:4918.

[75956] Another function of VGAM2207 is therefore inhibition of Mitochondrial Ribosomal Protein L13 (MRPL13, Accession NM_014078). Accordingly, utilities of VGAM2207 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL13. LOC220565 (Accession XM_165417) is another VGAM2207 host target gene. LOC220565 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220565, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220565 BINDING SITE, designated SEQ ID:43636, to the nucleotide sequence of VGAM2207 RNA, herein designated VGAM RNA, also designated SEQ ID:4918.

[75957] Another function of VGAM2207 is therefore inhibition of LOC220565 (Accession XM_165417). Accordingly, utilities of VGAM2207 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220565. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2208 (VGAM2208) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75958] VGAM2208 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2208 was detected is described hereinabove with reference to Figs. 1-8.

[75959] VGAM2208 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma Virus. VGAM2208 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75960] VGAM2208 gene encodes a VGAM2208 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2208 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2208 precursor RNA is designated SEQ ID:2194, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2194 is located at position 21539 relative to the genome of Myxoma Virus.

[75961] VGAM2208 precursor RNA folds onto itself, forming VGAM2208 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75962] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2208 folded precursor RNA into VGAM2208 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2208 RNA is designated SEQ ID:4919, and is provided hereinbelow with reference to the sequence listing part.

[75963] VGAM2208 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2208 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2208 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[75964] VGAM2208 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2208 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2208 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2208 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2208 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75965] The complementary binding of VGAM2208 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2208 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2208 host target RNA into VGAM2208 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75966] It is appreciated that VGAM2208 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2208 host target genes. The mRNA of each one of this plurality of VGAM2208 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2208 RNA, herein designated VGAM RNA, and which when bound by VGAM2208 RNA causes inhibition of translation of respective one or more VGAM2208 host target proteins.

[75967] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2208 gene, herein designated VGAM GENE, on one or more VGAM2208 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75968] It is yet further appreciated that a function of VGAM2208 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2208 include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific functions, and accordingly utilities, of VGAM2208 correlate with, and may be deduced from, the identity of the host target genes which VGAM2208 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[75969] Nucleotide sequences of the VGAM2208 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2208 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2208 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2208 are further described hereinbelow with reference to Table 1.

[75970] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2208 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2208 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75971] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2208 gene, herein designated VGAM is inhibition of expression of VGAM2208 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2208 correlate with, and may be deduced from, the identity of the target genes which VGAM2208 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75972] Potassium Channel, Subfamily K, Member 1 (KCNK1, Accession NM_002245) is a VGAM2208 host target gene.

KCNK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNK1 BINDING SITE, designated SEQ ID:8032, to the nucleotide sequence of VGAM2208 RNA, herein designated VGAM RNA, also designated SEQ ID:4919.

[75973] A function of VGAM2208 is therefore inhibition of Potassium Channel, Subfamily K, Member 1 (KCNK1, Accession NM_002245), a gene which is an inward rectifying potassium channel. Accordingly, utilities of VGAM2208 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK1. The function of KCNK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2209 (VGAM2209) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[75974] VGAM2209 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2209 was detected is described hereinabove with reference to Figs. 1-8.

[75975] VGAM2209 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma Virus. VGAM2209 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75976] VGAM2209 gene encodes a VGAM2209 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2209 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2209 precursor RNA is designated SEQ ID:2195, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2195 is located at position 1250 relative to the genome of Myxoma Virus.

[75977] VGAM2209 precursor RNA folds onto itself, forming VGAM2209 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75978] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2209 folded precursor RNA into VGAM2209 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2209 RNA is designated SEQ ID:4920, and is provided hereinbelow with reference to the sequence listing part.

[75979] VGAM2209 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2209 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2209 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75980] VGAM2209 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2209 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2209 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2209 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2209 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75981] The complementary binding of VGAM2209 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2209 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2209 host target RNA into VGAM2209 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75982] It is appreciated that VGAM2209 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2209 host target genes. The mRNA of each one of this plurality of VGAM2209 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2209 RNA, herein designated VGAM RNA, and which when bound by VGAM2209 RNA causes inhibition of translation of respective one or more VGAM2209 host target proteins.

[75983] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2209 gene, herein designated VGAM GENE, on one or more VGAM2209 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[75984] It is yet further appreciated that a function of VGAM2209 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2209 include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific functions, and accordingly utilities, of VGAM2209 correlate with, and may be deduced from, the identity of the host target genes which VGAM2209 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[75985] Nucleotide sequences of the VGAM2209 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2209 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2209 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2209 are further described hereinbelow with reference to Table 1.

[75986] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2209 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2209 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[75987] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2209 gene, herein designated VGAM is inhibition of expression of VGAM2209 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2209 correlate with, and may be deduced from, the identity of the target genes which VGAM2209 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[75988] FLJ10620 (Accession NM_018157) is a VGAM2209 host target gene. FLJ10620 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10620, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10620 BINDING SITE, designated SEQ ID:19973, to the nucleotide sequence of VGAM2209 RNA, herein designated VGAM RNA, also designated SEQ ID:4920.

[75989] A function of VGAM2209 is therefore inhibition of FLJ10620 (Accession NM_018157). Accordingly, utilities of VGAM2209 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10620. FLJ25415 (Accession NM_144708) is another VGAM2209 host target gene. FLJ25415 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ25415, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ25415 BINDING SITE, designated SEQ ID:29535, to the nucleotide sequence of VGAM2209 RNA, herein designated VGAM

RNA, also designated SEQ ID:4920.

[75990] Another function of VGAM2209 is therefore inhibition of FLJ25415 (Accession NM_144708). Accordingly, utilities of VGAM2209 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25415. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2210 (VGAM2210) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[75991] VGAM2210 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2210 was detected is described hereinabove with reference to Figs. 1-8.

[75992] VGAM2210 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma Virus. VGAM2210 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[75993] VGAM2210 gene encodes a VGAM2210 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2210 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2210 precursor RNA is designated SEQ ID:2196, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2196 is located at position 12338 relative to the genome of Myxoma Virus.

[75994] VGAM2210 precursor RNA folds onto itself, forming VGAM2210 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[75995] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2210 folded precursor RNA into VGAM2210 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2210 RNA is designated SEQ ID:4921, and is provided hereinbelow with reference to the sequence listing part.

[75996] VGAM2210 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2210 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2210 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[75997] VGAM2210 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2210 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2210 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2210 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2210 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[75998] The complementary binding of VGAM2210 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2210 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2210 host target RNA into VGAM2210 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[75999] It is appreciated that VGAM2210 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2210 host target genes. The mRNA of

each one of this plurality of VGAM2210 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2210 RNA, herein designated VGAM RNA, and which when bound by VGAM2210 RNA causes inhibition of translation of respective one or more VGAM2210 host target proteins.

[76000] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2210 gene, herein designated VGAM GENE, on one or more VGAM2210 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[76001] It is yet further appreciated that a function of VGAM2210 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2210 include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific functions, and accordingly utilities, of VGAM2210 correlate with, and may be deduced from, the identity of the host target genes which VGAM2210 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76002] Nucleotide sequences of the VGAM2210 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2210 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2210 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2210 are further described hereinbelow with reference to Table 1.

[76003] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2210 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2210 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76004] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2210 gene, herein designated VGAM is inhibition of expression of VGAM2210 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2210 correlate with, and may be deduced from, the identity of the target genes which VGAM2210 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76005] Tumor Necrosis Factor (ligand) Superfamily, Member 15 (TNFSF15, Accession NM_005118) is a VGAM2210 host target gene. TNFSF15 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TNFSF15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFSF15 BINDING SITE, designated SEQ ID:11600, to the nucleotide sequence of VGAM2210 RNA, herein designated VGAM RNA, also designated SEQ ID:4921.

[76006] A function of VGAM2210 is therefore inhibition of Tumor Necrosis Factor (ligand) Superfamily, Member 15

(TNFSF15, Accession NM_005118), a gene which acts as an autocrine factor to induce apoptosis in endothelial cells. Accordingly, utilities of VGAM2210 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFSF15. The function of TNFSF15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM350.KIAA1497 (Accession XM_041431) is another VGAM2210 host target gene. KIAA1497 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1497, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1497 BINDING SITE, designated SEQ ID:33525, to the nucleotide sequence of VGAM2210 RNA, herein designated VGAM RNA, also designated SEQ ID:4921.

[76007] Another function of VGAM2210 is therefore inhibition of KIAA1497 (Accession XM_041431). Accordingly, utilities of VGAM2210 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1497. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2211 (VGAM2211) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76008] VGAM2211 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2211 was detected is described hereinabove with reference to Figs. 1-8.

[76009] VGAM2211 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma Virus. VGAM2211 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76010] VGAM2211 gene encodes a VGAM2211 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2211 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2211 precursor RNA is designated SEQ ID:2197, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2197 is located at position 17880 relative to the genome of Myxoma Virus.

[76011] VGAM2211 precursor RNA folds onto itself, forming VGAM2211 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76012] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2211 folded precursor RNA into VGAM2211 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2211 RNA is designated SEQ ID:4922, and is provided hereinbelow with reference to the sequence listing part.

[76013] VGAM2211 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2211 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2211 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76014] VGAM2211 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2211 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2211 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2211 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2211 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76015] The complementary binding of VGAM2211 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2211 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2211 host target RNA into VGAM2211 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76016] It is appreciated that VGAM2211 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2211 host target genes. The mRNA of each one of this plurality of VGAM2211 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2211 RNA, herein designated VGAM RNA, and which when bound by VGAM2211 RNA causes inhibition of translation of respective one or more

VGAM2211 host target proteins.

[76017] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2211 gene, herein designated VGAM GENE, on one or more VGAM2211 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76018] It is yet further appreciated that a function of VGAM2211 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2211 include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific

functions, and accordingly utilities, of VGAM2211 correlate with, and may be deduced from, the identity of the host target genes which VGAM2211 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76019] Nucleotide sequences of the VGAM2211 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2211 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2211 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2211 are further described hereinbelow with reference to Table 1.

[76020] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2211 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2211 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76021] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2211 gene, herein designated VGAM is inhibition of expression of VGAM2211 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2211 correlate with, and may be deduced from, the identity of the target genes which VGAM2211 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76022] Contactin 2 (axonal) (CNTN2, Accession NM_005076) is a VGAM2211 host target gene. CNTN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNTN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNTN2 BINDING SITE, designated SEQ ID:11527, to the nucleotide sequence of VGAM2211 RNA, herein designated VGAM RNA, also designated SEQ ID:4922.

[76023] A function of VGAM2211 is therefore inhibition of Contactin 2 (axonal) (CNTN2, Accession NM_005076), a gene which may play a role in axonal growth and cell adhesion. Accordingly, utilities of VGAM2211 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNTN2. The function of CNTN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM259.DKFZP566I1024 (Accession XM_046506) is another VGAM2211 host target gene. DKFZP566I1024 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP566I1024, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566I1024 BINDING SITE, designated SEQ ID:34734, to the nucleotide sequence of VGAM2211 RNA, herein designated VGAM RNA, also designated SEQ ID:4922.

[76024] Another function of VGAM2211 is therefore inhibition of DKFZP566I1024 (Accession XM_046506). Accordingly, utilities of VGAM2211 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566I1024. FLJ12078 (Accession NM_024977) is another VGAM2211 host target gene. FLJ12078 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12078, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12078 BINDING SITE, designated SEQ ID:24536, to the

nucleotide sequence of VGAM2211 RNA, herein designated VGAM RNA, also designated SEQ ID:4922.

[76025] Another function of VGAM2211 is therefore inhibition of FLJ12078 (Accession NM_024977). Accordingly, utilities of VGAM2211 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12078. GK001 (Accession NM_020198) is another VGAM2211 host target gene. GK001 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GK001, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GK001 BINDING SITE, designated SEQ ID:21430, to the nucleotide sequence of VGAM2211 RNA, herein designated VGAM RNA, also designated SEQ ID:4922.

[76026] Another function of VGAM2211 is therefore inhibition of GK001 (Accession NM_020198). Accordingly, utilities of VGAM2211 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GK001. SCIN (Accession NM_033128) is another VGAM2211 host target gene. SCIN BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded

by SCIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCIN BINDING SITE, designated SEQ ID:26972, to the nucleotide sequence of VGAM2211 RNA, herein designated VGAM RNA, also designated SEQ ID:4922.

[76027] Another function of VGAM2211 is therefore inhibition of SCIN (Accession NM_033128). Accordingly, utilities of VGAM2211 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCIN. Zinc Finger Protein 323 (ZNF323, Accession NM_030899) is another VGAM2211 host target gene. ZNF323 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF323 BINDING SITE, designated SEQ ID:25167, to the nucleotide sequence of VGAM2211 RNA, herein designated VGAM RNA, also designated SEQ ID:4922.

[76028] Another function of VGAM2211 is therefore inhibition of Zinc Finger Protein 323 (ZNF323, Accession NM_030899).

Accordingly, utilities of VGAM2211 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF323. LOC152925 (Accession XM_087559) is another VGAM2211 host target gene. LOC152925 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152925, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152925 BINDING SITE, designated SEQ ID:39337, to the nucleotide sequence of VGAM2211 RNA, herein designated VGAM RNA, also designated SEQ ID:4922.

[76029] Another function of VGAM2211 is therefore inhibition of LOC152925 (Accession XM_087559). Accordingly, utilities of VGAM2211 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152925. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2212 (VGAM2212) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[76030] VGAM2212 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2212 was detected is described hereinabove with reference to Figs. 1-8.

[76031] VGAM2212 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma Virus. VGAM2212 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76032] VGAM2212 gene encodes a VGAM2212 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2212 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2212 precursor RNA is designated SEQ ID:2198, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2198 is located at position 11366 relative to the genome of Myxoma Virus.

[76033] VGAM2212 precursor RNA folds onto itself, forming VGAM2212 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76034] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2212 folded precursor RNA into VGAM2212 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2212 RNA is designated SEQ ID:4923, and is provided hereinbelow with reference to the sequence listing part.

[76035] VGAM2212 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2212 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2212 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76036] VGAM2212 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2212 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2212 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2212 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2212 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[76037] The complementary binding of VGAM2212 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2212 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2212 host target RNA into VGAM2212 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76038] It is appreciated that VGAM2212 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2212 host target genes. The mRNA of each one of this plurality of VGAM2212 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2212 RNA, herein designated VGAM RNA, and which when bound by VGAM2212 RNA causes inhibition of translation of respective one or more VGAM2212 host target proteins.

[76039] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2212 gene, herein designated VGAM GENE, on one

or more VGAM2212 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76040] It is yet further appreciated that a function of VGAM2212 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2212 include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific functions, and accordingly utilities, of VGAM2212 correlate with, and may be deduced from, the identity of the host target genes which VGAM2212 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76041] Nucleotide sequences of the VGAM2212 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2212 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2212 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2212 are further described hereinbelow with reference to Table 1.

[76042] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2212 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2212 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76043] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2212 gene, herein designated VGAM is inhibition of expression of VGAM2212 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2212 correlate with, and may be deduced from, the identity of the target genes which VGAM2212 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76044] Protein Kinase, CAMP-dependent, Regulatory, Type II, Al-

pha (PRKAR2A, Accession NM_004157) is a VGAM2212 host target gene. PRKAR2A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRKAR2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKAR2A BINDING SITE, designated SEQ ID:10370, to the nucleotide sequence of VGAM2212 RNA, herein designated VGAM RNA, also designated SEQ ID:4923.

[76045] A function of VGAM2212 is therefore inhibition of Protein Kinase, CAMP-dependent, Regulatory, Type II, Alpha (PRKAR2A, Accession NM_004157), a gene which mediates membrane association by binding to anchoring proteins, including the map2 kinase. Accordingly, utilities of VGAM2212 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKAR2A. The function of PRKAR2A has been established by previous studies. See 188830. Phosphorylation by cAMP-dependent protein kinases is essential for sperm motility. A cAMP-dependent protein kinase is bound to sperm flagella by a regulatory subunit (RII). Oyen et al. (1989) observed high testis-specific expression of a hu-

man homolog to the rat RII-alpha mRNA induced in haploid germ cells. They cloned a human cDNA that encodes a 404-amino acid polypeptide with a region (amino acids 45-75) divergent from that of the previously published mouse and rat sequences. By PCR and Southern blot analysis of somatic cell hybrid mapping panels and by radiation hybrid analysis, Tasken et al. (1998) mapped the PRKAR2A gene to chromosome 3p21.3-p21.2.

[76046] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[76047] Oyen, O.; Myklebust, F.; Scott, J. D.; Hansson, V.; Jahnsen, T. : Human testis cDNA for the regulatory subunit RII alpha of cAMP-dependent protein kinase encodes an alternate amino-terminal region. FEBS Lett. 246: 57-64, 1989. ; and

[76048] Tasken, K.; Naylor, S. L.; Solberg, R.; Jahnsen, T. : Mapping of the gene encoding the regulatory subunit RII-alpha of cAMP-dependent protein kinase (locus PRKAR2A) to human chromosome r.

[76049] Further studies establishing the function and utilities of PRKAR2A are found in John Hopkins OMIM database record ID 176910, and in sited publications numbered

1154-1155 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2213 (VGAM2213) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76050] VGAM2213 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2213 was detected is described hereinabove with reference to Figs. 1-8.

[76051] VGAM2213 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma Virus. VGAM2213 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76052] VGAM2213 gene encodes a VGAM2213 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2213 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2213 precursor RNA is desig-

nated SEQ ID:2199, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2199 is located at position 12976 relative to the genome of Myxoma Virus.

[76053] VGAM2213 precursor RNA folds onto itself, forming VGAM2213 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76054] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2213 folded precursor RNA into VGAM2213 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of VGAM2213 RNA is designated SEQ ID:4924, and is provided hereinbelow with reference to the sequence

listing part.

[76055] VGAM2213 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2213 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2213 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76056] VGAM2213 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2213 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2213 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2213 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2213 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76057] The complementary binding of VGAM2213 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2213 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2213 host target RNA into VGAM2213 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76058] It is appreciated that VGAM2213 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2213 host target genes. The mRNA of each one of this plurality of VGAM2213 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2213 RNA, herein designated VGAM

RNA, and which when bound by VGAM2213 RNA causes inhibition of translation of respective one or more VGAM2213 host target proteins.

[76059] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2213 gene, herein designated VGAM GENE, on one or more VGAM2213 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76060] It is yet further appreciated that a function of VGAM2213 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2213 include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific functions, and accordingly utilities, of VGAM2213 correlate with, and may be deduced from, the identity of the host target genes which VGAM2213 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76061] Nucleotide sequences of the VGAM2213 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2213 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2213 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2213 are further described hereinbelow with reference to Table 1.

[76062] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2213 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2213 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76063] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2213 gene, herein designated VGAM is

inhibition of expression of VGAM2213 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2213 correlate with, and may be deduced from, the identity of the target genes which VGAM2213 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76064] Extracellular Matrix Protein 2, Female Organ and Adipocyte Specific (ECM2, Accession NM_001393) is a VGAM2213 host target gene. ECM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ECM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ECM2 BINDING SITE, designated SEQ ID:7088, to the nucleotide sequence of VGAM2213 RNA, herein designated VGAM RNA, also designated SEQ ID:4924.

[76065] A function of VGAM2213 is therefore inhibition of Extracellular Matrix Protein 2, Female Organ and Adipocyte Specific (ECM2, Accession NM_001393). Accordingly, utilities of VGAM2213 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ECM2. PR Domain Containing 2, with ZNF Domain

(PRDM2, Accession NM_012231) is another VGAM2213 host target gene. PRDM2 BINDING SITE1 and PRDM2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PRDM2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRDM2 BINDING SITE1 and PRDM2 BINDING SITE2, designated SEQ ID:14536 and SEQ ID:18006 respectively, to the nucleotide sequence of VGAM2213 RNA, herein designated VGAM RNA, also designated SEQ ID:4924.

[76066] Another function of VGAM2213 is therefore inhibition of PR Domain Containing 2, with ZNF Domain (PRDM2, Accession NM_012231), a gene which plays a role in transcriptional regulation during neuronal differentiation and pathogenesis of retinoblastoma. Accordingly, utilities of VGAM2213 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDM2. The function of PRDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM120.FLJ10139 (Accession NM_018005) is another VGAM2213 host target gene. FLJ10139 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10139 BINDING SITE, designated SEQ ID:19736, to the nucleotide sequence of VGAM2213 RNA, herein designated VGAM RNA, also designated SEQ ID:4924.

[76067] Another function of VGAM2213 is therefore inhibition of FLJ10139 (Accession NM_018005). Accordingly, utilities of VGAM2213 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10139. KIAA1165 (Accession XM_041162) is another VGAM2213 host target gene. KIAA1165 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1165, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1165 BINDING SITE, designated SEQ ID:33475, to the nucleotide sequence of VGAM2213 RNA, herein designated VGAM RNA, also designated SEQ ID:4924.

[76068] Another function of VGAM2213 is therefore inhibition of

KIAA1165 (Accession XM_041162). Accordingly, utilities of VGAM2213 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1165. mPA-PLA1 (Accession NM_139248) is another VGAM2213 host target gene. mPA-PLA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by mPA-PLA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of mPA-PLA1 BINDING SITE, designated SEQ ID:29250, to the nucleotide sequence of VGAM2213 RNA, herein designated VGAM RNA, also designated SEQ ID:4924.

[76069] Another function of VGAM2213 is therefore inhibition of mPA-PLA1 (Accession NM_139248). Accordingly, utilities of VGAM2213 include diagnosis, prevention and treatment of diseases and clinical conditions associated with mPA-PLA1. MTCH1 (Accession NM_014341) is another VGAM2213 host target gene. MTCH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTCH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of MTCH1 BINDING SITE, designated SEQ ID:15661, to the nucleotide sequence of VGAM2213 RNA, herein designated VGAM RNA, also designated SEQ ID:4924.

[76070] Another function of VGAM2213 is therefore inhibition of MTCH1 (Accession NM_014341). Accordingly, utilities of VGAM2213 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTCH1. LOC158364 (Accession XM_088546) is another VGAM2213 host target gene. LOC158364 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158364, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158364 BINDING SITE, designated SEQ ID:39817, to the nucleotide sequence of VGAM2213 RNA, herein designated VGAM RNA, also designated SEQ ID:4924.

[76071] Another function of VGAM2213 is therefore inhibition of LOC158364 (Accession XM_088546). Accordingly, utilities of VGAM2213 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158364. LOC221773 (Accession XM_165802) is an-

other VGAM2213 host target gene. LOC221773 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221773, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221773 BINDING SITE, designated SEQ ID:43760, to the nucleotide sequence of VGAM2213 RNA, herein designated VGAM RNA, also designated SEQ ID:4924.

[76072] Another function of VGAM2213 is therefore inhibition of LOC221773 (Accession XM_165802). Accordingly, utilities of VGAM2213 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221773. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2214 (VGAM2214) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76073] VGAM2214 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2214 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[76074] VGAM2214 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Myxoma Virus. VGAM2214 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76075] VGAM2214 gene encodes a VGAM2214 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2214 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2214 precursor RNA is designated SEQ ID:2200, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2200 is located at position 20836 relative to the genome of Myxoma Virus.

[76076] VGAM2214 precursor RNA folds onto itself, forming VGAM2214 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76077] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2214 folded precursor RNA into VGAM2214 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2214 RNA is designated SEQ ID:4925, and is provided hereinbelow with reference to the sequence listing part.

[76078] VGAM2214 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2214 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2214 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76079] VGAM2214 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2214 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2214 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2214 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2214 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76080] The complementary binding of VGAM2214 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2214 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2214 host target RNA into VGAM2214 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76081] It is appreciated that VGAM2214 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2214 host target genes. The mRNA of each one of this plurality of VGAM2214 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2214 RNA, herein designated VGAM RNA, and which when bound by VGAM2214 RNA causes inhibition of translation of respective one or more VGAM2214 host target proteins.

[76082] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2214 gene, herein designated VGAM GENE, on one or more VGAM2214 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76083] It is yet further appreciated that a function of VGAM2214 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2214 include diagnosis, prevention and treatment of viral infection by Myxoma Virus. Specific functions, and accordingly utilities, of VGAM2214 correlate with, and may be deduced from, the identity of the host target genes which VGAM2214 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76084] Nucleotide sequences of the VGAM2214 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2214 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2214 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2214 are further described hereinbelow with reference to Table 1.

[76085] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2214 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2214 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76086] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2214 gene, herein designated VGAM is inhibition of expression of VGAM2214 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2214 correlate with, and may be deduced from, the identity of the target genes which VGAM2214 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76087] ATP Synthase, H+ Transporting, Mitochondrial F1 Complex, Beta Polypeptide (ATP5B, Accession XM_006710) is a VGAM2214 host target gene. ATP5B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ATP5B, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP5B BINDING SITE, designated SEQ ID:30008, to the nucleotide sequence of VGAM2214 RNA, herein designated VGAM RNA, also designated SEQ ID:4925.

[76088] A function of VGAM2214 is therefore inhibition of ATP Synthase, H+ Transporting, Mitochondrial F1 Complex, Beta Polypeptide (ATP5B, Accession XM_006710). Accordingly, utilities of VGAM2214 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP5B. Retinoschisis (X-linked, juvenile) 1 (RS1, Accession NM_000330) is another VGAM2214 host target gene. RS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RS1 BINDING SITE, designated SEQ ID:5877, to the nucleotide sequence of VGAM2214 RNA, herein designated VGAM RNA, also designated SEQ ID:4925.

[76089] Another function of VGAM2214 is therefore inhibition of Retinoschisis (X-linked, juvenile) 1 (RS1, Accession

NM_000330). Accordingly, utilities of VGAM2214 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RS1. ADP-ribosylation Factor Domain Protein 1, 64kDa (ARFD1, Accession NM_001656) is another VGAM2214 host target gene. ARFD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARFD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARFD1 BINDING SITE, designated SEQ ID:7372, to the nucleotide sequence of VGAM2214 RNA, herein designated VGAM RNA, also designated SEQ ID:4925.

[76090] Another function of VGAM2214 is therefore inhibition of ADP-ribosylation Factor Domain Protein 1, 64kDa (ARFD1, Accession NM_001656). Accordingly, utilities of VGAM2214 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARFD1. FLJ20666 (Accession NM_017922) is another VGAM2214 host target gene. FLJ20666 BINDING SITE1 and FLJ20666 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ20666, cor-

responding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20666 BINDING SITE1 and FLJ20666 BINDING SITE2, designated SEQ ID:19586 and SEQ ID:20337 respectively, to the nucleotide sequence of VGAM2214 RNA, herein designated VGAM RNA, also designated SEQ ID:4925.

[76091] Another function of VGAM2214 is therefore inhibition of FLJ20666 (Accession NM_017922). Accordingly, utilities of VGAM2214 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20666. Mitochondrial Ribosomal Protein L20 (MRPL20, Accession NM_017971) is another VGAM2214 host target gene. MRPL20 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPL20, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPL20 BINDING SITE, designated SEQ ID:19701, to the nucleotide sequence of VGAM2214 RNA, herein designated VGAM RNA, also designated SEQ ID:4925.

[76092] Another function of VGAM2214 is therefore inhibition of

Mitochondrial Ribosomal Protein L20 (MRPL20, Accession NM_017971). Accordingly, utilities of VGAM2214 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL20. Phosphatase, Orphan 1 (phospho1, Accession XM_091572) is another VGAM2214 host target gene. phospho1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by phospho1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of phospho1 BINDING SITE, designated SEQ ID:40058, to the nucleotide sequence of VGAM2214 RNA, herein designated VGAM RNA, also designated SEQ ID:4925.

[76093] Another function of VGAM2214 is therefore inhibition of Phosphatase, Orphan 1 (phospho1, Accession XM_091572). Accordingly, utilities of VGAM2214 include diagnosis, prevention and treatment of diseases and clinical conditions associated with phospho1. Unc-5 Homolog D (C. elegans) (UNC5D, Accession NM_080872) is another VGAM2214 host target gene. UNC5D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UNC5D, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UNC5D BINDING SITE, designated SEQ ID:28118, to the nucleotide sequence of VGAM2214 RNA, herein designated VGAM RNA, also designated SEQ ID:4925.

[76094] Another function of VGAM2214 is therefore inhibition of Unc-5 Homolog D (C. elegans) (UNC5D, Accession NM_080872). Accordingly, utilities of VGAM2214 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC5D. LOC130639 (Accession XM_059464) is another VGAM2214 host target gene. LOC130639 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC130639, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130639 BINDING SITE, designated SEQ ID:37003, to the nucleotide sequence of VGAM2214 RNA, herein designated VGAM RNA, also designated SEQ ID:4925.

[76095] Another function of VGAM2214 is therefore inhibition of LOC130639 (Accession XM_059464). Accordingly, utilities

of VGAM2214 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130639. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2215 (VGAM2215) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76096] VGAM2215 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2215 was detected is described hereinabove with reference to Figs. 1-8.

[76097] VGAM2215 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2215 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76098] VGAM2215 gene encodes a VGAM2215 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2215 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2215 precursor RNA is designated SEQ ID:2201, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2201 is located at position 9138 relative to the genome of Ectromelia Virus.

[76099] VGAM2215 precursor RNA folds onto itself, forming VGAM2215 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76100] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2215 folded precursor RNA into VGAM2215 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2215 RNA is designated SEQ ID:4926, and

is provided hereinbelow with reference to the sequence listing part.

[76101] VGAM2215 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2215 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2215 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76102] VGAM2215 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2215 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2215 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2215 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2215 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76103] The complementary binding of VGAM2215 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2215 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2215 host target RNA into VGAM2215 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76104] It is appreciated that VGAM2215 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2215 host target genes. The mRNA of each one of this plurality of VGAM2215 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2215 RNA, herein designated VGAM RNA, and which when bound by VGAM2215 RNA causes inhibition of translation of respective one or more VGAM2215 host target proteins.

[76105] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2215 gene, herein designated VGAM GENE, on one or more VGAM2215 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76106] It is yet further appreciated that a function of VGAM2215 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2215 correlate with, and may be deduced from, the identity of the host target genes which VGAM2215 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76107] Nucleotide sequences of the VGAM2215 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2215 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2215 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2215 are further described hereinbelow with reference to Table 1.

[76108] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2215 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2215 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76109] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2215 gene, herein designated VGAM is inhibition of expression of VGAM2215 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2215 correlate with, and may be deduced from, the identity of the target genes which VGAM2215 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76110] Adrenergic, Beta, Receptor Kinase 2 (ADRBK2, Accession NM_005160) is a VGAM2215 host target gene. ADRBK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADRBK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADRBK2 BINDING SITE, designated SEQ ID:11641, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76111] A function of VGAM2215 is therefore inhibition of Adrenergic, Beta, Receptor Kinase 2 (ADRBK2, Accession NM_005160), a gene which regulates desensitization of G protein-coupled receptors. Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with ADRBK2. The function of ADRBK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM806.EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838) is another VGAM2215 host target gene. EGFL5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EGFL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGFL5 BINDING SITE, designated SEQ ID:41872, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76112] Another function of VGAM2215 is therefore inhibition of EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGFL5. Poly (ADP-ribose) Glycohydrolase (PARG, Accession NM_003631) is another VGAM2215 host target gene. PARG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by PARG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PARG BINDING SITE, designated SEQ ID:9692, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76113] Another function of VGAM2215 is therefore inhibition of Poly (ADP-ribose) Glycohydrolase (PARG, Accession NM_003631), a gene which is found in many tissues and may be subject to proteolysis generating smaller, active products. Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PARG. The function of PARG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2207.Protein Kinase C, Nu (PRKCN, Accession NM_005813) is another VGAM2215 host target gene. PRKCN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKCN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of PRKCN BINDING SITE, designated SEQ ID:12394, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76114] Another function of VGAM2215 is therefore inhibition of Protein Kinase C, Nu (PRKCN, Accession NM_005813). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKCN. Runt-related Transcription Factor 3 (RUNX3, Accession NM_004350) is another VGAM2215 host target gene. RUNX3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RUNX3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RUNX3 BINDING SITE, designated SEQ ID:10546, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76115] Another function of VGAM2215 is therefore inhibition of Runt-related Transcription Factor 3 (RUNX3, Accession NM_004350), a gene which binds to the core site, 5'-pygpyggt-3', of a number of enhancers and promoters.

Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RUNX3. The function of RUNX3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1151.FLJ20004 (Accession XM_170889) is another VGAM2215 host target gene. FLJ20004 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20004, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20004 BINDING SITE, designated SEQ ID:45642, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76116] Another function of VGAM2215 is therefore inhibition of FLJ20004 (Accession XM_170889). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20004. HTCD37 (Accession XM_041884) is another VGAM2215 host target gene. HTCD37 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by HTCD37, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HTCD37 BINDING SITE, designated SEQ ID:33616, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76117] Another function of VGAM2215 is therefore inhibition of HTCD37 (Accession XM_041884). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTCD37. KIAA0841 (Accession XM_049237) is another VGAM2215 host target gene. KIAA0841 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0841 BINDING SITE, designated SEQ ID:35357, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76118] Another function of VGAM2215 is therefore inhibition of KIAA0841 (Accession XM_049237). Accordingly, utilities

of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0841. KIAA0855 (Accession NM_015003) is another VGAM2215 host target gene. KIAA0855 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0855, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0855 BINDING SITE, designated SEQ ID:17371, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76119] Another function of VGAM2215 is therefore inhibition of KIAA0855 (Accession NM_015003). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0855. KIAA1843 (Accession XM_030838) is another VGAM2215 host target gene. KIAA1843 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1843, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1843 BINDING SITE, designated SEQ ID:31160, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76120] Another function of VGAM2215 is therefore inhibition of KIAA1843 (Accession XM_030838). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1843. MGC2827 (Accession NM_023940) is another VGAM2215 host target gene. MGC2827 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2827, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2827 BINDING SITE, designated SEQ ID:23423, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76121] Another function of VGAM2215 is therefore inhibition of MGC2827 (Accession NM_023940). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2827. NXP-2 (Accession XM_048706) is another VGAM2215 host target gene. NXP-2 BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by NXP-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NXP-2 BINDING SITE, designated SEQ ID:35228, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76122] Another function of VGAM2215 is therefore inhibition of NXP-2 (Accession XM_048706). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXP-2. LOC148809 (Accession XM_086325) is another VGAM2215 host target gene. LOC148809 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148809, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148809 BINDING SITE, designated SEQ ID:38591, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76123] Another function of VGAM2215 is therefore inhibition of

LOC148809 (Accession XM_086325). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148809. LOC153387 (Accession XM_098369) is another VGAM2215 host target gene. LOC153387 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153387, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153387 BINDING SITE, designated SEQ ID:41633, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76124] Another function of VGAM2215 is therefore inhibition of LOC153387 (Accession XM_098369). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153387. LOC169225 (Accession XM_108531) is another VGAM2215 host target gene. LOC169225 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC169225, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC169225 BINDING SITE, designated SEQ ID:42203, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76125] Another function of VGAM2215 is therefore inhibition of LOC169225 (Accession XM_108531). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169225. LOC169966 (Accession XM_093010) is another VGAM2215 host target gene. LOC169966 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC169966, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169966 BINDING SITE, designated SEQ ID:40163, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76126] Another function of VGAM2215 is therefore inhibition of LOC169966 (Accession XM_093010). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169966. LOC51157 (Accession NM_016202) is an-

other VGAM2215 host target gene. LOC51157 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51157, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51157 BINDING SITE, designated SEQ ID:18297, to the nucleotide sequence of VGAM2215 RNA, herein designated VGAM RNA, also designated SEQ ID:4926.

[76127] Another function of VGAM2215 is therefore inhibition of LOC51157 (Accession NM_016202). Accordingly, utilities of VGAM2215 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51157. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2216 (VGAM2216) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76128] VGAM2216 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2216 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[76129] VGAM2216 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2216 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76130] VGAM2216 gene encodes a VGAM2216 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2216 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2216 precursor RNA is designated SEQ ID:2202, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2202 is located at position 192667 relative to the genome of Ectromelia Virus.

[76131] VGAM2216 precursor RNA folds onto itself, forming VGAM2216 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76132] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2216 folded precursor RNA into VGAM2216 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2216 RNA is designated SEQ ID:4927, and is provided hereinbelow with reference to the sequence listing part.

[76133] VGAM2216 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2216 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2216 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76134] VGAM2216 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2216 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2216 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2216 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2216 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76135] The complementary binding of VGAM2216 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2216 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2216 host target RNA into VGAM2216 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76136] It is appreciated that VGAM2216 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2216 host target genes. The mRNA of each one of this plurality of VGAM2216 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2216 RNA, herein designated VGAM RNA, and which when bound by VGAM2216 RNA causes inhibition of translation of respective one or more VGAM2216 host target proteins.

[76137] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2216 gene, herein designated VGAM GENE, on one or more VGAM2216 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76138] It is yet further appreciated that a function of VGAM2216 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2216 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2216 correlate with, and may be deduced from, the identity of the host target genes which VGAM2216 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76139] Nucleotide sequences of the VGAM2216 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2216 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2216 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2216 are further described hereinbelow with reference to Table 1.

[76140] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2216 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2216 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76141] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2216 gene, herein designated VGAM is inhibition of expression of VGAM2216 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2216 correlate with, and may be deduced from, the identity of the target genes which VGAM2216 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76142] Cytochrome P450, Subfamily IIIA (niphedipine oxidase), Polypeptide 4 (CYP3A4, Accession NM_017460) is a VGAM2216 host target gene. CYP3A4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP3A4, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP3A4 BINDING SITE, designated SEQ ID:18931, to the nucleotide sequence of VGAM2216 RNA, herein designated VGAM RNA, also designated SEQ ID:4927.

[76143] A function of VGAM2216 is therefore inhibition of Cytochrome P450, Subfamily IIIA (niphedipine oxidase), Polypeptide 4 (CYP3A4, Accession NM_017460), a gene which may be involved in an nadph-dependent electron transport pathway. Accordingly, utilities of VGAM2216 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP3A4. The function of CYP3A4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM955.Inducible T-cell Co-stimulator (ICOS, Accession NM_012092) is another VGAM2216 host target gene. ICOS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICOS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

ICOS BINDING SITE, designated SEQ ID:14382, to the nucleotide sequence of VGAM2216 RNA, herein designated VGAM RNA, also designated SEQ ID:4927.

[76144] Another function of VGAM2216 is therefore inhibition of Inducible T-cell Co-stimulator (ICOS, Accession NM_012092), a gene which forms homodimers and functions as an inducible T-cell co-stimulator. Accordingly, utilities of VGAM2216 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICOS. The function of ICOS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM18.LOC256790 (Accession XM_170679) is another VGAM2216 host target gene. LOC256790 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256790, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256790 BINDING SITE, designated SEQ ID:45459, to the nucleotide sequence of VGAM2216 RNA, herein designated VGAM RNA, also designated SEQ ID:4927.

[76145] Another function of VGAM2216 is therefore inhibition of LOC256790 (Accession XM_170679). Accordingly, utilities of VGAM2216 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256790. LOC91421 (Accession XM_038364) is another VGAM2216 host target gene. LOC91421 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91421, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91421 BINDING SITE, designated SEQ ID:32827, to the nucleotide sequence of VGAM2216 RNA, herein designated VGAM RNA, also designated SEQ ID:4927.

[76146] Another function of VGAM2216 is therefore inhibition of LOC91421 (Accession XM_038364). Accordingly, utilities of VGAM2216 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91421. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2217 (VGAM2217) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[76147] VGAM2217 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2217 was detected is described hereinabove with reference to Figs. 1-8.

[76148] VGAM2217 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2217 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76149] VGAM2217 gene encodes a VGAM2217 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2217 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2217 precursor RNA is designated SEQ ID:2203, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2203 is located at position 198184 relative to the genome of Ectromelia Virus.

[76150] VGAM2217 precursor RNA folds onto itself, forming VGAM2217 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76151] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2217 folded precursor RNA into VGAM2217 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2217 RNA is designated SEQ ID:4928, and is provided hereinbelow with reference to the sequence listing part.

[76152] VGAM2217 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2217 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2217 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76153] VGAM2217 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2217 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2217 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2217 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2217 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76154] The complementary binding of VGAM2217 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2217 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2217 host target RNA into VGAM2217 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76155] It is appreciated that VGAM2217 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2217 host target genes. The mRNA of each one of this plurality of VGAM2217 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2217 RNA, herein designated VGAM RNA, and which when bound by VGAM2217 RNA causes inhibition of translation of respective one or more VGAM2217 host target proteins.

[76156] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2217 gene, herein designated VGAM GENE, on one or more VGAM2217 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76157] It is yet further appreciated that a function of VGAM2217 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2217 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2217 correlate with, and may be deduced from, the identity of the host target genes which VGAM2217 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[76158] Nucleotide sequences of the VGAM2217 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2217 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2217 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2217 are further described hereinbelow with reference to Table 1.

[76159] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2217 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2217 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76160] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2217 gene, herein designated VGAM is inhibition of expression of VGAM2217 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2217 correlate with, and may be deduced from, the identity of the target genes which VGAM2217 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76161] Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977) is a VGAM2217 host target gene. SLC22A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC22A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC22A3 BINDING SITE, designated SEQ ID:22503, to the nucleotide sequence of VGAM2217 RNA, herein designated VGAM RNA, also designated SEQ ID:4928.

[76162] A function of VGAM2217 is therefore inhibition of Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977), a gene which is a sodium-ion dependent, high affinity carnitine transporter. also transports organic cations without the involvement of sodium. involved in the active cellular uptake of carnitine. Accordingly, utilities of VGAM2217 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC22A3. The function of SLC22A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM2147.Solute Carrier Family 6 (neurotransmitter transporter, betaine/GABA), Member 12 (SLC6A12, Accession NM_003044) is another VGAM2217 host target gene. SLC6A12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC6A12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC6A12 BINDING SITE, designated SEQ ID:9010, to the nucleotide sequence of VGAM2217 RNA, herein designated VGAM RNA, also designated SEQ ID:4928.

[76163] Another function of VGAM2217 is therefore inhibition of Solute Carrier Family 6 (neurotransmitter transporter, betaine/GABA), Member 12 (SLC6A12, Accession NM_003044), a gene which transports betaine and gaba. Accordingly, utilities of VGAM2217 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A12. The function of SLC6A12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM293.Chromosome 22 Open Reading Frame 23

(C22orf23, Accession NM_032561) is another VGAM2217 host target gene. C22orf23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C22orf23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C22orf23 BINDING SITE, designated SEQ ID:26287, to the nucleotide sequence of VGAM2217 RNA, herein designated VGAM RNA, also designated SEQ ID:4928.

[76164] Another function of VGAM2217 is therefore inhibition of Chromosome 22 Open Reading Frame 23 (C22orf23, Accession NM_032561). Accordingly, utilities of VGAM2217 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C22orf23.

FLJ10159 (Accession NM_018013) is another VGAM2217 host target gene. FLJ10159 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10159, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10159 BINDING SITE, designated SEQ ID:19748, to the nucleotide sequence of

VGAM2217 RNA, herein designated VGAM RNA, also designated SEQ ID:4928.

[76165] Another function of VGAM2217 is therefore inhibition of FLJ10159 (Accession NM_018013). Accordingly, utilities of VGAM2217 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10159. KIAA1323 (Accession XM_032146) is another VGAM2217 host target gene. KIAA1323 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1323 BINDING SITE, designated SEQ ID:31566, to the nucleotide sequence of VGAM2217 RNA, herein designated VGAM RNA, also designated SEQ ID:4928.

[76166] Another function of VGAM2217 is therefore inhibition of KIAA1323 (Accession XM_032146). Accordingly, utilities of VGAM2217 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1323. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2218 (VGAM2218) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76167] VGAM2218 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2218 was detected is described hereinabove with reference to Figs. 1-8.

[76168] VGAM2218 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2218 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76169] VGAM2218 gene encodes a VGAM2218 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2218 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2218 precursor RNA is designated SEQ ID:2204, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2204 is located at position 188178 relative to the genome of Ectromelia Virus.

[76170] VGAM2218 precursor RNA folds onto itself, forming VGAM2218 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76171] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2218 folded precursor RNA into VGAM2218 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2218 RNA is designated SEQ ID:4929, and is provided hereinbelow with reference to the sequence listing part.

[76172] VGAM2218 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2218 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2218 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76173] VGAM2218 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2218 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2218 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2218 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2218 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76174] The complementary binding of VGAM2218 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2218 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2218 host target RNA into VGAM2218 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76175] It is appreciated that VGAM2218 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2218 host target genes. The mRNA of each one of this plurality of VGAM2218 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2218 RNA, herein designated VGAM RNA, and which when bound by VGAM2218 RNA causes inhibition of translation of respective one or more VGAM2218 host target proteins.

[76176] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2218 gene, herein designated VGAM GENE, on one or more VGAM2218 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76177] It is yet further appreciated that a function of VGAM2218 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2218 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2218 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2218 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76178] Nucleotide sequences of the VGAM2218 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2218 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2218 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2218 are further described hereinbelow with reference to Table 1.

[76179] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2218 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2218 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76180] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2218 gene, herein designated VGAM is inhibition of expression of VGAM2218 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2218 correlate with, and may be deduced from, the identity of the target genes which VGAM2218

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76181] FLJ13072 (Accession XM_117117) is a VGAM2218 host target gene. FLJ13072 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13072, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13072 BINDING SITE, designated SEQ ID:43233, to the nucleotide sequence of VGAM2218 RNA, herein designated VGAM RNA, also designated SEQ ID:4929.

[76182] A function of VGAM2218 is therefore inhibition of FLJ13072 (Accession XM_117117). Accordingly, utilities of VGAM2218 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13072. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2219 (VGAM2219) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76183] VGAM2219 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2219 was detected is described hereinabove with reference to Figs. 1-8.

[76184] VGAM2219 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2219 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76185] VGAM2219 gene encodes a VGAM2219 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2219 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2219 precursor RNA is designated SEQ ID:2205, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2205 is located at position 190763 relative to the genome of Ectromelia Virus.

[76186] VGAM2219 precursor RNA folds onto itself, forming VGAM2219 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76187] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2219 folded precursor RNA into VGAM2219 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2219 RNA is designated SEQ ID:4930, and is provided hereinbelow with reference to the sequence listing part.

[76188] VGAM2219 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2219 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2219 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[76189] VGAM2219 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2219 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2219 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2219 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2219 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76190] The complementary binding of VGAM2219 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2219 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2219 host target RNA into VGAM2219 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76191] It is appreciated that VGAM2219 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2219 host target genes. The mRNA of each one of this plurality of VGAM2219 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2219 RNA, herein designated VGAM RNA, and which when bound by VGAM2219 RNA causes inhibition of translation of respective one or more VGAM2219 host target proteins.

[76192] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2219 gene, herein designated VGAM GENE, on one or more VGAM2219 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76193] It is yet further appreciated that a function of VGAM2219 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2219 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2219 correlate with, and may be deduced from, the identity of the host target genes which VGAM2219 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76194] Nucleotide sequences of the VGAM2219 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2219 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2219 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2219 are further described hereinbelow with reference to Table 1.

[76195] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2219 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2219 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76196] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2219 gene, herein designated VGAM is inhibition of expression of VGAM2219 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2219 correlate with, and may be deduced from, the identity of the target genes which VGAM2219 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76197] Protocadherin Beta 16 (PCDHB16, Accession NM_020957) is a VGAM2219 host target gene. PCDHB16 BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHB16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHB16 BINDING SITE, designated SEQ ID:21945, to the nucleotide sequence of VGAM2219 RNA, herein designated VGAM RNA, also designated SEQ ID:4930.

[76198] A function of VGAM2219 is therefore inhibition of Protocadherin Beta 16 (PCDHB16, Accession NM_020957), a gene which is a potential calcium-dependent cell-adhesion protein. Accordingly, utilities of VGAM2219 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB16. The function of PCDHB16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM931.LOC221474 (Accession XM_166464) is another VGAM2219 host target gene. LOC221474 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221474, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC221474 BINDING SITE, designated SEQ ID:44382, to the nucleotide sequence of VGAM2219 RNA, herein designated VGAM RNA, also designated SEQ ID:4930.

[76199] Another function of VGAM2219 is therefore inhibition of LOC221474 (Accession XM_166464). Accordingly, utilities of VGAM2219 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221474. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2220 (VGAM2220) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76200] VGAM2220 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2220 was detected is described hereinabove with reference to Figs. 1-8.

[76201] VGAM2220 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2220 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[76202] VGAM2220 gene encodes a VGAM2220 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2220 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2220 precursor RNA is designated SEQ ID:2206, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2206 is located at position 196292 relative to the genome of Ectromelia Virus.

[76203] VGAM2220 precursor RNA folds onto itself, forming VGAM2220 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76204] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2220 folded precursor RNA into VGAM2220 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2220 RNA is designated SEQ ID:4931, and is provided hereinbelow with reference to the sequence listing part.

[76205] VGAM2220 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2220 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2220 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76206] VGAM2220 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2220 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2220 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2220 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2220 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76207] The complementary binding of VGAM2220 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2220 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2220 host target RNA into VGAM2220 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76208] It is appreciated that VGAM2220 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2220 host target genes. The mRNA of each one of this plurality of VGAM2220 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2220 RNA, herein designated VGAM RNA, and which when bound by VGAM2220 RNA causes inhibition of translation of respective one or more VGAM2220 host target proteins.

[76209] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2220 gene, herein designated VGAM GENE, on one or more VGAM2220 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76210] It is yet further appreciated that a function of VGAM2220 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2220 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2220 correlate with, and may be deduced from, the identity of the host target genes which VGAM2220 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76211] Nucleotide sequences of the VGAM2220 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2220 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2220 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2220 are further described hereinbelow with reference to Table 1.

[76212] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2220 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2220 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76213] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2220 gene, herein designated VGAM is inhibition of expression of VGAM2220 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2220 correlate with, and may be deduced from, the identity of the target genes which VGAM2220 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76214] PRO2435 (Accession NM_018527) is a VGAM2220 host target gene. PRO2435 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2435 BINDING SITE, designated SEQ ID:20598, to the nucleotide sequence of VGAM2220 RNA, herein designated VGAM RNA, also designated SEQ ID:4931.

[76215] A function of VGAM2220 is therefore inhibition of PRO2435 (Accession NM_018527). Accordingly, utilities of VGAM2220 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2435. LOC143425 (Accession XM_113695) is another VGAM2220 host target gene. LOC143425 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143425, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143425 BINDING SITE, designated SEQ ID:42354, to the nucleotide sequence of VGAM2220 RNA, herein designated VGAM RNA, also designated SEQ ID:4931.

[76216] Another function of VGAM2220 is therefore inhibition of LOC143425 (Accession XM_113695). Accordingly, utilities of VGAM2220 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143425. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2221 (VGAM2221) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[76217] VGAM2221 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2221 was detected is described hereinabove with reference to Figs. 1-8.

[76218] VGAM2221 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2221 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76219] VGAM2221 gene encodes a VGAM2221 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2221 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2221 precursor RNA is designated SEQ ID:2207, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2207 is located at position 161928 relative to the genome of Equine Herpesvirus 2.

[76220] VGAM2221 precursor RNA folds onto itself, forming VGAM2221 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76221] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2221 folded precursor RNA into VGAM2221 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2221 RNA is designated SEQ ID:4932, and is provided hereinbelow with reference to the sequence listing part.

[76222] VGAM2221 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2221 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2221 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76223] VGAM2221 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2221 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2221 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2221 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2221 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76224] The complementary binding of VGAM2221 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2221 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2221 host target RNA into VGAM2221 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76225] It is appreciated that VGAM2221 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2221 host target genes. The mRNA of each one of this plurality of VGAM2221 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2221 RNA, herein designated VGAM RNA, and which when bound by VGAM2221 RNA causes inhibition of translation of respective one or more VGAM2221 host target proteins.

[76226] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2221 gene, herein designated VGAM GENE, on one or more VGAM2221 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76227] It is yet further appreciated that a function of VGAM2221 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2221 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2221 correlate with, and may be deduced from, the identity of the host target genes which VGAM2221 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[76228] Nucleotide sequences of the VGAM2221 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2221 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2221 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2221 are further described hereinbelow with reference to Table 1.

[76229] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2221 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2221 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76230] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2221 gene, herein designated VGAM is inhibition of expression of VGAM2221 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2221 correlate with, and may be deduced from, the identity of the target genes which VGAM2221 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76231] Chromodomain Helicase DNA Binding Protein 2 (CHD2, Accession NM_001271) is a VGAM2221 host target gene. CHD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHD2 BINDING SITE, designated SEQ ID:6936, to the nucleotide sequence of VGAM2221 RNA, herein designated VGAM RNA, also designated SEQ ID:4932.

[76232] A function of VGAM2221 is therefore inhibition of Chromodomain Helicase DNA Binding Protein 2 (CHD2, Accession NM_001271). Accordingly, utilities of VGAM2221 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHD2. Coenzyme Q7 Homolog, Ubiquinone (yeast) (COQ7, Accession NM_016138) is another VGAM2221 host target gene. COQ7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COQ7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COQ7 BINDING SITE, designated SEQ ID:18222,

to the nucleotide sequence of VGAM2221 RNA, herein designated VGAM RNA, also designated SEQ ID:4932.

[76233] Another function of VGAM2221 is therefore inhibition of Coenzyme Q7 Homolog, Ubiquinone (yeast) (COQ7, Accession NM_016138). Accordingly, utilities of VGAM2221 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COQ7. KIAA1969 (Accession XM_086098) is another VGAM2221 host target gene. KIAA1969 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1969, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1969 BINDING SITE, designated SEQ ID:38490, to the nucleotide sequence of VGAM2221 RNA, herein designated VGAM RNA, also designated SEQ ID:4932.

[76234] Another function of VGAM2221 is therefore inhibition of KIAA1969 (Accession XM_086098). Accordingly, utilities of VGAM2221 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1969. LOC153196 (Accession XM_098323) is another VGAM2221 host target gene. LOC153196 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153196 BINDING SITE, designated SEQ ID:41586, to the nucleotide sequence of VGAM2221 RNA, herein designated VGAM RNA, also designated SEQ ID:4932.

[76235] Another function of VGAM2221 is therefore inhibition of LOC153196 (Accession XM_098323). Accordingly, utilities of VGAM2221 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153196. LOC169026 (Accession XM_095471) is another VGAM2221 host target gene. LOC169026 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC169026, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169026 BINDING SITE, designated SEQ ID:40260, to the nucleotide sequence of VGAM2221 RNA, herein designated VGAM RNA, also designated SEQ ID:4932.

[76236] Another function of VGAM2221 is therefore inhibition of

LOC169026 (Accession XM_095471). Accordingly, utilities of VGAM2221 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169026. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2222 (VGAM2222) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76237] VGAM2222 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2222 was detected is described hereinabove with reference to Figs. 1-8.

[76238] VGAM2222 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2222 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76239] VGAM2222 gene encodes a VGAM2222 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2222 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2222 precursor RNA is designated SEQ ID:2208, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2208 is located at position 11521 relative to the genome of Equine Herpesvirus 2.

[76240] VGAM2222 precursor RNA folds onto itself, forming VGAM2222 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76241] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2222 folded precursor RNA into VGAM2222 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide se-

quence of VGAM2222 RNA is designated SEQ ID:4933, and is provided hereinbelow with reference to the sequence listing part.

[76242] VGAM2222 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2222 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2222 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76243] VGAM2222 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2222 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2222 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2222 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2222 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76244] The complementary binding of VGAM2222 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2222 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2222 host target RNA into VGAM2222 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76245] It is appreciated that VGAM2222 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2222 host target genes. The mRNA of each one of this plurality of VGAM2222 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2222 RNA, herein designated VGAM RNA, and which when bound by VGAM2222 RNA causes inhibition of translation of respective one or more VGAM2222 host target proteins.

[76246] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2222 gene, herein designated VGAM GENE, on one or more VGAM2222 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76247] It is yet further appreciated that a function of VGAM2222

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2222 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2222 correlate with, and may be deduced from, the identity of the host target genes which VGAM2222 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76248] Nucleotide sequences of the VGAM2222 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2222 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2222 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2222 are further described hereinbelow with reference to Table 1.

[76249] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2222 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2222 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76250] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2222 gene, herein designated VGAM is inhibition of expression of VGAM2222 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2222 correlate with, and may be deduced from, the identity of the target genes which VGAM2222 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76251] CSE-C (Accession XM_166163) is a VGAM2222 host target gene. CSE-C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSE-C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSE-C BINDING SITE, designated SEQ ID:43982, to the nucleotide sequence of VGAM2222 RNA, herein designated VGAM RNA, also designated SEQ ID:4933.

[76252] A function of VGAM2222 is therefore inhibition of CSE-C (Accession XM_166163). Accordingly, utilities of VGAM2222 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSE-C. DKFZP434N178 (Accession XM_050278) is another

VGAM2222 host target gene. DKFZP434N178 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434N178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434N178 BINDING SITE, designated SEQ ID:35599, to the nucleotide sequence of VGAM2222 RNA, herein designated VGAM RNA, also designated SEQ ID:4933.

[76253] Another function of VGAM2222 is therefore inhibition of DKFZP434N178 (Accession XM_050278). Accordingly, utilities of VGAM2222 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434N178. LOC203411 (Accession XM_117547) is another VGAM2222 host target gene. LOC203411 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203411, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203411 BINDING SITE, designated SEQ ID:43566, to the nucleotide sequence of VGAM2222 RNA,

herein designated VGAM RNA, also designated SEQ ID:4933.

[76254] Another function of VGAM2222 is therefore inhibition of LOC203411 (Accession XM_117547). Accordingly, utilities of VGAM2222 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203411. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2223 (VGAM2223) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76255] VGAM2223 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2223 was detected is described hereinabove with reference to Figs. 1-8.

[76256] VGAM2223 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2223 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76257] VGAM2223 gene encodes a VGAM2223 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2223 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2223 precursor RNA is designated SEQ ID:2209, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2209 is located at position 2065 relative to the genome of Equine Herpesvirus 2.

[76258] VGAM2223 precursor RNA folds onto itself, forming VGAM2223 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76259] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2223 folded precursor RNA into VGAM2223 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2223 RNA is designated SEQ ID:4934, and is provided hereinbelow with reference to the sequence listing part.

[76260] VGAM2223 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2223 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2223 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76261] VGAM2223 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2223 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2223 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2223 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2223 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76262] The complementary binding of VGAM2223 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2223 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2223 host target RNA into VGAM2223 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76263] It is appreciated that VGAM2223 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2223 host target genes. The mRNA of each one of this plurality of VGAM2223 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2223 RNA, herein designated VGAM RNA, and which when bound by VGAM2223 RNA causes inhibition of translation of respective one or more VGAM2223 host target proteins.

[76264] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2223 gene, herein designated VGAM GENE, on one or more VGAM2223 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76265] It is yet further appreciated that a function of VGAM2223 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2223 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2223 correlate with, and may be deduced from, the identity of the host target genes which VGAM2223 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76266] Nucleotide sequences of the VGAM2223 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2223 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2223 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2223 are further described hereinbelow with reference to Table 1.

[76267] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2223 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2223 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76268] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2223 gene, herein designated VGAM is inhibition of expression of VGAM2223 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2223 correlate with, and may be deduced from, the identity of the target genes which VGAM2223 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76269] EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838) is a VGAM2223 host target gene. EGFL5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EGFL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGFL5 BINDING SITE, designated SEQ ID:41871, to the nucleotide sequence of VGAM2223 RNA, herein designated VGAM RNA, also designated SEQ ID:4934.

[76270] A function of VGAM2223 is therefore inhibition of EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838).

Accordingly, utilities of VGAM2223 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGFL5. Egl Nine Homolog 1 (C. elegans) (EGLN1, Accession NM_022051) is another VGAM2223 host target gene. EGLN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EGLN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGLN1 BINDING SITE, designated SEQ ID:22586, to the nucleotide sequence of VGAM2223 RNA, herein designated VGAM RNA, also designated SEQ ID:4934.

[76271] Another function of VGAM2223 is therefore inhibition of Egl Nine Homolog 1 (C. elegans) (EGLN1, Accession NM_022051), a gene which is expressed in the cytoplasm of arterial smooth muscle cells. Accordingly, utilities of VGAM2223 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGLN1. The function of EGLN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM216.Erbb2 Interacting Protein (ERBB2IP, Accession

NM_018695) is another VGAM2223 host target gene. ERBB2IP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERBB2IP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERBB2IP BINDING SITE, designated SEQ ID:20769, to the nucleotide sequence of VGAM2223 RNA, herein designated VGAM RNA, also designated SEQ ID:4934.

[76272] Another function of VGAM2223 is therefore inhibition of Erbb2 Interacting Protein (ERBB2IP, Accession NM_018695), a gene which ERBB2 interacting protein; acts as an adaptor for the receptor ERBB2/HER2. Accordingly, utilities of VGAM2223 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERBB2IP. The function of ERBB2IP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1019.FOG2 (Accession NM_012082) is another VGAM2223 host target gene. FOG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FOG2,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOG2 BINDING SITE, designated SEQ ID:14371, to the nucleotide sequence of VGAM2223 RNA, herein designated VGAM RNA, also designated SEQ ID:4934.

[76273] Another function of VGAM2223 is therefore inhibition of FOG2 (Accession NM_012082), a gene which Interacts with and modulates activities of GATA-1 and mCtBP2. Accordingly, utilities of VGAM2223 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOG2. The function of FOG2 has been established by previous studies. Svensson et al. (1999) showed that mouse Fog2 associates physically with the N-terminal zinc finger of Gata4 both in vitro and in vivo. This interaction appears to modulate specifically the transcriptional activity of Gata4 because overexpression of Fog2 in both NIH 3T3 cells and primary rat cardiomyocytes repressed Gata4-dependent transcription from multiple cardiac-restricted promoters. Taken together, these results implicated FOG2 as a novel modulator of GATA4 function during cardiac development and suggested a paradigm in which tissue-specific interactions between different FOG

and GATA proteins regulate the differentiation of distinct mesodermal cell lineages. Animal model experiments lend further support to the function of FOG2. GATA4 is a zinc finger transcription factor with a role in early cardiac development. GATA4-deficient mice fail to form a ventral heart tube and die of circulatory failure at embryonic day (E)8.5. Zfpm2, also know as Fog2, is a multi-zinc-finger protein that is coexpressed with Gata4 in the developing heart beginning at E8.5. Zfpm2 interacts specifically with the N-terminal zinc finger of Gata4 and represses Gata4-dependent transcription. Svensson et al. (2000) used targeted mutagenesis to explore the role of Zfpm2 in normal cardiac development. Zfpm2-deficient mice died of congestive heart failure at E13 with a syndrome of tricuspid atresia (OMIM Ref. No. 605067) that included an absent tricuspid valve, a large atrial septal defect, a ventral septal defect, an elongated left ventricular outflow tract, rightward displacement of the aortic valve, and pulmonic stenosis. These mice also displayed hypoplasia of the compact zone of the left ventricle. Findings indicated the importance of Zfpm2 in the normal looping and septation of the heart and suggested a genetic basis for the syndrome of tricuspid atresia.

[76274] It is appreciated that the abovementioned animal model for FOG2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[76275] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[76276] Svensson, E. C.; Huggins, G. S.; Lin, H.; Clendenin, C.; Jiang, F.; Tufts, R.; Dardik, F. B.; Leiden, J. M. : A syndrome of tricuspid atresia in mice with a targeted mutation of the gene encoding Fog-2. Nature Genet. 25: 353-356, 2000. ; and

[76277] Svensson, E. C.; Tufts, R. L.; Polk, C. E.; Leiden, J. M. : Molecular cloning of FOG-2: a modulator of transcription factor GATA-4 in cardiomyocytes. Proc. Nat. Acad. Sci. 96: 956-961.

[76278] Further studies establishing the function and utilities of FOG2 are found in John Hopkins OMIM database record ID 603693, and in sited publications numbered 991 and 9919-4953 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.TNF Receptor-associated Factor 5 (TRAF5, Accession NM_004619) is another VGAM2223 host target gene.

TRAF5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRAF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:10963, to the nucleotide sequence of VGAM2223 RNA, herein designated VGAM RNA, also designated SEQ ID:4934.

[76279] Another function of VGAM2223 is therefore inhibition of TNF Receptor-associated Factor 5 (TRAF5, Accession NM_004619), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of VGAM2223 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5. The function of TRAF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM76.KIAA0643 (Accession NM_024793) is another VGAM2223 host target gene. KIAA0643 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0643, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0643 BINDING SITE, designated SEQ ID:24172, to the nucleotide sequence of VGAM2223 RNA, herein designated VGAM RNA, also designated SEQ ID:4934.

[76280] Another function of VGAM2223 is therefore inhibition of KIAA0643 (Accession NM_024793). Accordingly, utilities of VGAM2223 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0643. KIAA1676 (Accession XM_167612) is another VGAM2223 host target gene. KIAA1676 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1676, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1676 BINDING SITE, designated SEQ ID:44725, to the nucleotide sequence of VGAM2223 RNA, herein designated VGAM RNA, also designated SEQ ID:4934.

[76281] Another function of VGAM2223 is therefore inhibition of KIAA1676 (Accession XM_167612). Accordingly, utilities of VGAM2223 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1676. LOC199725 (Accession XM_117119) is another VGAM2223 host target gene. LOC199725 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199725, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199725 BINDING SITE, designated SEQ ID:43240, to the nucleotide sequence of VGAM2223 RNA, herein designated VGAM RNA, also designated SEQ ID:4934.

[76282] Another function of VGAM2223 is therefore inhibition of LOC199725 (Accession XM_117119). Accordingly, utilities of VGAM2223 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199725. LOC200347 (Accession XM_114219) is another VGAM2223 host target gene. LOC200347 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200347, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200347 BINDING SITE, designated SEQ ID:42805, to

the nucleotide sequence of VGAM2223 RNA, herein designated VGAM RNA, also designated SEQ ID:4934.

[76283] Another function of VGAM2223 is therefore inhibition of LOC200347 (Accession XM_114219). Accordingly, utilities of VGAM2223 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200347. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2224 (VGAM2224) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76284] VGAM2224 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2224 was detected is described hereinabove with reference to Figs. 1-8.

[76285] VGAM2224 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2224 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76286] VGAM2224 gene encodes a VGAM2224 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2224 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2224 precursor RNA is designated SEQ ID:2210, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2210 is located at position 2628 relative to the genome of Equine Herpesvirus 2.

[76287] VGAM2224 precursor RNA folds onto itself, forming VGAM2224 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76288] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2224 folded precursor RNA into VGAM2224 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2224 RNA is designated SEQ ID:4935, and is provided hereinbelow with reference to the sequence listing part.

[76289] VGAM2224 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2224 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2224 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76290] VGAM2224 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2224 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2224 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2224 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2224 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76291] The complementary binding of VGAM2224 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2224 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2224 host target RNA into VGAM2224 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76292] It is appreciated that VGAM2224 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2224 host target genes. The mRNA of each one of this plurality of VGAM2224 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2224 RNA, herein designated VGAM RNA, and which when bound by VGAM2224 RNA causes inhibition of translation of respective one or more VGAM2224 host target proteins.

[76293] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2224 gene, herein designated VGAM GENE, on one or more VGAM2224 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76294] It is yet further appreciated that a function of VGAM2224 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2224 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2224 correlate with, and may be deduced from, the identity of the host target genes which VGAM2224 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76295] Nucleotide sequences of the VGAM2224 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2224 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2224 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2224 are further described hereinbelow with reference to Table 1.

[76296] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2224 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2224 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76297] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2224 gene, herein designated VGAM is inhibition of expression of VGAM2224 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2224 correlate with, and may be deduced from, the identity of the target genes which VGAM2224 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76298] Adenylate Cyclase 6 (ADCY6, Accession NM_015270) is a VGAM2224 host target gene. ADCY6 BINDING SITE1 and ADCY6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ADCY6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADCY6 BINDING SITE1 and ADCY6 BINDING SITE2, designated SEQ ID:17586 and SEQ ID:21974 respectively, to the nucleotide sequence of VGAM2224 RNA, herein designated VGAM RNA, also designated SEQ ID:4935.

[76299] A function of VGAM2224 is therefore inhibition of Adenylate Cyclase 6 (ADCY6, Accession NM_015270), a gene which this a membrane-bound, ca(2+)-inhibitable adenylyl cyclase (by similarity). Accordingly, utilities of VGAM2224 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY6. The function of ADCY6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM22.Zinc Finger Protein 36 (KOX 18) (ZNF36, Accession XM_168302) is another VGAM2224 host target gene. ZNF36 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF36, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF36 BINDING SITE, designated SEQ ID:45102, to the nucleotide sequence of VGAM2224 RNA, herein designated VGAM RNA, also designated SEQ ID:4935.

[76300] Another function of VGAM2224 is therefore inhibition of Zinc Finger Protein 36 (KOX 18) (ZNF36, Accession XM_168302), a gene which may be involved in transcrip-

tional regulation. Accordingly, utilities of VGAM2224 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF36. The function of ZNF36 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM804.A Kinase (PRKA) Anchor Protein 11 (AKAP11, Accession NM_016248) is another VGAM2224 host target gene. AKAP11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKAP11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP11 BINDING SITE, designated SEQ ID:18371, to the nucleotide sequence of VGAM2224 RNA, herein designated VGAM RNA, also designated SEQ ID:4935.

[76301] Another function of VGAM2224 is therefore inhibition of A Kinase (PRKA) Anchor Protein 11 (AKAP11, Accession NM_016248). Accordingly, utilities of VGAM2224 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP11. Fig. 1 further provides a conceptual description of a novel bioinformatically

detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2225 (VGAM2225) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76302] VGAM2225 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2225 was detected is described hereinabove with reference to Figs. 1-8.

[76303] VGAM2225 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2225 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76304] VGAM2225 gene encodes a VGAM2225 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2225 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2225 precursor RNA is designated SEQ ID:2211, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2211 is located at position 9536 relative to the

genome of Equine Herpesvirus 2.

[76305] VGAM2225 precursor RNA folds onto itself, forming VGAM2225 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76306] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2225 folded precursor RNA into VGAM2225 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2225 RNA is designated SEQ ID:4936, and is provided hereinbelow with reference to the sequence listing part.

[76307] VGAM2225 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2225 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2225 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76308] VGAM2225 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2225 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2225 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2225 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2225 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76309] The complementary binding of VGAM2225 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2225 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2225 host target RNA into VGAM2225 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76310] It is appreciated that VGAM2225 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2225 host target genes. The mRNA of each one of this plurality of VGAM2225 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2225 RNA, herein designated VGAM RNA, and which when bound by VGAM2225 RNA causes inhibition of translation of respective one or more VGAM2225 host target proteins.

[76311] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2225 gene, herein designated VGAM GENE, on one or more VGAM2225 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76312] It is yet further appreciated that a function of VGAM2225 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2225 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2225

correlate with, and may be deduced from, the identity of the host target genes which VGAM2225 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76313] Nucleotide sequences of the VGAM2225 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2225 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2225 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2225 are further described hereinbelow with reference to Table 1.

[76314] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2225 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2225 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76315] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2225 gene, herein designated VGAM is inhibition of expression of VGAM2225 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2225 correlate with, and may be deduced

from, the identity of the target genes which VGAM2225 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76316] Exostoses (multiple)-like 3 (EXTL3, Accession NM_001440) is a VGAM2225 host target gene. EXTL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EXTL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EXTL3 BINDING SITE, designated SEQ ID:7166, to the nucleotide sequence of VGAM2225 RNA, herein designated VGAM RNA, also designated SEQ ID:4936.

[76317] A function of VGAM2225 is therefore inhibition of Exostoses (multiple)-like 3 (EXTL3, Accession NM_001440), a gene which a member of the multiple exostoses gene family. Accordingly, utilities of VGAM2225 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EXTL3. The function of EXTL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM95.LanC Lantibiotic Synthetase Component C-like 1 (bacterial)

(LANCL1, Accession NM_006055) is another VGAM2225 host target gene. LANCL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LANCL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LANCL1 BINDING SITE, designated SEQ ID:12693, to the nucleotide sequence of VGAM2225 RNA, herein designated VGAM RNA, also designated SEQ ID:4936.

[76318] Another function of VGAM2225 is therefore inhibition of LanC Lantibiotic Synthetase Component C-like 1 (bacterial) (LANCL1, Accession NM_006055), a gene which binds the C-terminus of stomatin. Accordingly, utilities of VGAM2225 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LANCL1. The function of LANCL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM656.Lipoprotein Lipase (LPL, Accession NM_000237) is another VGAM2225 host target gene. LPL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LPL, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LPL BINDING SITE, designated SEQ ID:5750, to the nucleotide sequence of VGAM2225 RNA, herein designated VGAM RNA, also designated SEQ ID:4936.

[76319] Another function of VGAM2225 is therefore inhibition of Lipoprotein Lipase (LPL, Accession NM_000237), a gene which is the hydrolysis of triglycerides of circulating chylomicrons and very low density lipoproteins (vldl). the enzyme functions in the presence of apolipoprotein c-2 on the luminal surface of vascular. Accordingly, utilities of VGAM2225 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPL. The function of LPL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.FLJ22746 (Accession NM_024785) is another VGAM2225 host target gene. FLJ22746 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22746, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ22746 BINDING SITE, designated SEQ ID:24162, to the nucleotide sequence of VGAM2225 RNA, herein designated VGAM RNA, also designated SEQ ID:4936.

[76320] Another function of VGAM2225 is therefore inhibition of FLJ22746 (Accession NM_024785). Accordingly, utilities of VGAM2225 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22746. LOC128077 (Accession XM_059208) is another VGAM2225 host target gene. LOC128077 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC128077, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC128077 BINDING SITE, designated SEQ ID:36917, to the nucleotide sequence of VGAM2225 RNA, herein designated VGAM RNA, also designated SEQ ID:4936.

[76321] Another function of VGAM2225 is therefore inhibition of LOC128077 (Accession XM_059208). Accordingly, utilities of VGAM2225 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128077. LOC151201 (Accession XM_098021) is an-

other VGAM2225 host target gene. LOC151201 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151201, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151201 BINDING SITE, designated SEQ ID:41320, to the nucleotide sequence of VGAM2225 RNA, herein designated VGAM RNA, also designated SEQ ID:4936.

[76322] Another function of VGAM2225 is therefore inhibition of LOC151201 (Accession XM_098021). Accordingly, utilities of VGAM2225 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151201. LOC152286 (Accession XM_098188) is another VGAM2225 host target gene. LOC152286 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152286, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152286 BINDING SITE, designated SEQ ID:41460, to the nucleotide sequence of VGAM2225 RNA, herein designated VGAM RNA, also designated SEQ ID:4936.

[76323] Another function of VGAM2225 is therefore inhibition of LOC152286 (Accession XM_098188). Accordingly, utilities of VGAM2225 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152286. LOC221747 (Accession XM_166460) is another VGAM2225 host target gene. LOC221747 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221747, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221747 BINDING SITE, designated SEQ ID:44364, to the nucleotide sequence of VGAM2225 RNA, herein designated VGAM RNA, also designated SEQ ID:4936.

[76324] Another function of VGAM2225 is therefore inhibition of LOC221747 (Accession XM_166460). Accordingly, utilities of VGAM2225 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221747. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2226 (VGAM2226) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[76325] VGAM2226 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2226 was detected is described hereinabove with reference to Figs. 1-8.

[76326] VGAM2226 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2226 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76327] VGAM2226 gene encodes a VGAM2226 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2226 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2226 precursor RNA is designated SEQ ID:2212, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2212 is located at position 161798 relative to the genome of Equine Herpesvirus 2.

[76328] VGAM2226 precursor RNA folds onto itself, forming VGAM2226 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76329] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2226 folded precursor RNA into VGAM2226 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2226 RNA is designated SEQ ID:4937, and is provided hereinbelow with reference to the sequence listing part.

[76330] VGAM2226 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2226 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2226 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76331] VGAM2226 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2226 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2226 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2226 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2226 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76332] The complementary binding of VGAM2226 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2226 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2226 host target RNA into VGAM2226 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76333] It is appreciated that VGAM2226 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2226 host target genes. The mRNA of each one of this plurality of VGAM2226 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2226 RNA, herein designated VGAM RNA, and which when bound by VGAM2226 RNA causes inhibition of translation of respective one or more VGAM2226 host target proteins.

[76334] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2226 gene, herein designated VGAM GENE, on one or more VGAM2226 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76335] It is yet further appreciated that a function of VGAM2226 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2226 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2226 correlate with, and may be deduced from, the identity of the host target genes which VGAM2226 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[76336] Nucleotide sequences of the VGAM2226 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2226 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2226 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2226 are further described hereinbelow with reference to Table 1.

[76337] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2226 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2226 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76338] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2226 gene, herein designated VGAM is inhibition of expression of VGAM2226 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2226 correlate with, and may be deduced from, the identity of the target genes which VGAM2226 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76339] B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6, Accession NM_001706) is a VGAM2226 host target gene. BCL6 BINDING SITE1 and BCL6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by BCL6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL6 BINDING SITE1 and BCL6 BINDING SITE2, designated SEQ ID:7428 and SEQ ID:29055 respectively, to the nucleotide sequence of VGAM2226 RNA, herein designated VGAM RNA, also designated SEQ ID:4937.

[76340] A function of VGAM2226 is therefore inhibition of B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6, Accession NM_001706), a gene which is involved in the generation and maintenance of both T and B cells during immune responses. Accordingly, utilities of VGAM2226 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL6. The function of BCL6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM481.Diacylglycerol Kinase, Gamma 90kDa (DGKG,

Accession NM_001346) is another VGAM2226 host target gene. DGKG BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DGKG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGKG BINDING SITE, designated SEQ ID:7024, to the nucleotide sequence of VGAM2226 RNA, herein designated VGAM RNA, also designated SEQ ID:4937.

[76341] Another function of VGAM2226 is therefore inhibition of Diacylglycerol Kinase, Gamma 90kDa (DGKG, Accession NM_001346), a gene which may convert diacylglycerol to phosphatidic acid. Accordingly, utilities of VGAM2226 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGKG. The function of DGKG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM451.Heterogeneous Nuclear Ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa) (HNRPD, Accession NM_002138) is another VGAM2226 host target gene. HNRPD BINDING SITE1 and HNRPD BINDING SITE2 are HOST TARGET binding sites found in untranslated re-

gions of mRNA encoded by HNRPD, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNRPD BINDING SITE1 and HNRPD BINDING SITE2, designated SEQ ID:7913 and SEQ ID:25363 respectively, to the nucleotide sequence of VGAM2226 RNA, herein designated VGAM RNA, also designated SEQ ID:4937.

[76342] Another function of VGAM2226 is therefore inhibition of Heterogeneous Nuclear Ribonucleoprotein D (AU-rich element RNA binding protein 1, 37kDa) (HNRPD, Accession NM_002138). Accordingly, utilities of VGAM2226 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNRPD. Platelet Derived Growth Factor C (PDGFC, Accession NM_016205) is another VGAM2226 host target gene. PDGFC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDGFC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDGFC BINDING SITE, designated SEQ ID:18300, to the nucleotide sequence of VGAM2226 RNA, herein designated VGAM RNA,

also designated SEQ ID:4937.

[76343] Another function of VGAM2226 is therefore inhibition of Platelet Derived Growth Factor C (PDGFC, Accession NM_016205). Accordingly, utilities of VGAM2226 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFC. SENP7 (Accession NM_020654) is another VGAM2226 host target gene. SENP7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SENP7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SENP7 BINDING SITE, designated SEQ ID:21821, to the nucleotide sequence of VGAM2226 RNA, herein designated VGAM RNA, also designated SEQ ID:4937.

[76344] Another function of VGAM2226 is therefore inhibition of SENP7 (Accession NM_020654). Accordingly, utilities of VGAM2226 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SENP7. SNRK (Accession NM_017719) is another VGAM2226 host target gene. SNRK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by SNRK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNRK BINDING SITE, designated SEQ ID:19305, to the nucleotide sequence of VGAM2226 RNA, herein designated VGAM RNA, also designated SEQ ID:4937.

[76345] Another function of VGAM2226 is therefore inhibition of SNRK (Accession NM_017719). Accordingly, utilities of VGAM2226 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNRK. T-box 19 (TBX19, Accession NM_005149) is another VGAM2226 host target gene. TBX19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBX19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBX19 BINDING SITE, designated SEQ ID:11622, to the nucleotide sequence of VGAM2226 RNA, herein designated VGAM RNA, also designated SEQ ID:4937.

[76346] Another function of VGAM2226 is therefore inhibition of T-box 19 (TBX19, Accession NM_005149). Accordingly,

utilities of VGAM2226 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBX19. LOC154282 (Accession XM_098505) is another VGAM2226 host target gene. LOC154282 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154282, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154282 BINDING SITE, designated SEQ ID:41695, to the nucleotide sequence of VGAM2226 RNA, herein designated VGAM RNA, also designated SEQ ID:4937.

[76347] Another function of VGAM2226 is therefore inhibition of LOC154282 (Accession XM_098505). Accordingly, utilities of VGAM2226 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154282. LOC92539 (Accession XM_045632) is another VGAM2226 host target gene. LOC92539 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92539, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC92539 BINDING SITE, designated SEQ ID:34495, to the nucleotide sequence of VGAM2226 RNA, herein designated VGAM RNA, also designated SEQ ID:4937.

[76348] Another function of VGAM2226 is therefore inhibition of LOC92539 (Accession XM_045632). Accordingly, utilities of VGAM2226 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92539. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2227 (VGAM2227) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76349] VGAM2227 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2227 was detected is described hereinabove with reference to Figs. 1-8.

[76350] VGAM2227 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2227 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76351] VGAM2227 gene encodes a VGAM2227 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2227 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2227 precursor RNA is designated SEQ ID:2213, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2213 is located at position 161250 relative to the genome of Equine Herpesvirus 2.

[76352] VGAM2227 precursor RNA folds onto itself, forming VGAM2227 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76353] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2227 folded precursor RNA into VGAM2227 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2227 RNA is designated SEQ ID:4938, and is provided hereinbelow with reference to the sequence listing part.

[76354] VGAM2227 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2227 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2227 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76355] VGAM2227 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2227 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2227 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2227 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2227 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76356] The complementary binding of VGAM2227 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2227 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2227 host target RNA into VGAM2227 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76357] It is appreciated that VGAM2227 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2227 host target genes. The mRNA of each one of this plurality of VGAM2227 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2227 RNA, herein designated VGAM RNA, and which when bound by VGAM2227 RNA causes inhibition of translation of respective one or more VGAM2227 host target proteins.

[76358] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2227 gene, herein designated VGAM GENE, on one or more VGAM2227 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76359] It is yet further appreciated that a function of VGAM2227 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2227 correlate with, and may be deduced from, the identity of the host target genes which VGAM2227 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76360] Nucleotide sequences of the VGAM2227 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2227 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2227 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2227 are further described hereinbelow with reference to Table 1.

[76361] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2227 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2227 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76362] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2227 gene, herein designated VGAM is inhibition of expression of VGAM2227 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2227 correlate with, and may be deduced from, the identity of the target genes which VGAM2227 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76363] A Kinase (PRKA) Anchor Protein 13 (AKAP13, Accession XM_116974) is a VGAM2227 host target gene. AKAP13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKAP13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP13 BINDING SITE, designated SEQ ID:43183, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76364] A function of VGAM2227 is therefore inhibition of A Ki-

nase (PRKA) Anchor Protein 13 (AKAP13, Accession XM_116974), a gene which regulates subcellular localization of type II cAMP-dependent PKA. Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP13. The function of AKAP13 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM17.Aldehyde Dehydrogenase 8 Family, Member A1 (ALDH8A1, Accession NM_022568) is another VGAM2227 host target gene. ALDH8A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALDH8A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALDH8A1 BINDING SITE, designated SEQ ID:22890, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76365] Another function of VGAM2227 is therefore inhibition of Aldehyde Dehydrogenase 8 Family, Member A1 (ALDH8A1, Accession NM_022568). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with ALDH8A1. ATPase, Na+/K+ Transporting, Beta 2 Polypeptide (ATP1B2, Accession NM_001678) is another VGAM2227 host target gene. ATP1B2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP1B2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP1B2 BINDING SITE, designated SEQ ID:7396, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76366] Another function of VGAM2227 is therefore inhibition of ATPase, Na+/K+ Transporting, Beta 2 Polypeptide (ATP1B2, Accession NM_001678), a gene which catalyzes the hydrolysis of ATP coupled with the exchange of Na +/K+ ions across the plasma membrane. Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1B2. The function of ATP1B2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.Cytoplasmic Linker Associated

Protein 1 (CLASP1, Accession XM_037105) is another VGAM2227 host target gene. CLASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLASP1 BINDING SITE, designated SEQ ID:32543, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76367] Another function of VGAM2227 is therefore inhibition of Cytoplasmic Linker Associated Protein 1 (CLASP1, Accession XM_037105), a gene which plays a role in the local regulation of microtubule dynamics . Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLASP1. The function of CLASP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM298.Potassium Voltage-gated Channel, Shaker-related Subfamily, Member 3 (KCNA3, Accession NM_002232) is another VGAM2227 host target gene. KCNA3 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by KCNA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNA3 BINDING SITE, designated SEQ ID:8014, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76368] Another function of VGAM2227 is therefore inhibition of Potassium Voltage-gated Channel, Shaker-related Subfamily, Member 3 (KCNA3, Accession NM_002232). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNA3. Leptin (obesity homolog, mouse) (LEP, Accession NM_000230) is another VGAM2227 host target gene. LEP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LEP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LEP BINDING SITE, designated SEQ ID:5737, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76369] Another function of VGAM2227 is therefore inhibition of Leptin (obesity homolog, mouse) (LEP, Accession NM_000230). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LEP. Mastermind-like 1 (Drosophila) (MAML1, Accession NM_014757) is another VGAM2227 host target gene. MAML1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAML1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAML1 BINDING SITE, designated SEQ ID:16501, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76370] Another function of VGAM2227 is therefore inhibition of Mastermind-like 1 (Drosophila) (MAML1, Accession NM_014757), a gene which MAML1 functions as a transcriptional coactivator for Notch signaling. Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAML1. The function of MAML1 and its association with various diseases and clinical conditions, has been es-

tablished by previous studies, as described hereinabove with reference to VGAM556.Neuroepithelial Cell Transforming Gene 1 (NET1, Accession NM_005863) is another VGAM2227 host target gene. NET1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NET1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NET1 BINDING SITE, designated SEQ ID:12475, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76371] Another function of VGAM2227 is therefore inhibition of Neuroepithelial Cell Transforming Gene 1 (NET1, Accession NM_005863), a gene which is induced morphologic alterations and conferred a malignant phenotype in vitro and in nude mice. Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NET1. The function of NET1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1333.Polymerase (DNA directed), Theta (POLQ, Ac-

cession NM_006596) is another VGAM2227 host target gene. POLQ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POLQ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POLQ BINDING SITE, designated SEQ ID:13366, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76372] Another function of VGAM2227 is therefore inhibition of Polymerase (DNA directed), Theta (POLQ, Accession NM_006596), a gene which enhances untargeted mutagenesis. Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLQ. The function of POLQ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM922.RAD50 Homolog (S. cerevisiae) (RAD50, Accession NM_133482) is another VGAM2227 host target gene. RAD50 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAD50, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD50 BINDING SITE, designated SEQ ID:28553, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76373] Another function of VGAM2227 is therefore inhibition of RAD50 Homolog (S. cerevisiae) (RAD50, Accession NM_133482), a gene which is involved in dna double-strand break repair (dsbr). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD50. The function of RAD50 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM132.AD022 (Accession XM_165725) is another VGAM2227 host target gene. AD022 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AD022, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AD022 BINDING SITE, designated SEQ ID:43738, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA,

also designated SEQ ID:4938.

[76374] Another function of VGAM2227 is therefore inhibition of AD022 (Accession XM_165725). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AD022. Butyrophilin, Subfamily 2, Member A2 (BTN2A2, Accession NM_006995) is another VGAM2227 host target gene. BTN2A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTN2A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTN2A2 BINDING SITE, designated SEQ ID:13862, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76375] Another function of VGAM2227 is therefore inhibition of Butyrophilin, Subfamily 2, Member A2 (BTN2A2, Accession NM_006995). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN2A2. Chromosome 21 Open Reading Frame 42 (C21orf42, Accession NM_058184) is another VGAM2227 host target gene.

C21orf42 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C21orf42, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C21orf42 BINDING SITE, designated SEQ ID:27750, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76376] Another function of VGAM2227 is therefore inhibition of Chromosome 21 Open Reading Frame 42 (C21orf42, Accession NM_058184). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf42. DKFZp547D155 (Accession XM_046977) is another VGAM2227 host target gene. DKFZp547D155 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp547D155, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547D155 BINDING SITE, designated SEQ ID:34871, to the nucleotide sequence of VGAM2227 RNA,

herein designated VGAM RNA, also designated SEQ ID:4938.

[76377] Another function of VGAM2227 is therefore inhibition of DKFZp547D155 (Accession XM_046977). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547D155. F-box Protein 30 (FBXO30, Accession NM_032145) is another VGAM2227 host target gene. FBXO30 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXO30, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXO30 BINDING SITE, designated SEQ ID:25838, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76378] Another function of VGAM2227 is therefore inhibition of F-box Protein 30 (FBXO30, Accession NM_032145). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO30. FLJ31978 (Accession NM_144669) is another VGAM2227 host target gene.

FLJ31978 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ31978, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ31978 BINDING SITE, designated SEQ ID:29491, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76379] Another function of VGAM2227 is therefore inhibition of FLJ31978 (Accession NM_144669). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31978. HSU24186 (Accession NM_013347) is another VGAM2227 host target gene. HSU24186 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HSU24186, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSU24186 BINDING SITE, designated SEQ ID:14991, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76380] Another function of VGAM2227 is therefore inhibition of HSU24186 (Accession NM_013347). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSU24186. KIAA0939 (Accession XM_030524) is another VGAM2227 host target gene. KIAA0939 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0939, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0939 BINDING SITE, designated SEQ ID:31070, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76381] Another function of VGAM2227 is therefore inhibition of KIAA0939 (Accession XM_030524). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0939. KIAA1145 (Accession XM_037790) is another VGAM2227 host target gene. KIAA1145 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1145, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1145 BINDING SITE, designated SEQ ID:32681, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76382] Another function of VGAM2227 is therefore inhibition of KIAA1145 (Accession XM_037790). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1145. KIAA1432 (Accession XM_039698) is another VGAM2227 host target gene. KIAA1432 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1432, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1432 BINDING SITE, designated SEQ ID:33158, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76383] Another function of VGAM2227 is therefore inhibition of KIAA1432 (Accession XM_039698). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1432. KIAA1950 (Accession XM_166532) is another VGAM2227 host target gene. KIAA1950 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1950, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1950 BINDING SITE, designated SEQ ID:44493, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76384] Another function of VGAM2227 is therefore inhibition of KIAA1950 (Accession XM_166532). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1950. MFN2 (Accession NM_014874) is another VGAM2227 host target gene. MFN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MFN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MFN2 BINDING SITE, designated SEQ ID:17013, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4938.

[76385] Another function of VGAM2227 is therefore inhibition of MFN2 (Accession NM_014874). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MFN2. MGC21738 (Accession NM_145044) is another VGAM2227 host target gene. MGC21738 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC21738, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC21738 BINDING SITE, designated SEQ ID:29678, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76386] Another function of VGAM2227 is therefore inhibition of MGC21738 (Accession NM_145044). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21738. Signal Transducer and Activator of Transcription 5A (STAT5A, Accession NM_003152) is another VGAM2227 host target gene. STAT5A BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by STAT5A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAT5A BINDING SITE, designated SEQ ID:9130, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76387] Another function of VGAM2227 is therefore inhibition of Signal Transducer and Activator of Transcription 5A (STAT5A, Accession NM_003152). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAT5A. LOC143872 (Accession XM_084665) is another VGAM2227 host target gene. LOC143872 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143872, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143872 BINDING SITE, designated SEQ ID:37655, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76388] Another function of VGAM2227 is therefore inhibition of

LOC143872 (Accession XM_084665). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143872. LOC144321 (Accession XM_096578) is another VGAM2227 host target gene. LOC144321 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144321, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144321 BINDING SITE, designated SEQ ID:40410, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76389] Another function of VGAM2227 is therefore inhibition of LOC144321 (Accession XM_096578). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144321. LOC145482 (Accession XM_085154) is another VGAM2227 host target gene. LOC145482 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145482, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC145482 BINDING SITE, designated SEQ ID:37878, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76390] Another function of VGAM2227 is therefore inhibition of LOC145482 (Accession XM_085154). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145482. LOC146782 (Accession XM_083963) is another VGAM2227 host target gene. LOC146782 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146782, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146782 BINDING SITE, designated SEQ ID:37525, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76391] Another function of VGAM2227 is therefore inhibition of LOC146782 (Accession XM_083963). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146782. LOC221474 (Accession XM_166464) is an-

other VGAM2227 host target gene. LOC221474 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221474, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221474 BINDING SITE, designated SEQ ID:44381, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76392] Another function of VGAM2227 is therefore inhibition of LOC221474 (Accession XM_166464). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221474. LOC90092 (Accession XM_028862) is another VGAM2227 host target gene. LOC90092 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90092 BINDING SITE, designated SEQ ID:30792, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76393] Another function of VGAM2227 is therefore inhibition of LOC90092 (Accession XM_028862). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90092. LOC92344 (Accession XM_044455) is another VGAM2227 host target gene. LOC92344 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92344, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92344 BINDING SITE, designated SEQ ID:34210, to the nucleotide sequence of VGAM2227 RNA, herein designated VGAM RNA, also designated SEQ ID:4938.

[76394] Another function of VGAM2227 is therefore inhibition of LOC92344 (Accession XM_044455). Accordingly, utilities of VGAM2227 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92344. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2228 (VGAM2228) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[76395] VGAM2228 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2228 was detected is described hereinabove with reference to Figs. 1-8.

[76396] VGAM2228 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2228 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76397] VGAM2228 gene encodes a VGAM2228 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2228 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2228 precursor RNA is designated SEQ ID:2214, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2214 is located at position 162465 relative to the genome of Equine Herpesvirus 2.

[76398] VGAM2228 precursor RNA folds onto itself, forming VGAM2228 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76399] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2228 folded precursor RNA into VGAM2228 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2228 RNA is designated SEQ ID:4939, and is provided hereinbelow with reference to the sequence listing part.

[76400] VGAM2228 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2228 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2228 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76401] VGAM2228 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2228 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2228 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2228 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2228 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76402] The complementary binding of VGAM2228 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2228 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2228 host target RNA into VGAM2228 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76403] It is appreciated that VGAM2228 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2228 host target genes. The mRNA of each one of this plurality of VGAM2228 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2228 RNA, herein designated VGAM RNA, and which when bound by VGAM2228 RNA causes inhibition of translation of respective one or more VGAM2228 host target proteins.

[76404] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2228 gene, herein designated VGAM GENE, on one or more VGAM2228 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76405] It is yet further appreciated that a function of VGAM2228 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2228 correlate with, and may be deduced from, the identity of the host target genes which VGAM2228 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[76406] Nucleotide sequences of the VGAM2228 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2228 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2228 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2228 are further described hereinbelow with reference to Table 1.

[76407] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2228 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2228 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76408] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2228 gene, herein designated VGAM is inhibition of expression of VGAM2228 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2228 correlate with, and may be deduced from, the identity of the target genes which VGAM2228 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76409] Calcium Channel, Voltage-dependent, Gamma Subunit 7 (CACNG7, Accession NM_031896) is a VGAM2228 host target gene. CACNG7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CACNG7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CACNG7 BINDING SITE, designated SEQ ID:25641, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76410] A function of VGAM2228 is therefore inhibition of Calcium Channel, Voltage-dependent, Gamma Subunit 7 (CACNG7, Accession NM_031896), a gene which may stabilize the calcium channel in an inactivated (closed) state. Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNG7. The function of CACNG7 has been established by previous studies. Voltage-dependent calcium channels couple membrane depolarization in a number of cellular processes. These activities are regulated by distinct channels composed of the pore-forming alpha-1 subunit (e.g., CACNA1D; 114206) and the modulatory

beta (e.g., CACNB1; 114207), alpha-2/delta (e.g., CACNA2D1; 114204), and gamma (e.g., CACNG1; 114209) subunits. By RT-PCR and genomic sequence analysis, Burgess et al. (2001) determined that the CACNG7 gene, like CACNG6 and CACNG8, contains 4 exons.

[76411] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[76412] Burgess, D. L.; Gefrides, L. A.; Foreman, P. J.; Noebels, J. L. : A cluster of three novel Ca(2+) channel gamma subunit genes on chromosome 19q13.4: evolution and expression profile of the gamma subunit gene family. Genomics 71: 339-350, 2001. ; and

[76413] Chu, P.-J.; Robertson, H. M.; Best, P. M. : Calcium channel gamma subunits provide insights into the evolution of this gene family. Gene 280: 37-48, 2001.

[76414] Further studies establishing the function and utilities of CACNG7 are found in John Hopkins OMIM database record ID 606899, and in sited publications numbered 4526-4527 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Glutamate Receptor, Ionotropic, N-methyl D-

aspartate-like 1A (GRINL1A, Accession XM_045376) is another VGAM2228 host target gene. GRINL1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRINL1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRINL1A BINDING SITE, designated SEQ ID:34447, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76415] Another function of VGAM2228 is therefore inhibition of Glutamate Receptor, Ionotropic, N-methyl D-aspartate-like 1A (GRINL1A, Accession XM_045376), a gene which plays a role in the development and function of the mammalian brain. Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRINL1A. The function of GRINL1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM53.Heparan Sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4, Accession XM_056254) is another VGAM2228 host target gene. HS3ST4 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HS3ST4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HS3ST4 BINDING SITE, designated SEQ ID:36372, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76416] Another function of VGAM2228 is therefore inhibition of Heparan Sulfate (glucosamine) 3-O-sulfotransferase 4 (HS3ST4, Accession XM_056254). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HS3ST4. Integrin, Beta 3 (platelet glycoprotein IIIa, antigen CD61) (ITGB3, Accession NM_000212) is another VGAM2228 host target gene. ITGB3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGB3 BINDING SITE, designated SEQ ID:5708, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4939.

[76417] Another function of VGAM2228 is therefore inhibition of Integrin, Beta 3 (platelet glycoprotein IIIa, antigen CD61) (ITGB3, Accession NM_000212). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGB3. Pre-B-cell Leukemia Transcription Factor 2 (PBX2, Accession NM_002586) is another VGAM2228 host target gene. PBX2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PBX2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PBX2 BINDING SITE, designated SEQ ID:8448, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76418] Another function of VGAM2228 is therefore inhibition of Pre-B-cell Leukemia Transcription Factor 2 (PBX2, Accession NM_002586), a gene which binds the sequence 5'-atcaatcaa-3'. Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PBX2. The function of PBX2 and its association with various diseases and clinical con-

ditions, has been established by previous studies, as described hereinabove with reference to VGAM1063.Zinc Finger Protein 264 (ZNF264, Accession NM_003417) is another VGAM2228 host target gene. ZNF264 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF264, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF264 BINDING SITE, designated SEQ ID:9461, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76419] Another function of VGAM2228 is therefore inhibition of Zinc Finger Protein 264 (ZNF264, Accession NM_003417). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF264. CG012 (Accession XM_096710) is another VGAM2228 host target gene. CG012 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CG012, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of CG012 BINDING SITE, designated SEQ ID:40489, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76420] Another function of VGAM2228 is therefore inhibition of CG012 (Accession XM_096710). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CG012. FLJ12604 (Accession XM_035022) is another VGAM2228 host target gene. FLJ12604 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12604, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12604 BINDING SITE, designated SEQ ID:32190, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76421] Another function of VGAM2228 is therefore inhibition of FLJ12604 (Accession XM_035022). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12604. Interleukin 1 Receptor Accessory Protein-like 1

(IL1RAPL1, Accession NM_014271) is another VGAM2228 host target gene. IL1RAPL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IL1RAPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1RAPL1 BINDING SITE, designated SEQ ID:15553, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76422] Another function of VGAM2228 is therefore inhibition of Interleukin 1 Receptor Accessory Protein-like 1 (IL1RAPL1, Accession NM_014271). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1RAPL1. KIAA1069 (Accession XM_042635) is another VGAM2228 host target gene. KIAA1069 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1069, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1069 BINDING SITE, designated SEQ ID:33724, to the

nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76423] Another function of VGAM2228 is therefore inhibition of KIAA1069 (Accession XM_042635). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1069. KIAA1318 (Accession XM_041080) is another VGAM2228 host target gene. KIAA1318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1318 BINDING SITE, designated SEQ ID:33432, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76424] Another function of VGAM2228 is therefore inhibition of KIAA1318 (Accession XM_041080). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1318. KIAA1468 (Accession XM_166289) is another VGAM2228 host target gene. KIAA1468 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1468, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1468 BINDING SITE, designated SEQ ID:44100, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76425] Another function of VGAM2228 is therefore inhibition of KIAA1468 (Accession XM_166289). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1468. SAE1 (Accession NM_005500) is another VGAM2228 host target gene. SAE1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SAE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SAE1 BINDING SITE, designated SEQ ID:12005, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76426] Another function of VGAM2228 is therefore inhibition of SAE1 (Accession NM_005500). Accordingly, utilities of

VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SAE1. Zinc Finger Protein 36, C3H Type-like 2 (ZFP36L2, Accession NM_006887) is another VGAM2228 host target gene. ZFP36L2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZFP36L2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZFP36L2 BINDING SITE, designated SEQ ID:13754, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76427] Another function of VGAM2228 is therefore inhibition of Zinc Finger Protein 36, C3H Type-like 2 (ZFP36L2, Accession NM_006887). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP36L2. LOC151571 (Accession XM_098088) is another VGAM2228 host target gene. LOC151571 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151571, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151571 BINDING SITE, designated SEQ ID:41373, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76428] Another function of VGAM2228 is therefore inhibition of LOC151571 (Accession XM_098088). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151571. LOC158219 (Accession XM_088514) is another VGAM2228 host target gene. LOC158219 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158219 BINDING SITE, designated SEQ ID:39764, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76429] Another function of VGAM2228 is therefore inhibition of LOC158219 (Accession XM_088514). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC158219. LOC257415 (Accession XM_171177) is another VGAM2228 host target gene. LOC257415 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257415, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257415 BINDING SITE, designated SEQ ID:45959, to the nucleotide sequence of VGAM2228 RNA, herein designated VGAM RNA, also designated SEQ ID:4939.

[76430] Another function of VGAM2228 is therefore inhibition of LOC257415 (Accession XM_171177). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257415. LOC57019 (Accession NM_020313) is another VGAM2228 host target gene. LOC57019 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57019, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57019 BINDING SITE, designated SEQ ID:21570, to the nucleotide sequence of VGAM2228 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4939.

[76431] Another function of VGAM2228 is therefore inhibition of LOC57019 (Accession NM_020313). Accordingly, utilities of VGAM2228 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57019. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2229 (VGAM2229) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76432] VGAM2229 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2229 was detected is described hereinabove with reference to Figs. 1-8.

[76433] VGAM2229 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato Aucuba Mosaic Virus. VGAM2229 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76434] VGAM2229 gene encodes a VGAM2229 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2229 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2229 precursor RNA is designated SEQ ID:2215, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2215 is located at position 827 relative to the genome of Potato Aucuba Mosaic Virus.

[76435] VGAM2229 precursor RNA folds onto itself, forming VGAM2229 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76436] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2229 folded precursor RNA into VGAM2229 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2229 RNA is designated SEQ ID:4940, and is provided hereinbelow with reference to the sequence listing part.

[76437] VGAM2229 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2229 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2229 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76438] VGAM2229 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2229 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2229 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2229 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2229 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76439] The complementary binding of VGAM2229 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2229 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2229 host target RNA into VGAM2229 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76440] It is appreciated that VGAM2229 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2229 host target genes. The mRNA of

each one of this plurality of VGAM2229 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2229 RNA, herein designated VGAM RNA, and which when bound by VGAM2229 RNA causes inhibition of translation of respective one or more VGAM2229 host target proteins.

[76441] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2229 gene, herein designated VGAM GENE, on one or more VGAM2229 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76442] It is yet further appreciated that a function of VGAM2229 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2229 include diagnosis, prevention and treatment of viral infection by Potato Aucuba Mosaic Virus. Specific functions, and accordingly utilities, of

VGAM2229 correlate with, and may be deduced from, the identity of the host target genes which VGAM2229 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76443] Nucleotide sequences of the VGAM2229 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2229 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2229 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2229 are further described hereinbelow with reference to Table 1.

[76444] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2229 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2229 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76445] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2229 gene, herein designated VGAM is inhibition of expression of VGAM2229 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2229 correlate with, and may be deduced

from, the identity of the target genes which VGAM2229 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76446] Pleiomorphic Adenoma Gene 1 (PLAG1, Accession NM_002655) is a VGAM2229 host target gene. PLAG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLAG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLAG1 BINDING SITE, designated SEQ ID:8516, to the nucleotide sequence of VGAM2229 RNA, herein designated VGAM RNA, also designated SEQ ID:4940.

[76447] A function of VGAM2229 is therefore inhibition of Pleiomorphic Adenoma Gene 1 (PLAG1, Accession NM_002655), a gene which contains a zinc finger domain. Accordingly, utilities of VGAM2229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAG1. The function of PLAG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM29.FLJ10140 (Accession NM_018006) is another VGAM2229 host target

gene. FLJ10140 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10140 BINDING SITE, designated SEQ ID:19737, to the nucleotide sequence of VGAM2229 RNA, herein designated VGAM RNA, also designated SEQ ID:4940.

[76448] Another function of VGAM2229 is therefore inhibition of FLJ10140 (Accession NM_018006). Accordingly, utilities of VGAM2229 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10140. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2230 (VGAM2230) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76449] VGAM2230 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2230 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[76450] VGAM2230 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato Aucuba Mosaic Virus. VGAM2230 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76451] VGAM2230 gene encodes a VGAM2230 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2230 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2230 precursor RNA is designated SEQ ID:2216, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2216 is located at position 1300 relative to the genome of Potato Aucuba Mosaic Virus.

[76452] VGAM2230 precursor RNA folds onto itself, forming VGAM2230 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76453] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2230 folded precursor RNA into VGAM2230 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2230 RNA is designated SEQ ID:4941, and is provided hereinbelow with reference to the sequence listing part.

[76454] VGAM2230 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2230 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2230 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76455] VGAM2230 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2230 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2230 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2230 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2230 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76456] The complementary binding of VGAM2230 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2230 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2230 host target RNA into VGAM2230 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76457] It is appreciated that VGAM2230 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2230 host target genes. The mRNA of each one of this plurality of VGAM2230 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2230 RNA, herein designated VGAM RNA, and which when bound by VGAM2230 RNA causes inhibition of translation of respective one or more VGAM2230 host target proteins.

[76458] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2230 gene, herein designated VGAM GENE, on one or more VGAM2230 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76459] It is yet further appreciated that a function of VGAM2230 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of viral infection by Potato Aucuba Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2230 correlate with, and may be deduced from, the identity of the host target genes which VGAM2230 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76460] Nucleotide sequences of the VGAM2230 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2230 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2230 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2230 are further described hereinbelow with reference to Table 1.

[76461] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2230 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2230 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76462] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2230 gene, herein designated VGAM is inhibition of expression of VGAM2230 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2230 correlate with, and may be deduced from, the identity of the target genes which VGAM2230 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76463] BIG1 (Accession NM_006421) is a VGAM2230 host target gene. BIG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BIG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Ta-

ble 2 illustrates the complementarity of the nucleotide sequences of BIG1 BINDING SITE, designated SEQ ID:13139, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76464] A function of VGAM2230 is therefore inhibition of BIG1 (Accession NM_006421), a gene which is a guanine nucleotide-exchange protein, has a role in vesicular transport. Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIG1. The function of BIG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1190.Ca2+-dependent Activator Protein For Secretion (CADPS, Accession XM_036915) is another VGAM2230 host target gene. CADPS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CADPS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CADPS BINDING SITE, designated SEQ ID:32508, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4941.

[76465] Another function of VGAM2230 is therefore inhibition of Ca2+-dependent Activator Protein For Secretion (CADPS, Accession XM_036915), a gene which is required for the Ca2+-regulated exocytosis of secretory vesicles. Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CADPS. The function of CADPS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1315.Centaurin, Delta 1 (CENTD1, Accession NM_139182) is another VGAM2230 host target gene. CENTD1 BINDING SITE1 and CENTD1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CENTD1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CENTD1 BINDING SITE1 and CENTD1 BINDING SITE2, designated SEQ ID:29201 and SEQ ID:17563 respectively, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76466] Another function of VGAM2230 is therefore inhibition of

Centaurin, Delta 1 (CENTD1, Accession NM_139182), a gene which is nvolved in cell signaling/communication. Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENTD1. The function of CENTD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM445.Protein Phosphatase 3 (formerly 2B), Catalytic Subunit, Alpha Isoform (calcineurin A alpha) (PPP3CA, Accession NM_000944) is another VGAM2230 host target gene. PPP3CA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP3CA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP3CA BINDING SITE, designated SEQ ID:6646, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76467] Another function of VGAM2230 is therefore inhibition of Protein Phosphatase 3 (formerly 2B), Catalytic Subunit, Alpha Isoform (calcineurin A alpha) (PPP3CA, Accession

NM_000944), a gene which is the catalytic subunit of calcium-dependent, calmodulin-stimulated protein phosphatase. Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP3CA. The function of PPP3CA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM497.Phosphoribosyl Pyrophosphate Synthetase 2 (PRPS2, Accession NM_002765) is another VGAM2230 host target gene. PRPS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRPS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRPS2 BINDING SITE, designated SEQ ID:8657, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76468] Another function of VGAM2230 is therefore inhibition of Phosphoribosyl Pyrophosphate Synthetase 2 (PRPS2, Accession NM_002765), a gene which generates the PRPP needed for initiation of purine biosynthesis. Accordingly,

utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRPS2. The function of PRPS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM828.RNA Binding Motif Protein 8A (RBM8A, Accession NM_005105) is another VGAM2230 host target gene. RBM8A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBM8A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBM8A BINDING SITE, designated SEQ ID:11581, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76469] Another function of VGAM2230 is therefore inhibition of RNA Binding Motif Protein 8A (RBM8A, Accession NM_005105), a gene which involves in the pathway of gene expression postsplicing nuclear preexport mRNPs, and newly exported cytoplasmic mRNPs. Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with RBM8A. The function of RBM8A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1864.V-yes-1 Yamaguchi Sarcoma Viral Oncogene Homolog 1 (YES1, Accession NM_005433) is another VGAM2230 host target gene. YES1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by YES1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YES1 BINDING SITE, designated SEQ ID:11915, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76470] Another function of VGAM2230 is therefore inhibition of V-yes-1 Yamaguchi Sarcoma Viral Oncogene Homolog 1 (YES1, Accession NM_005433), a gene which is a putative protein-tyrosine kinase. Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YES1. The function of YES1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM74.Calmegin (CLGN, Accession NM_004362) is another VGAM2230 host target gene. CLGN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLGN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLGN BINDING SITE, designated SEQ ID:10569, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76471] Another function of VGAM2230 is therefore inhibition of Calmegin (CLGN, Accession NM_004362). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLGN. Cyclin M1 (CNNM1, Accession NM_020348) is another VGAM2230 host target gene. CNNM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNNM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNNM1 BINDING SITE, designated SEQ ID:21610, to the nucleotide sequence of VGAM2230 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4941.

[76472] Another function of VGAM2230 is therefore inhibition of Cyclin M1 (CNNM1, Accession NM_020348). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNNM1. DKFZp434C0923 (Accession NM_017598) is another VGAM2230 host target gene. DKFZp434C0923 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp434C0923, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434C0923 BINDING SITE, designated SEQ ID:19066, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76473] Another function of VGAM2230 is therefore inhibition of DKFZp434C0923 (Accession NM_017598). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434C0923. FLJ10704 (Accession NM_018185) is another VGAM2230 host target gene. FLJ10704 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by FLJ10704, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10704 BINDING SITE, designated SEQ ID:20034, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76474] Another function of VGAM2230 is therefore inhibition of FLJ10704 (Accession NM_018185). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10704. FLJ11267 (Accession NM_019607) is another VGAM2230 host target gene. FLJ11267 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ11267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11267 BINDING SITE, designated SEQ ID:21225, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76475] Another function of VGAM2230 is therefore inhibition of FLJ11267 (Accession NM_019607). Accordingly, utilities of

VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11267. FLJ13962 (Accession NM_024862) is another VGAM2230 host target gene. FLJ13962 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13962, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13962 BINDING SITE, designated SEQ ID:24298, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76476] Another function of VGAM2230 is therefore inhibition of FLJ13962 (Accession NM_024862). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13962. FLJ20413 (Accession NM_017808) is another VGAM2230 host target gene. FLJ20413 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20413, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20413

BINDING SITE, designated SEQ ID:19455, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76477] Another function of VGAM2230 is therefore inhibition of FLJ20413 (Accession NM_017808). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20413. FLJ20729 (Accession NM_017953) is another VGAM2230 host target gene. FLJ20729 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20729, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20729 BINDING SITE, designated SEQ ID:19657, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76478] Another function of VGAM2230 is therefore inhibition of FLJ20729 (Accession NM_017953). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20729. KIAA0237 (Accession NM_014747) is another VGAM2230 host target gene. KIAA0237 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0237, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0237 BINDING SITE, designated SEQ ID:16453, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76479] Another function of VGAM2230 is therefore inhibition of KIAA0237 (Accession NM_014747). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0237. KIAA0746 (Accession XM_045277) is another VGAM2230 host target gene. KIAA0746 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0746, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0746 BINDING SITE, designated SEQ ID:34415, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76480] Another function of VGAM2230 is therefore inhibition of

KIAA0746 (Accession XM_045277). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0746. KIAA0788 (Accession XM_049108) is another VGAM2230 host target gene. KIAA0788 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0788, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0788 BINDING SITE, designated SEQ ID:35344, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76481] Another function of VGAM2230 is therefore inhibition of KIAA0788 (Accession XM_049108). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0788. KIAA0795 (Accession NM_025010) is another VGAM2230 host target gene. KIAA0795 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0795, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0795 BINDING SITE, designated SEQ ID:24586, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76482] Another function of VGAM2230 is therefore inhibition of KIAA0795 (Accession NM_025010). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0795. KIAA1977 (Accession XM_058800) is another VGAM2230 host target gene. KIAA1977 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1977, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1977 BINDING SITE, designated SEQ ID:36746, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76483] Another function of VGAM2230 is therefore inhibition of KIAA1977 (Accession XM_058800). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1977. KR18 (Accession NM_033288) is another

VGAM2230 host target gene. KR18 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KR18, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KR18 BINDING SITE, designated SEQ ID:27121, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76484] Another function of VGAM2230 is therefore inhibition of KR18 (Accession NM_033288). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KR18. LIG-1 (Accession XM_033712) is another VGAM2230 host target gene. LIG-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIG-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIG-1 BINDING SITE, designated SEQ ID:31954, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76485] Another function of VGAM2230 is therefore inhibition of LIG-1 (Accession XM_033712). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIG-1. Nucleoporin 133kDa (NUP133, Accession NM_018230) is another VGAM2230 host target gene. NUP133 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUP133, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUP133 BINDING SITE, designated SEQ ID:20168, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76486] Another function of VGAM2230 is therefore inhibition of Nucleoporin 133kDa (NUP133, Accession NM_018230). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUP133. Pleiomorphic Adenoma Gene-like 2 (PLAGL2, Accession XM_047007) is another VGAM2230 host target gene. PLAGL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLAGL2, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLAGL2 BINDING SITE, designated SEQ ID:34880, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76487] Another function of VGAM2230 is therefore inhibition of Pleiomorphic Adenoma Gene-like 2 (PLAGL2, Accession XM_047007). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAGL2. RAN, Member RAS Oncogene Family (RAN, Accession NM_006325) is another VGAM2230 host target gene. RAN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAN BINDING SITE, designated SEQ ID:13017, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76488] Another function of VGAM2230 is therefore inhibition of RAN, Member RAS Oncogene Family (RAN, Accession

NM_006325). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAN. Roundabout, Axon Guidance Receptor, Homolog 2 (Drosophila) (ROBO2, Accession XM_031246) is another VGAM2230 host target gene. ROBO2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ROBO2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ROBO2 BINDING SITE, designated SEQ ID:31317, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76489] Another function of VGAM2230 is therefore inhibition of Roundabout, Axon Guidance Receptor, Homolog 2 (Drosophila) (ROBO2, Accession XM_031246). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ROBO2. SEC15B (Accession XM_039570) is another VGAM2230 host target gene. SEC15B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC15B, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC15B BINDING SITE, designated SEQ ID:33125, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76490] Another function of VGAM2230 is therefore inhibition of SEC15B (Accession XM_039570). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC15B. SH3 Domain Binding Glutamic Acid-rich Protein Like (SH3BGRL, Accession XM_030373) is another VGAM2230 host target gene. SH3BGRL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3BGRL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3BGRL BINDING SITE, designated SEQ ID:31027, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76491] Another function of VGAM2230 is therefore inhibition of SH3 Domain Binding Glutamic Acid-rich Protein Like

(SH3BGRL, Accession XM_030373). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BGRL. TRIP-Br2 (Accession NM_014755) is another VGAM2230 host target gene. TRIP-Br2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIP-Br2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIP-Br2 BINDING SITE, designated SEQ ID:16494, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76492] Another function of VGAM2230 is therefore inhibition of TRIP-Br2 (Accession NM_014755). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIP-Br2. LOC157507 (Accession XM_088312) is another VGAM2230 host target gene. LOC157507 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157507, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC157507 BINDING SITE, designated SEQ ID:39607, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76493] Another function of VGAM2230 is therefore inhibition of LOC157507 (Accession XM_088312). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157507. LOC161742 (Accession XM_091095) is another VGAM2230 host target gene. LOC161742 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC161742, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161742 BINDING SITE, designated SEQ ID:40028, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76494] Another function of VGAM2230 is therefore inhibition of LOC161742 (Accession XM_091095). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161742. LOC162239 (Accession XM_091439) is an-

other VGAM2230 host target gene. LOC162239 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC162239, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162239 BINDING SITE, designated SEQ ID:40053, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76495] Another function of VGAM2230 is therefore inhibition of LOC162239 (Accession XM_091439). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162239. LOC199704 (Accession XM_113994) is another VGAM2230 host target gene. LOC199704 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199704, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199704 BINDING SITE, designated SEQ ID:42602, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76496] Another function of VGAM2230 is therefore inhibition of LOC199704 (Accession XM_113994). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199704. LOC220469 (Accession XM_084334) is another VGAM2230 host target gene. LOC220469 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220469, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220469 BINDING SITE, designated SEQ ID:37554, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76497] Another function of VGAM2230 is therefore inhibition of LOC220469 (Accession XM_084334). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220469. LOC221002 (Accession XM_166156) is another VGAM2230 host target gene. LOC221002 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221002, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221002 BINDING SITE, designated SEQ ID:43975, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76498] Another function of VGAM2230 is therefore inhibition of LOC221002 (Accession XM_166156). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221002. LOC56965 (Accession NM_020213) is another VGAM2230 host target gene. LOC56965 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC56965, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56965 BINDING SITE, designated SEQ ID:21454, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76499] Another function of VGAM2230 is therefore inhibition of LOC56965 (Accession NM_020213). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC56965. LOC91050 (Accession XM_035703) is another VGAM2230 host target gene. LOC91050 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91050, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91050 BINDING SITE, designated SEQ ID:32337, to the nucleotide sequence of VGAM2230 RNA, herein designated VGAM RNA, also designated SEQ ID:4941.

[76500] Another function of VGAM2230 is therefore inhibition of LOC91050 (Accession XM_035703). Accordingly, utilities of VGAM2230 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91050. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2231 (VGAM2231) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76501] VGAM2231 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2231 was detected is described hereinabove with reference to Figs. 1-8.

[76502] VGAM2231 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Potato Aucuba Mosaic Virus. VGAM2231 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76503] VGAM2231 gene encodes a VGAM2231 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2231 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2231 precursor RNA is designated SEQ ID:2217, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2217 is located at position 1079 relative to the genome of Potato Aucuba Mosaic Virus.

[76504] VGAM2231 precursor RNA folds onto itself, forming VGAM2231 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76505] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2231 folded precursor RNA into VGAM2231 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2231 RNA is designated SEQ ID:4942, and is provided hereinbelow with reference to the sequence listing part.

[76506] VGAM2231 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2231 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2231 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76507] VGAM2231 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2231 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2231 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2231 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2231 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76508] The complementary binding of VGAM2231 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2231 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2231 host target RNA into VGAM2231 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76509] It is appreciated that VGAM2231 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2231 host target genes. The mRNA of each one of this plurality of VGAM2231 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2231 RNA, herein designated VGAM RNA, and which when bound by VGAM2231 RNA causes inhibition of translation of respective one or more VGAM2231 host target proteins.

[76510] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2231 gene, herein designated VGAM GENE, on one or more VGAM2231 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76511] It is yet further appreciated that a function of VGAM2231 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of viral infection by Potato Aucuba Mosaic Virus. Specific functions, and accordingly utilities, of VGAM2231 correlate with, and may be deduced from, the identity of the host target genes which VGAM2231 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76512] Nucleotide sequences of the VGAM2231 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2231 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2231 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2231 are further described hereinbelow with reference to Table 1.

[76513] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2231 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2231 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76514] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2231 gene, herein designated VGAM is inhibition of expression of VGAM2231 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2231 correlate with, and may be deduced from, the identity of the target genes which VGAM2231 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76515] ATPase, Na+/K+ Transporting, Alpha 2 (+) Polypeptide (ATP1A2, Accession NM_000702) is a VGAM2231 host target gene. ATP1A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA en-

coded by ATP1A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP1A2 BINDING SITE, designated SEQ ID:6367, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76516] A function of VGAM2231 is therefore inhibition of ATPase, Na+/K+ Transporting, Alpha 2 (+) Polypeptide (ATP1A2, Accession NM_000702). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1A2. Protocadherin Alpha 9 (PCDHA9, Accession NM_014005) is another VGAM2231 host target gene. PCDHA9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHA9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA9 BINDING SITE, designated SEQ ID:15214, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76517] Another function of VGAM2231 is therefore inhibition of Protocadherin Alpha 9 (PCDHA9, Accession NM_014005), a gene which is a calcium-dependent cell-adhesion protein. Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA9. The function of PCDHA9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM71.Protein Tyrosine Phosphatase, Receptor Type, A (PTPRA, Accession NM_002836) is another VGAM2231 host target gene. PTPRA BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PTPRA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRA BINDING SITE, designated SEQ ID:8715, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76518] Another function of VGAM2231 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, A (PTPRA, Accession NM_002836), a gene which is the human homolog of the murine PTPase. Accordingly, utilities of

VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRA. The function of PTPRA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1205.Splicing Factor, Arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1, Accession NM_006924) is another VGAM2231 host target gene. SFRS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFRS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRS1 BINDING SITE, designated SEQ ID:13803, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76519] Another function of VGAM2231 is therefore inhibition of Splicing Factor, Arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1, Accession NM_006924), a gene which plays an essential role in pre-mRNA splicing. Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRS1. The function of SFRS1 and its

association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM323.Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977) is another VGAM2231 host target gene. SLC22A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC22A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC22A3 BINDING SITE, designated SEQ ID:22504, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76520] Another function of VGAM2231 is therefore inhibition of Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977), a gene which is a sodium-ion dependent, high affinity carnitine transporter. also transports organic cations without the involvement of sodium. involved in the active cellular uptake of carnitine. Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC22A3. The

function of SLC22A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2147.Vanin 1 (VNN1, Accession NM_004666) is another VGAM2231 host target gene. VNN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VNN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VNN1 BINDING SITE, designated SEQ ID:11040, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76521] Another function of VGAM2231 is therefore inhibition of Vanin 1 (VNN1, Accession NM_004666), a gene which may regulate steps in thymus homing and play a role in mammalian sexual development. Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VNN1. The function of VNN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM419.Zinc Finger Protein 124 (HZF-16) (ZNF124,

Accession NM_003431) is another VGAM2231 host target gene. ZNF124 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF124, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF124 BINDING SITE, designated SEQ ID:9484, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76522] Another function of VGAM2231 is therefore inhibition of Zinc Finger Protein 124 (HZF-16) (ZNF124, Accession NM_003431). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF124. Chromosome 22 Open Reading Frame 19 (C22orf19, Accession NM_003678) is another VGAM2231 host target gene. C22orf19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C22orf19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C22orf19 BINDING SITE, designated SEQ

ID:9776, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76523] Another function of VGAM2231 is therefore inhibition of Chromosome 22 Open Reading Frame 19 (C22orf19, Accession NM_003678). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C22orf19. Chromosome 8 Open Reading Frame 2 (C8orf2, Accession NM_007175) is another VGAM2231 host target gene. C8orf2 BINDING SITE1 and C8orf2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by C8orf2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C8orf2 BINDING SITE1 and C8orf2 BINDING SITE2, designated SEQ ID:14024 and SEQ ID:14025 respectively, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76524] Another function of VGAM2231 is therefore inhibition of Chromosome 8 Open Reading Frame 2 (C8orf2, Accession NM_007175). Accordingly, utilities of VGAM2231 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with C8orf2. FLJ23132 (Accession XM_171194) is another VGAM2231 host target gene. FLJ23132 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23132, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23132 BINDING SITE, designated SEQ ID:45982, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76525] Another function of VGAM2231 is therefore inhibition of FLJ23132 (Accession XM_171194). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23132. HRD1 (Accession XM_045498) is another VGAM2231 host target gene. HRD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HRD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRD1 BINDING SITE,

designated SEQ ID:34475, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76526] Another function of VGAM2231 is therefore inhibition of HRD1 (Accession XM_045498). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRD1. KIAA0009 (Accession NM_014637) is another VGAM2231 host target gene. KIAA0009 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0009, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0009 BINDING SITE, designated SEQ ID:16022, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76527] Another function of VGAM2231 is therefore inhibition of KIAA0009 (Accession NM_014637). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0009. MGC13523 (Accession NM_033411) is another VGAM2231 host target gene. MGC13523 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC13523, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13523 BINDING SITE, designated SEQ ID:27234, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76528] Another function of VGAM2231 is therefore inhibition of MGC13523 (Accession NM_033411). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13523. LOC150481 (Accession XM_086929) is another VGAM2231 host target gene. LOC150481 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150481, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150481 BINDING SITE, designated SEQ ID:38979, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76529] Another function of VGAM2231 is therefore inhibition of

LOC150481 (Accession XM_086929). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150481. LOC158191 (Accession XM_088505) is another VGAM2231 host target gene. LOC158191 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158191, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158191 BINDING SITE, designated SEQ ID:39758, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76530] Another function of VGAM2231 is therefore inhibition of LOC158191 (Accession XM_088505). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158191. LOC201516 (Accession XM_113974) is another VGAM2231 host target gene. LOC201516 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC201516 BINDING SITE, designated SEQ ID:42582, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76531] Another function of VGAM2231 is therefore inhibition of LOC201516 (Accession XM_113974). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201516. LOC219672 (Accession XM_166111) is another VGAM2231 host target gene. LOC219672 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219672, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219672 BINDING SITE, designated SEQ ID:43890, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76532] Another function of VGAM2231 is therefore inhibition of LOC219672 (Accession XM_166111). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219672. LOC219988 (Accession XM_166223) is an-

other VGAM2231 host target gene. LOC219988 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219988, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219988 BINDING SITE, designated SEQ ID:44042, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76533] Another function of VGAM2231 is therefore inhibition of LOC219988 (Accession XM_166223). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219988. LOC90190 (Accession XM_029758) is another VGAM2231 host target gene. LOC90190 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90190, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90190 BINDING SITE, designated SEQ ID:30947, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76534] Another function of VGAM2231 is therefore inhibition of LOC90190 (Accession XM_029758). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90190. LOC91380 (Accession XM_038134) is another VGAM2231 host target gene. LOC91380 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91380, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91380 BINDING SITE, designated SEQ ID:32758, to the nucleotide sequence of VGAM2231 RNA, herein designated VGAM RNA, also designated SEQ ID:4942.

[76535] Another function of VGAM2231 is therefore inhibition of LOC91380 (Accession XM_038134). Accordingly, utilities of VGAM2231 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91380. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2232 (VGAM2232) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[76536] VGAM2232 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2232 was detected is described hereinabove with reference to Figs. 1-8.

[76537] VGAM2232 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2232 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76538] VGAM2232 gene encodes a VGAM2232 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2232 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2232 precursor RNA is designated SEQ ID:2218, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2218 is located at position 2170 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76539] VGAM2232 precursor RNA folds onto itself, forming VGAM2232 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76540] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2232 folded precursor RNA into VGAM2232 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2232 RNA is designated SEQ ID:4943, and is provided hereinbelow with reference to the sequence listing part.

[76541] VGAM2232 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2232 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2232 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76542] VGAM2232 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2232 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2232 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2232 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2232 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76543] The complementary binding of VGAM2232 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2232 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2232 host target RNA into VGAM2232 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76544] It is appreciated that VGAM2232 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2232 host target genes. The mRNA of each one of this plurality of VGAM2232 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2232 RNA, herein designated VGAM RNA, and which when bound by VGAM2232 RNA causes inhibition of translation of respective one or more VGAM2232 host target proteins.

[76545] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2232 gene, herein designated VGAM GENE, on one or more VGAM2232 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76546] It is yet further appreciated that a function of VGAM2232 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGAM2232 correlate with, and may be deduced from, the identity of the host target genes which VGAM2232 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[76547] Nucleotide sequences of the VGAM2232 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2232 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2232 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2232 are further described hereinbelow with reference to Table 1.

[76548] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2232 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2232 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76549] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2232 gene, herein designated VGAM is inhibition of expression of VGAM2232 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2232 correlate with, and may be deduced from, the identity of the target genes which VGAM2232 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76550] ATPase, Cu++ Transporting, Alpha Polypeptide (Menkes syndrome) (ATP7A, Accession NM_000052) is a VGAM2232 host target gene. ATP7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:5494, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76551] A function of VGAM2232 is therefore inhibition of ATPase, Cu++ Transporting, Alpha Polypeptide (Menkes syndrome) (ATP7A, Accession NM_000052). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7A. Branched Chain Aminotransferase 1, Cytosolic (BCAT1, Accession XM_038659) is another VGAM2232 host target gene. BCAT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCAT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of BCAT1 BINDING SITE, designated SEQ ID:32894, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76552] Another function of VGAM2232 is therefore inhibition of Branched Chain Aminotransferase 1, Cytosolic (BCAT1, Accession XM_038659), a gene which catalyzes of the essential branched chain leucine, isoleucine, and valine. Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCAT1. The function of BCAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1367.Frizzled Homolog 4 (Drosophila) (FZD4, Accession NM_012193) is another VGAM2232 host target gene. FZD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FZD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FZD4 BINDING SITE, designated SEQ ID:14481, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4943.

[76553] Another function of VGAM2232 is therefore inhibition of Frizzled Homolog 4 (Drosophila) (FZD4, Accession NM_012193), a gene which may function in cell polarity, cell fate specification and cancer; similar to frizzled receptor family, has seven transmembrane domains. Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FZD4. The function of FZD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM309.Mitogen-activated Protein Kinase 1 (MAPK1, Accession NM_002745) is another VGAM2232 host target gene. MAPK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAPK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPK1 BINDING SITE, designated SEQ ID:8618, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76554] Another function of VGAM2232 is therefore inhibition of

Mitogen-activated Protein Kinase 1 (MAPK1, Accession NM_002745), a gene which phosphorylates microtubule-associated protein-2 (map2). myelin basic protein (mbp), and elk-1; may promote entry in the cell cycle. Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK1. The function of MAPK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM217.RAD52 Homolog (S. cerevisiae) (RAD52, Accession NM_134422) is another VGAM2232 host target gene. RAD52 BINDING SITE1 through RAD52 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RAD52, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD52 BINDING SITE1 through RAD52 BINDING SITE3, designated SEQ ID:28641, SEQ ID:28651 and SEQ ID:28660 respectively, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76555] Another function of VGAM2232 is therefore inhibition of

RAD52 Homolog (S. cerevisiae) (RAD52, Accession NM_134422). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD52. DKFZP434C171 (Accession NM_015621) is another VGAM2232 host target gene. DKFZP434C171 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434C171, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434C171 BINDING SITE, designated SEQ ID:17881, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76556] Another function of VGAM2232 is therefore inhibition of DKFZP434C171 (Accession NM_015621). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434C171. KIAA0285 (Accession NM_014807) is another VGAM2232 host target gene. KIAA0285 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0285, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0285 BINDING SITE, designated SEQ ID:16747, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76557] Another function of VGAM2232 is therefore inhibition of KIAA0285 (Accession NM_014807). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0285. KIAA0408 (Accession NM_014702) is another VGAM2232 host target gene. KIAA0408 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0408, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0408 BINDING SITE, designated SEQ ID:16237, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76558] Another function of VGAM2232 is therefore inhibition of KIAA0408 (Accession NM_014702). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0408. KIAA1871 (Accession XM_028409) is another VGAM2232 host target gene. KIAA1871 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1871 BINDING SITE, designated SEQ ID:30707, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76559] Another function of VGAM2232 is therefore inhibition of KIAA1871 (Accession XM_028409). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1871. Phosphatase, Orphan 1 (phospho1, Accession XM_091572) is another VGAM2232 host target gene. phospho1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by phospho1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of phospho1 BINDING SITE, designated SEQ ID:40065, to the nucleotide sequence of VGAM2232 RNA,

herein designated VGAM RNA, also designated SEQ ID:4943.

[76560] Another function of VGAM2232 is therefore inhibition of Phosphatase, Orphan 1 (phospho1, Accession XM_091572). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with phospho1. PPI5PIV (Accession NM_019892) is another VGAM2232 host target gene. PPI5PIV BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPI5PIV, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPI5PIV BINDING SITE, designated SEQ ID:21273, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76561] Another function of VGAM2232 is therefore inhibition of PPI5PIV (Accession NM_019892). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPI5PIV. Thiamine Triphosphatase (THTPA, Accession NM_024328) is another VGAM2232 host target gene. THTPA BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by THTPA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of THTPA BINDING SITE, designated SEQ ID:23621, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76562] Another function of VGAM2232 is therefore inhibition of Thiamine Triphosphatase (THTPA, Accession NM_024328). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THTPA. TSPEAR (Accession NM_144991) is another VGAM2232 host target gene. TSPEAR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TSPEAR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TSPEAR BINDING SITE, designated SEQ ID:29594, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76563] Another function of VGAM2232 is therefore inhibition of TSPEAR (Accession NM_144991). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSPEAR. Zinc Finger Protein 297B (ZNF297B, Accession XM_088524) is another VGAM2232 host target gene. ZNF297B BINDING SITE1 and ZNF297B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ZNF297B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF297B BINDING SITE1 and ZNF297B BINDING SITE2, designated SEQ ID:39769 and SEQ ID:15218 respectively, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76564] Another function of VGAM2232 is therefore inhibition of Zinc Finger Protein 297B (ZNF297B, Accession XM_088524). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF297B. LOC146520 (Accession XM_085492) is another VGAM2232 host target gene. LOC146520 BINDING SITE is HOST TARGET binding

site found in the 5` untranslated region of mRNA encoded by LOC146520, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146520 BINDING SITE, designated SEQ ID:38188, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76565] Another function of VGAM2232 is therefore inhibition of LOC146520 (Accession XM_085492). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146520. LOC149566 (Accession XM_097670) is another VGAM2232 host target gene. LOC149566 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149566, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149566 BINDING SITE, designated SEQ ID:41013, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76566] Another function of VGAM2232 is therefore inhibition of

LOC149566 (Accession XM_097670). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149566. LOC155435 (Accession XM_088257) is another VGAM2232 host target gene. LOC155435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155435 BINDING SITE, designated SEQ ID:39565, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76567] Another function of VGAM2232 is therefore inhibition of LOC155435 (Accession XM_088257). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155435. LOC202460 (Accession XM_114493) is another VGAM2232 host target gene. LOC202460 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202460, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC202460 BINDING SITE, designated SEQ ID:42981, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76568] Another function of VGAM2232 is therefore inhibition of LOC202460 (Accession XM_114493). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202460. LOC203080 (Accession XM_114623) is another VGAM2232 host target gene. LOC203080 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203080, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203080 BINDING SITE, designated SEQ ID:43003, to the nucleotide sequence of VGAM2232 RNA, herein designated VGAM RNA, also designated SEQ ID:4943.

[76569] Another function of VGAM2232 is therefore inhibition of LOC203080 (Accession XM_114623). Accordingly, utilities of VGAM2232 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203080. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2233 (VGAM2233) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76570] VGAM2233 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2233 was detected is described hereinabove with reference to Figs. 1-8.

[76571] VGAM2233 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2233 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76572] VGAM2233 gene encodes a VGAM2233 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2233 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2233 precursor RNA is designated SEQ ID:2219, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2219 is located at position 17365 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76573] VGAM2233 precursor RNA folds onto itself, forming VGAM2233 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76574] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2233 folded precursor RNA into VGAM2233 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2233 RNA is designated SEQ ID:4944, and is provided hereinbelow with reference to the sequence listing part.

[76575] VGAM2233 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2233 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2233 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76576] VGAM2233 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2233 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2233 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2233 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2233 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76577] The complementary binding of VGAM2233 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2233 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2233 host target RNA into VGAM2233 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76578] It is appreciated that VGAM2233 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2233 host target genes. The mRNA of each one of this plurality of VGAM2233 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2233 RNA, herein designated VGAM RNA, and which when bound by VGAM2233 RNA causes inhibition of translation of respective one or more

VGAM2233 host target proteins.

[76579] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2233 gene, herein designated VGAM GENE, on one or more VGAM2233 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76580] It is yet further appreciated that a function of VGAM2233 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea

Virus. Specific functions, and accordingly utilities, of VGAM2233 correlate with, and may be deduced from, the identity of the host target genes which VGAM2233 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76581] Nucleotide sequences of the VGAM2233 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2233 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2233 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2233 are further described hereinbelow with reference to Table 1.

[76582] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2233 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2233 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76583] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2233 gene, herein designated VGAM is inhibition of expression of VGAM2233 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2233 correlate with, and may be deduced from, the identity of the target genes which VGAM2233 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76584] SRY (sex determining region Y)-box 12 (SOX12, Accession NM_006943) is a VGAM2233 host target gene. SOX12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX12 BINDING SITE, designated SEQ ID:13829, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76585] A function of VGAM2233 is therefore inhibition of SRY (sex determining region Y)-box 12 (SOX12, Accession NM_006943). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX12. Bromodomain and PHD Finger Containing, 3 (BRPF3, Accession XM_166450) is another VGAM2233 host target gene. BRPF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BRPF3, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRPF3 BINDING SITE, designated SEQ ID:44344, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76586] Another function of VGAM2233 is therefore inhibition of Bromodomain and PHD Finger Containing, 3 (BRPF3, Accession XM_166450). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRPF3. KIAA1202 (Accession XM_050478) is another VGAM2233 host target gene. KIAA1202 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1202, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1202 BINDING SITE, designated SEQ ID:35638, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76587] Another function of VGAM2233 is therefore inhibition of KIAA1202 (Accession XM_050478). Accordingly, utilities

of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1202. Lipoma HMGIC Fusion Partner-like 2 (LHFPL2, Accession XM_046054) is another VGAM2233 host target gene. LHFPL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LHFPL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LHFPL2 BINDING SITE, designated SEQ ID:34658, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76588] Another function of VGAM2233 is therefore inhibition of Lipoma HMGIC Fusion Partner-like 2 (LHFPL2, Accession XM_046054). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHFPL2. MGC1842 (Accession XM_037797) is another VGAM2233 host target gene. MGC1842 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC1842, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC1842 BINDING SITE, designated SEQ ID:32684, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76589] Another function of VGAM2233 is therefore inhibition of MGC1842 (Accession XM_037797). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC1842. p21(CDKN1A)-activated Kinase 7 (PAK7, Accession XM_045653) is another VGAM2233 host target gene. PAK7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAK7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAK7 BINDING SITE, designated SEQ ID:34509, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76590] Another function of VGAM2233 is therefore inhibition of p21(CDKN1A)-activated Kinase 7 (PAK7, Accession XM_045653). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PAK7. RALGPS1A (Accession NM_014636) is another VGAM2233 host target gene. RALGPS1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RALGPS1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RALGPS1A BINDING SITE, designated SEQ ID:16014, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76591] Another function of VGAM2233 is therefore inhibition of RALGPS1A (Accession NM_014636). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RALGPS1A. Serine Protease Inhibitor-like, with Kunitz and WAP Domains 1 (eppin) (SPINLW1, Accession NM_020398) is another VGAM2233 host target gene. SPINLW1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPINLW1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

SPINLW1 BINDING SITE, designated SEQ ID:21666, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76592] Another function of VGAM2233 is therefore inhibition of Serine Protease Inhibitor-like, with Kunitz and WAP Domains 1 (eppin) (SPINLW1, Accession NM_020398). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPINLW1. LOC127435 (Accession XM_072088) is another VGAM2233 host target gene. LOC127435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC127435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127435 BINDING SITE, designated SEQ ID:37460, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76593] Another function of VGAM2233 is therefore inhibition of LOC127435 (Accession XM_072088). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC127435. LOC144866 (Accession XM_096699) is another VGAM2233 host target gene. LOC144866 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144866, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144866 BINDING SITE, designated SEQ ID:40474, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76594] Another function of VGAM2233 is therefore inhibition of LOC144866 (Accession XM_096699). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144866. LOC163231 (Accession XM_092094) is another VGAM2233 host target gene. LOC163231 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC163231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163231 BINDING SITE, designated SEQ ID:40091, to the nucleotide sequence of VGAM2233 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4944.

[76595] Another function of VGAM2233 is therefore inhibition of LOC163231 (Accession XM_092094). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163231. LOC201952 (Accession XM_117345) is another VGAM2233 host target gene. LOC201952 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201952, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201952 BINDING SITE, designated SEQ ID:43393, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76596] Another function of VGAM2233 is therefore inhibition of LOC201952 (Accession XM_117345). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201952. LOC253675 (Accession XM_172990) is another VGAM2233 host target gene. LOC253675 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253675, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253675 BINDING SITE, designated SEQ ID:46264, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76597] Another function of VGAM2233 is therefore inhibition of LOC253675 (Accession XM_172990). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253675. LOC92080 (Accession XM_042704) is another VGAM2233 host target gene. LOC92080 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92080, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92080 BINDING SITE, designated SEQ ID:33756, to the nucleotide sequence of VGAM2233 RNA, herein designated VGAM RNA, also designated SEQ ID:4944.

[76598] Another function of VGAM2233 is therefore inhibition of LOC92080 (Accession XM_042704). Accordingly, utilities of VGAM2233 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC92080. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2234 (VGAM2234) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76599] VGAM2234 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2234 was detected is described hereinabove with reference to Figs. 1-8.

[76600] VGAM2234 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2234 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76601] VGAM2234 gene encodes a VGAM2234 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2234 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2234 precursor RNA is desig-

nated SEQ ID:2220, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2220 is located at position 15172 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76602] VGAM2234 precursor RNA folds onto itself, forming VGAM2234 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76603] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2234 folded precursor RNA into VGAM2234 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2234 RNA is designated SEQ ID:4945, and is provided hereinbelow with reference to the sequence

listing part.

[76604] VGAM2234 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2234 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2234 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76605] VGAM2234 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2234 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2234 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2234 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2234 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76606] The complementary binding of VGAM2234 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2234 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2234 host target RNA into VGAM2234 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76607] It is appreciated that VGAM2234 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2234 host target genes. The mRNA of each one of this plurality of VGAM2234 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2234 RNA, herein designated VGAM

RNA, and which when bound by VGAM2234 RNA causes inhibition of translation of respective one or more VGAM2234 host target proteins.

[76608] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2234 gene, herein designated VGAM GENE, on one or more VGAM2234 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76609] It is yet further appreciated that a function of VGAM2234 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2234 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGAM2234 correlate with, and may be deduced from, the identity of the host target genes which VGAM2234 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76610] Nucleotide sequences of the VGAM2234 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2234 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2234 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2234 are further described hereinbelow with reference to Table 1.

[76611] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2234 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2234 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76612] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2234 gene, herein designated VGAM is

inhibition of expression of VGAM2234 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2234 correlate with, and may be deduced from, the identity of the target genes which VGAM2234 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76613] Ankyrin 3, Node of Ranvier (ankyrin G) (ANK3, Accession NM_020987) is a VGAM2234 host target gene. ANK3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANK3 BINDING SITE, designated SEQ ID:21982, to the nucleotide sequence of VGAM2234 RNA, herein designated VGAM RNA, also designated SEQ ID:4945.

[76614] A function of VGAM2234 is therefore inhibition of Ankyrin 3, Node of Ranvier (ankyrin G) (ANK3, Accession NM_020987), a gene which plays key roles in activities such as cell motility, activation, proliferation. Accordingly, utilities of VGAM2234 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANK3. The function of ANK3 and its association with

various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1527.EPB72 (Accession NM_004099) is another VGAM2234 host target gene. EPB72 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPB72, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPB72 BINDING SITE, designated SEQ ID:10305, to the nucleotide sequence of VGAM2234 RNA, herein designated VGAM RNA, also designated SEQ ID:4945.

[76615] Another function of VGAM2234 is therefore inhibition of EPB72 (Accession NM_004099), a gene which may regulate cation conductance. Accordingly, utilities of VGAM2234 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPB72. The function of EPB72 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1560.A Kinase (PRKA) Anchor Protein 6 (AKAP6, Accession NM_004274) is another VGAM2234 host target gene. AKAP6 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by AKAP6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP6 BINDING SITE, designated SEQ ID:10489, to the nucleotide sequence of VGAM2234 RNA, herein designated VGAM RNA, also designated SEQ ID:4945.

[76616] Another function of VGAM2234 is therefore inhibition of A Kinase (PRKA) Anchor Protein 6 (AKAP6, Accession NM_004274). Accordingly, utilities of VGAM2234 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP6. Kelch-like 8 (Drosophila) (KLHL8, Accession XM_031735) is another VGAM2234 host target gene. KLHL8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLHL8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLHL8 BINDING SITE, designated SEQ ID:31476, to the nucleotide sequence of VGAM2234 RNA, herein designated VGAM RNA, also designated SEQ ID:4945.

[76617] Another function of VGAM2234 is therefore inhibition of Kelch-like 8 (Drosophila) (KLHL8, Accession XM_031735). Accordingly, utilities of VGAM2234 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLHL8. LOC200150 (Accession XM_114131) is another VGAM2234 host target gene. LOC200150 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200150, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200150 BINDING SITE, designated SEQ ID:42711, to the nucleotide sequence of VGAM2234 RNA, herein designated VGAM RNA, also designated SEQ ID:4945.

[76618] Another function of VGAM2234 is therefore inhibition of LOC200150 (Accession XM_114131). Accordingly, utilities of VGAM2234 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200150. LOC257319 (Accession XM_171049) is another VGAM2234 host target gene. LOC257319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257319, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257319 BINDING SITE, designated SEQ ID:45834, to the nucleotide sequence of VGAM2234 RNA, herein designated VGAM RNA, also designated SEQ ID:4945.

[76619] Another function of VGAM2234 is therefore inhibition of LOC257319 (Accession XM_171049). Accordingly, utilities of VGAM2234 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257319. LOC89932 (Accession XM_027341) is another VGAM2234 host target gene. LOC89932 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC89932, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC89932 BINDING SITE, designated SEQ ID:30491, to the nucleotide sequence of VGAM2234 RNA, herein designated VGAM RNA, also designated SEQ ID:4945.

[76620] Another function of VGAM2234 is therefore inhibition of LOC89932 (Accession XM_027341). Accordingly, utilities of VGAM2234 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC89932. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2235 (VGAM2235) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76621] VGAM2235 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2235 was detected is described hereinabove with reference to Figs. 1-8.

[76622] VGAM2235 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2235 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76623] VGAM2235 gene encodes a VGAM2235 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2235 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2235 precursor RNA is desig-

nated SEQ ID:2221, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2221 is located at position 19252 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76624] VGAM2235 precursor RNA folds onto itself, forming VGAM2235 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76625] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2235 folded precursor RNA into VGAM2235 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2235 RNA is designated SEQ ID:4946, and is provided hereinbelow with reference to the sequence

listing part.

[76626] VGAM2235 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2235 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2235 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76627] VGAM2235 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2235 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2235 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2235 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2235 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76628] The complementary binding of VGAM2235 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2235 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2235 host target RNA into VGAM2235 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76629] It is appreciated that VGAM2235 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2235 host target genes. The mRNA of each one of this plurality of VGAM2235 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2235 RNA, herein designated VGAM

RNA, and which when bound by VGAM2235 RNA causes inhibition of translation of respective one or more VGAM2235 host target proteins.

[76630] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2235 gene, herein designated VGAM GENE, on one or more VGAM2235 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76631] It is yet further appreciated that a function of VGAM2235 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2235 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGAM2235 correlate with, and may be deduced from, the identity of the host target genes which VGAM2235 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76632] Nucleotide sequences of the VGAM2235 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2235 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2235 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2235 are further described hereinbelow with reference to Table 1.

[76633] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2235 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2235 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76634] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2235 gene, herein designated VGAM is

inhibition of expression of VGAM2235 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2235 correlate with, and may be deduced from, the identity of the target genes which VGAM2235 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76635] Arachidonate 15-lipoxygenase (ALOX15, Accession NM_001140) is a VGAM2235 host target gene. ALOX15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALOX15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALOX15 BINDING SITE, designated SEQ ID:6808, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76636] A function of VGAM2235 is therefore inhibition of Arachidonate 15-lipoxygenase (ALOX15, Accession NM_001140), a gene which converts arachidonic acid to 15s- hydroperoxyeicosatetraenoic acid. Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with ALOX15. The function of ALOX15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM282.ATPase, Class I, Type 8B, Member 2 (ATP8B2, Accession XM_036933) is another VGAM2235 host target gene. ATP8B2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ATP8B2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP8B2 BINDING SITE, designated SEQ ID:32515, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76637] Another function of VGAM2235 is therefore inhibition of ATPase, Class I, Type 8B, Member 2 (ATP8B2, Accession XM_036933). Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8B2. Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858) is another VGAM2235 host target gene. COL19A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL19A1, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL19A1 BINDING SITE, designated SEQ ID:7598, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76638] Another function of VGAM2235 is therefore inhibition of Collagen, Type XIX, Alpha 1 (COL19A1, Accession NM_001858), a gene which may act as a cross-bridge between fibrils and other extracellular matrix molecules. Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL19A1. The function of COL19A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM19.Carboxypeptidase N, Polypeptide 1, 50kD (CPN1, Accession NM_001308) is another VGAM2235 host target gene. CPN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CPN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of CPN1 BINDING SITE, designated SEQ ID:6990, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76639] Another function of VGAM2235 is therefore inhibition of Carboxypeptidase N, Polypeptide 1, 50kD (CPN1, Accession NM_001308), a gene which cleaves basic amino acid residues from the C terminal of peptides and proteins. Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPN1. The function of CPN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1965.Catenin (cadherin-associated protein), Delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2, Accession NM_001332) is another VGAM2235 host target gene. CTNND2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTNND2 BINDING SITE, designated SEQ ID:7014, to the nucleotide sequence of VGAM2235 RNA,

herein designated VGAM RNA, also designated SEQ ID:4946.

[76640] Another function of VGAM2235 is therefore inhibition of Catenin (cadherin-associated protein), Delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2, Accession NM_001332), a gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo family. Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTNND2. The function of CTNND2 has been established by previous studies. Armadillo-like proteins are characterized by a series of armadillo repeats, first defined in the Drosophila 'armadillo' gene product, that are typically 42 to 45 amino acids long. These proteins can be divided into subfamilies based on the number of repeats, their overall sequence similarity, and the dispersion of the repeats throughout their sequences. Members of the p120(ctn)/plakophilin subfamily of Armadillo-like proteins, including CTNND1 (OMIM Ref. No. 601045), CTNND2, PKP1 (OMIM Ref. No. 601975), PKP2 (OMIM Ref. No. 602861), PKP4 (OMIM Ref. No. 604276), and ARVCF (OMIM Ref. No. 602269), have 10 armadillo repeats each In a search for proteins with se-

quence homology to PKP1, Paffenholz and Franke (1997) identified a human cDNA with 45% amino acid identity to PKP1 in a segment within the armadillo (arm) repeat units. Antibodies raised against the arm repeat region recognized 2 polypeptide bands of approximately 150 and 160 kD in immunoblots of mouse brain and a weak band of approximately 160 kD in mouse skeletal muscle and pancreas. The authors, therefore, named the protein NPRAP for 'neural plakophilin-related arm-repeat protein.' Paffenholz and Franke (1997) isolated 2 partial human cDNA clones from a human fetal brain cDNA library. The longer displays 91% identity to the complete mouse cDNA. Northern blot analysis of a number of human and bovine cell lines and tissues detected CTNND2 expression as 5- and 6-kb transcripts only in human fetal brain RNA

[76641] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[76642] Paffenholz, R.; Franke, W. W. : Identification and localization of a neurally expressed member of the plakoglobin/armadillo multigene family. Differentiation 61: 293-304, 1997. ; and

[76643] Medina, M.; Marinescu, R. C.; Overhauser, J.; Kosik, K. S. :

Hemizygosity of delta-catenin (CTNND2) is associated with severe mental retardation in cri-du-chat syndrome. Genomics 63: 157.

[76644] Further studies establishing the function and utilities of CTNND2 are found in John Hopkins OMIM database record ID 604275, and in sited publications numbered 702 and 7385-7387 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Interleukin 12 Receptor, Beta 2 (IL12RB2, Accession NM_001559) is another VGAM2235 host target gene. IL12RB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL12RB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL12RB2 BINDING SITE, designated SEQ ID:7279, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76645] Another function of VGAM2235 is therefore inhibition of Interleukin 12 Receptor, Beta 2 (IL12RB2, Accession NM_001559), a gene which is involved in il-12 transduction. binds to il-12 with a low affinity. Accordingly, utili-

ties of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL12RB2. The function of IL12RB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM326.Pre-B-cell Leukemia Transcription Factor 3 (PBX3, Accession NM_006195) is another VGAM2235 host target gene. PBX3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PBX3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PBX3 BINDING SITE, designated SEQ ID:12868, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76646] Another function of VGAM2235 is therefore inhibition of Pre-B-cell Leukemia Transcription Factor 3 (PBX3, Accession NM_006195). Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PBX3. Protein Phosphatase 3 (formerly 2B), Catalytic Subunit, Alpha Isoform (calcineurin A alpha) (PPP3CA, Accession NM_000944) is

another VGAM2235 host target gene. PPP3CA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP3CA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP3CA BINDING SITE, designated SEQ ID:6643, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76647] Another function of VGAM2235 is therefore inhibition of Protein Phosphatase 3 (formerly 2B), Catalytic Subunit, Alpha Isoform (calcineurin A alpha) (PPP3CA, Accession NM_000944), a gene which is the catalytic subunit of calcium-dependent, calmodulin-stimulated protein phosphatase. Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP3CA. The function of PPP3CA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM497.Peroxisomal Farnesylated Protein (PXF, Accession NM_002857) is another VGAM2235 host target gene. PXF BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by PXF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PXF BINDING SITE, designated SEQ ID:8750, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76648] Another function of VGAM2235 is therefore inhibition of Peroxisomal Farnesylated Protein (PXF, Accession NM_002857), a gene which may function in peroxisomal biogenesis or assembly. Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PXF. The function of PXF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM193.Regulatory Factor X-associated Protein (RFXAP, Accession NM_000538) is another VGAM2235 host target gene. RFXAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RFXAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of RFXAP BINDING SITE, designated SEQ ID:6134, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76649] Another function of VGAM2235 is therefore inhibition of Regulatory Factor X-associated Protein (RFXAP, Accession NM_000538), a gene which binds to the x-box of mhc ii promoters and is a transcriptional regulator. Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFXAP. The function of RFXAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM797.HSA243666 (Accession NM_017582) is another VGAM2235 host target gene. HSA243666 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSA243666, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSA243666 BINDING SITE, designated SEQ ID:19019, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4946.

[76650] Another function of VGAM2235 is therefore inhibition of HSA243666 (Accession NM_017582). Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSA243666. MCM10 Minichromosome Maintenance Deficient 10 (S. cerevisiae) (MCM10, Accession NM_018518) is another VGAM2235 host target gene. MCM10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MCM10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MCM10 BINDING SITE, designated SEQ ID:20592, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76651] Another function of VGAM2235 is therefore inhibition of MCM10 Minichromosome Maintenance Deficient 10 (S. cerevisiae) (MCM10, Accession NM_018518). Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCM10. Neuropilin (NRP) and Tolloid (TLL)-like 1 (NETO1, Accession NM_138966) is another VGAM2235

host target gene. NETO1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NETO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NETO1 BINDING SITE, designated SEQ ID:29070, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76652] Another function of VGAM2235 is therefore inhibition of Neuropilin (NRP) and Tolloid (TLL)-like 1 (NETO1, Accession NM_138966). Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NETO1. PEPP3 (Accession NM_014935) is another VGAM2235 host target gene. PEPP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PEPP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEPP3 BINDING SITE, designated SEQ ID:17233, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76653] Another function of VGAM2235 is therefore inhibition of PEPP3 (Accession NM_014935). Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEPP3. ZID (Accession NM_006626) is another VGAM2235 host target gene. ZID BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZID, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZID BINDING SITE, designated SEQ ID:13414, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76654] Another function of VGAM2235 is therefore inhibition of ZID (Accession NM_006626). Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZID. Zinc Finger Protein 237 (ZNF237, Accession NM_014242) is another VGAM2235 host target gene. ZNF237 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF237, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of ZNF237 BINDING SITE, designated SEQ ID:15504, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76655] Another function of VGAM2235 is therefore inhibition of Zinc Finger Protein 237 (ZNF237, Accession NM_014242). Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF237. LOC122786 (Accession XM_058660) is another VGAM2235 host target gene. LOC122786 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC122786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122786 BINDING SITE, designated SEQ ID:36697, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76656] Another function of VGAM2235 is therefore inhibition of LOC122786 (Accession XM_058660). Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC122786. LOC124801 (Accession XM_058850) is another VGAM2235 host target gene. LOC124801 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC124801, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124801 BINDING SITE, designated SEQ ID:36762, to the nucleotide sequence of VGAM2235 RNA, herein designated VGAM RNA, also designated SEQ ID:4946.

[76657] Another function of VGAM2235 is therefore inhibition of LOC124801 (Accession XM_058850). Accordingly, utilities of VGAM2235 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124801. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2236 (VGAM2236) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76658] VGAM2236 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2236 was detected is described hereinabove with reference to Figs. 1-8.

[76659] VGAM2236 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2236 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76660] VGAM2236 gene encodes a VGAM2236 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2236 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2236 precursor RNA is designated SEQ ID:2222, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2222 is located at position 3556 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76661] VGAM2236 precursor RNA folds onto itself, forming VGAM2236 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76662] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2236 folded precursor RNA into VGAM2236 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2236 RNA is designated SEQ ID:4947, and is provided hereinbelow with reference to the sequence listing part.

[76663] VGAM2236 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2236 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2236 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76664] VGAM2236 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2236 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2236 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2236 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2236 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76665] The complementary binding of VGAM2236 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2236 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2236 host target RNA into VGAM2236 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76666] It is appreciated that VGAM2236 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2236 host target genes. The mRNA of each one of this plurality of VGAM2236 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2236 RNA, herein designated VGAM RNA, and which when bound by VGAM2236 RNA causes inhibition of translation of respective one or more VGAM2236 host target proteins.

[76667] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2236 gene, herein designated VGAM GENE, on one or more VGAM2236 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76668] It is yet further appreciated that a function of VGAM2236 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGAM2236 correlate with, and may be deduced from, the identity of the host target genes which VGAM2236 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76669] Nucleotide sequences of the VGAM2236 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2236 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2236 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2236 are further described hereinbelow with reference to Table 1.

[76670] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2236 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2236 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76671] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2236 gene, herein designated VGAM is inhibition of expression of VGAM2236 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2236 correlate with, and may be deduced from, the identity of the target genes which VGAM2236 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76672] A Kinase (PRKA) Anchor Protein 2 (AKAP2, Accession NM_007203) is a VGAM2236 host target gene. AKAP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKAP2, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP2 BINDING SITE, designated SEQ ID:14062, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76673] A function of VGAM2236 is therefore inhibition of A Kinase (PRKA) Anchor Protein 2 (AKAP2, Accession NM_007203), a gene which binds to regulatory subunit (rii) of protein kinase a. Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP2. The function of AKAP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM18.Autocrine Motility Factor Receptor (AMFR, Accession NM_138958) is another VGAM2236 host target gene. AMFR BINDING SITE1 and AMFR BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AMFR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AMFR BINDING SITE1

and AMFR BINDING SITE2, designated SEQ ID:29067 and SEQ ID:6811 respectively, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76674] Another function of VGAM2236 is therefore inhibition of Autocrine Motility Factor Receptor (AMFR, Accession NM_138958), a gene which acts to stimulate migration of fibrosarcoma cells. Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMFR. The function of AMFR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM440.Diptheria Toxin Resistance Protein Required For Diphthamide Biosynthesis-like 2 (S. cerevisiae) (DPH2L2, Accession NM_001384) is another VGAM2236 host target gene. DPH2L2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DPH2L2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DPH2L2 BINDING SITE, designated SEQ ID:7060, to the nucleotide sequence of VGAM2236 RNA,

herein designated VGAM RNA, also designated SEQ ID:4947.

[76675] Another function of VGAM2236 is therefore inhibition of Diptheria Toxin Resistance Protein Required For Diphthamide Biosynthesis-like 2 (S. cerevisiae) (DPH2L2, Accession NM_001384), a gene which is required for diphthamide biosynthesis. Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPH2L2. The function of DPH2L2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1221.Hemoglobin, Epsilon 1 (HBE1, Accession NM_005330) is another VGAM2236 host target gene. HBE1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HBE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HBE1 BINDING SITE, designated SEQ ID:11805, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76676] Another function of VGAM2236 is therefore inhibition of

Hemoglobin, Epsilon 1 (HBE1, Accession NM_005330), a gene which modulates erythrocyte metabolism and senescence, a source of physiological active catabolites. Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HBE1. The function of HBE1 has been established by previous studies. The epsilon locus determines the epsilon, or non-alpha, chain of embryonic hemoglobin (originally known as Gower-2). No mutations affecting the epsilon chain have yet been identified. Gower-1 is a tetramer of epsilon chains. The epsilon locus may be linked to the delta-beta complex. The amino acid sequence of the epsilon chain is similar to those of the delta and beta chains. Furthermore, the homologous chain in the mouse is linked to the beta locus (Gilman and Smithies, 1968). Shen and Smithies (1982) determined the complete nucleotide sequence of the 3.4-kb stretch of DNA 5-prime to the epsilon gene where a pseudogene (psi-beta-2) was thought to reside (Fritsch et al., 1980). They concluded that no globin-related gene exists there and provided a possible explanation for the earlier contrary conclusion. By studies in transgenic mice, Raich et al. (1992) demonstrated that deletion of a 'negative element'

located between -182 and -467 bp upstream of the HBE gene cap site resulted in continuation of HBE gene expression in the definitive erythroblasts of the fetal liver and in the red blood cells of adult animals. The findings provided direct in vivo evidence that cis-acting silencing elements are involved in the developmental control of the HBE gene. He and Russell (2002) analyzed the anti-sickling properties of HBE both in vitro as well as in vivo in a well-established mouse model of sickle cell anemia (OMIM Ref. No. 603903). These animals, expressing 100% of human Hb S (141900.0243), display a chronic hemolytic anemia with compensatory marrow and extramedullary erythropoiesis, abundant circulating sickled erythrocytes, and chronic tissue damage evidenced by parallel histopathologic and functional deficits. By comparison, related mice that coexpress Hb S as well as HBE exhibited normal physiologic, morphologic, histologic, and functional attributes. Subsequent in vitro analyses substantiated results from whole-animal studies, indicating that the polymerization of deoxygenated Hb S can be significantly slowed by relatively small quantities of HBE. Together, the in vivo and in vitro analyses suggested that reactivation of epsilon-globin gene expression would be

therapeutically beneficial to adults with sickle phenotypes, and provide a rationale for detailed investigations into the molecular basis for its developmental silencing.

[76677] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[76678] Shen, S.-H.; Smithies, O. : Human globin psi-beta-2 is not a globin-related sequence. Nucleic Acids Res. 10: 7809-7818, 1982. ; and

[76679] He, Z.; Russell, J. E. : A human embryonic hemoglobin inhibits Hb S polymerization in vitro and restores a normal phenotype to mouse models of sickle cell disease. Proc. Nat. Acad. Sci.

[76680] Further studies establishing the function and utilities of HBE1 are found in John Hopkins OMIM database record ID 142100, and in sited publications numbered 11689-11699 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Heat Shock 70kDa Protein 4 (HSPA4, Accession XM_114482) is another VGAM2236 host target gene. HSPA4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSPA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPA4 BINDING SITE, designated SEQ ID:42975, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76681] Another function of VGAM2236 is therefore inhibition of Heat Shock 70kDa Protein 4 (HSPA4, Accession XM_114482). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPA4. V-ski Sarcoma Viral Oncogene Homolog (avian) (SKI, Accession NM_003036) is another VGAM2236 host target gene. SKI BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SKI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SKI BINDING SITE, designated SEQ ID:8990, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76682] Another function of VGAM2236 is therefore inhibition of V-ski Sarcoma Viral Oncogene Homolog (avian) (SKI, Accession NM_003036). Accordingly, utilities of VGAM2236

include diagnosis, prevention and treatment of diseases and clinical conditions associated with SKI. Transmembrane Protease, Serine 2 (TMPRSS2, Accession NM_005656) is another VGAM2236 host target gene. TMPRSS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TMPRSS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMPRSS2 BINDING SITE, designated SEQ ID:12196, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76683] Another function of VGAM2236 is therefore inhibition of Transmembrane Protease, Serine 2 (TMPRSS2, Accession NM_005656). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMPRSS2. Chromosome 20 Open Reading Frame 150 (C20orf150, Accession XM_037265) is another VGAM2236 host target gene. C20orf150 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf150, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf150 BINDING SITE, designated SEQ ID:32599, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76684] Another function of VGAM2236 is therefore inhibition of Chromosome 20 Open Reading Frame 150 (C20orf150, Accession XM_037265). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf150. Cleavage Stimulation Factor, 3' Pre-RNA, Subunit 1, 50kDa (CSTF1, Accession NM_001324) is another VGAM2236 host target gene. CSTF1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CSTF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSTF1 BINDING SITE, designated SEQ ID:7009, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76685] Another function of VGAM2236 is therefore inhibition of

Cleavage Stimulation Factor, 3' Pre-RNA, Subunit 1, 50kDa (CSTF1, Accession NM_001324). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSTF1. FLJ12700 (Accession NM_024910) is another VGAM2236 host target gene. FLJ12700 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12700, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12700 BINDING SITE, designated SEQ ID:24414, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76686] Another function of VGAM2236 is therefore inhibition of FLJ12700 (Accession NM_024910). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12700. FLJ20320 (Accession NM_017765) is another VGAM2236 host target gene. FLJ20320 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20320, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20320 BINDING SITE, designated SEQ ID:19383, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76687] Another function of VGAM2236 is therefore inhibition of FLJ20320 (Accession NM_017765). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20320. Glycoprotein V (platelet) (GP5, Accession NM_004488) is another VGAM2236 host target gene. GP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GP5 BINDING SITE, designated SEQ ID:10821, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76688] Another function of VGAM2236 is therefore inhibition of Glycoprotein V (platelet) (GP5, Accession NM_004488). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with GP5. KIAA0649 (Accession NM_014811) is another VGAM2236 host target gene. KIAA0649 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0649, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0649 BINDING SITE, designated SEQ ID:16773, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76689] Another function of VGAM2236 is therefore inhibition of KIAA0649 (Accession NM_014811). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0649. KIAA1383 (Accession XM_045859) is another VGAM2236 host target gene. KIAA1383 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1383, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1383 BINDING SITE, designated SEQ ID:34585, to the

nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76690] Another function of VGAM2236 is therefore inhibition of KIAA1383 (Accession XM_045859). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1383. PA26 (Accession NM_014454) is another VGAM2236 host target gene. PA26 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PA26, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PA26 BINDING SITE, designated SEQ ID:15808, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76691] Another function of VGAM2236 is therefore inhibition of PA26 (Accession NM_014454). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PA26. Solute Carrier Family 5 (choline transporter), Member 7 (SLC5A7, Accession NM_021815) is another VGAM2236 host target gene. SLC5A7 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by SLC5A7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC5A7 BINDING SITE, designated SEQ ID:22394, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76692] Another function of VGAM2236 is therefore inhibition of Solute Carrier Family 5 (choline transporter), Member 7 (SLC5A7, Accession NM_021815). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC5A7. LOC118987 (Accession XM_058361) is another VGAM2236 host target gene. LOC118987 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC118987, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC118987 BINDING SITE, designated SEQ ID:36609, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76693] Another function of VGAM2236 is therefore inhibition of LOC118987 (Accession XM_058361). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118987. LOC150245 (Accession XM_097843) is another VGAM2236 host target gene. LOC150245 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150245, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150245 BINDING SITE, designated SEQ ID:41164, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76694] Another function of VGAM2236 is therefore inhibition of LOC150245 (Accession XM_097843). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150245. LOC151162 (Accession XM_098012) is another VGAM2236 host target gene. LOC151162 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151162, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151162 BINDING SITE, designated SEQ ID:41309, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76695] Another function of VGAM2236 is therefore inhibition of LOC151162 (Accession XM_098012). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151162. LOC158056 (Accession XM_088463) is another VGAM2236 host target gene. LOC158056 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158056, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158056 BINDING SITE, designated SEQ ID:39719, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76696] Another function of VGAM2236 is therefore inhibition of LOC158056 (Accession XM_088463). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC158056. LOC202134 (Accession XM_117365) is another VGAM2236 host target gene. LOC202134 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202134, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202134 BINDING SITE, designated SEQ ID:43414, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76697] Another function of VGAM2236 is therefore inhibition of LOC202134 (Accession XM_117365). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202134. LOC203377 (Accession XM_117540) is another VGAM2236 host target gene. LOC203377 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203377, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203377 BINDING SITE, designated SEQ ID:43544, to the nucleotide sequence of VGAM2236 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4947.

[76698] Another function of VGAM2236 is therefore inhibition of LOC203377 (Accession XM_117540). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203377. LOC220988 (Accession XM_165561) is another VGAM2236 host target gene. LOC220988 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220988, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220988 BINDING SITE, designated SEQ ID:43683, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76699] Another function of VGAM2236 is therefore inhibition of LOC220988 (Accession XM_165561). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220988. LOC221271 (Accession XM_166307) is another VGAM2236 host target gene. LOC221271 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221271, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221271 BINDING SITE, designated SEQ ID:44123, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76700] Another function of VGAM2236 is therefore inhibition of LOC221271 (Accession XM_166307). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221271. LOC92370 (Accession XM_044665) is another VGAM2236 host target gene. LOC92370 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92370, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92370 BINDING SITE, designated SEQ ID:34259, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76701] Another function of VGAM2236 is therefore inhibition of LOC92370 (Accession XM_044665). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC92370. LOC93048 (Accession XM_048903) is another VGAM2236 host target gene. LOC93048 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93048, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93048 BINDING SITE, designated SEQ ID:35296, to the nucleotide sequence of VGAM2236 RNA, herein designated VGAM RNA, also designated SEQ ID:4947.

[76702] Another function of VGAM2236 is therefore inhibition of LOC93048 (Accession XM_048903). Accordingly, utilities of VGAM2236 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93048. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2237 (VGAM2237) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76703] VGAM2237 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2237 was detected is described hereinabove with reference to Figs. 1-8.

[76704] VGAM2237 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2237 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76705] VGAM2237 gene encodes a VGAM2237 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2237 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2237 precursor RNA is designated SEQ ID:2223, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2223 is located at position 26770 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76706] VGAM2237 precursor RNA folds onto itself, forming VGAM2237 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76707] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2237 folded precursor RNA into VGAM2237 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2237 RNA is designated SEQ ID:4948, and is provided hereinbelow with reference to the sequence listing part.

[76708] VGAM2237 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2237 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2237 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76709] VGAM2237 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2237 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2237 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2237 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2237 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76710] The complementary binding of VGAM2237 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2237 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2237 host target RNA into VGAM2237 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76711] It is appreciated that VGAM2237 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2237 host target genes. The mRNA of each one of this plurality of VGAM2237 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2237 RNA, herein designated VGAM RNA, and which when bound by VGAM2237 RNA causes inhibition of translation of respective one or more VGAM2237 host target proteins.

[76712] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2237 gene, herein designated VGAM GENE, on one or more VGAM2237 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76713] It is yet further appreciated that a function of VGAM2237 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGAM2237 correlate with, and may be deduced from, the identity of the host target genes which VGAM2237 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76714] Nucleotide sequences of the VGAM2237 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2237 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2237 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2237 are further described hereinbelow with reference to Table 1.

[76715] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2237 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2237 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76716] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2237 gene, herein designated VGAM is inhibition of expression of VGAM2237 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2237 correlate with, and may be deduced from, the identity of the target genes which VGAM2237 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76717] Core-binding Factor, Runt Domain, Alpha Subunit 2; Translocated To, 3 (CBFA2T3, Accession NM_005187) is a VGAM2237 host target gene. CBFA2T3 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CBFA2T3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBFA2T3 BINDING SITE, designated SEQ ID:11689, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76718] A function of VGAM2237 is therefore inhibition of Core-binding Factor, Runt Domain, Alpha Subunit 2; Translocated To, 3 (CBFA2T3, Accession NM_005187). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T3. DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide, Y Chromosome (DBY, Accession NM_004660) is another VGAM2237 host target gene. DBY BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DBY, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DBY BINDING SITE, designated SEQ ID:11025, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA,

also designated SEQ ID:4948.

[76719] Another function of VGAM2237 is therefore inhibition of DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide, Y Chromosome (DBY, Accession NM_004660), a gene which plays a key role in the spermatogenic process. Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DBY. The function of DBY and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM374.Deafness, Autosomal Dominant 5 (DFNA5, Accession NM_004403) is another VGAM2237 host target gene. DFNA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DFNA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DFNA5 BINDING SITE, designated SEQ ID:10654, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76720] Another function of VGAM2237 is therefore inhibition of Deafness, Autosomal Dominant 5 (DFNA5, Accession

NM_004403). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DFNA5. Histamine N-methyltransferase (HNMT, Accession NM_006895) is another VGAM2237 host target gene. HNMT BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HNMT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNMT BINDING SITE, designated SEQ ID:13767, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76721] Another function of VGAM2237 is therefore inhibition of Histamine N-methyltransferase (HNMT, Accession NM_006895), a gene which inactivates histamine by n-methylation. Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNMT. The function of HNMT has been established by previous studies. Preuss et al. (1998) demonstrated a common 314C-T polymorphism in the HNMT gene resulting in a thr105-to-ile amino acid substitution (605238.0001). The 314T allele is

associated with decreased levels of both HNMT enzymatic activity and immunoreactive protein; therefore, the presence of the 314T allele would be expected to result in reduced histamine metabolism and increased bronchoconstriction. Yan et al. (2000) characterized the common, functionally significant 314T polymorphism in DNA samples from 237 randomly selected Caucasian control subjects and 192 samples from Caucasian asthmatic patients. The frequency of the 314T allele of the HNMT gene was 0.08 in the control samples and 0.14 in samples from Caucasian asthmatic patients (odds ratio = 1.9, P less than 0.01), indicating a significant increase in the frequency of subjects with low HNMT activity among asthmatics.

[76722] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[76723] Preuss, C. V.; Wood, T. C.; Szumlanski, C. L.; Raftogianis, R. B.; Otterness, D. M.; Girard, B.; Scott, M. C.; Weinshilboum, R. M. : Human histamine N-methyltransferase pharmacogenetics: common genetic polymorphisms that alter activity. Molec. Pharm. 53: 708-717, 1998. ; and

[76724] Yan, L.; Galinsky, R. E.; Bernstein, J. A.; Liggett, S. B.;

Weinshilboum, R. M. : Histamine N-methyltransferase pharmacogenetics: association of a common functional polymorphism with asthma.

[76725] Further studies establishing the function and utilities of HNMT are found in John Hopkins OMIM database record ID 605238, and in sited publications numbered 7488-7493 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Junctophilin 2 (JPH2, Accession XM_170491) is another VGAM2237 host target gene. JPH2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by JPH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JPH2 BINDING SITE, designated SEQ ID:45333, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76726] Another function of VGAM2237 is therefore inhibition of Junctophilin 2 (JPH2, Accession XM_170491), a gene which mediates cross talk between cell surface and intracellular ion channels. Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with JPH2. The function of JPH2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM295.Neurobeachin (NBEA, Accession XM_170732) is another VGAM2237 host target gene. NBEA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NBEA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NBEA BINDING SITE, designated SEQ ID:45494, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76727] Another function of VGAM2237 is therefore inhibition of Neurobeachin (NBEA, Accession XM_170732), a gene which may mediate protein-protein interactions. Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NBEA. The function of NBEA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM459.Translin (TSN, Accession

NM_004622) is another VGAM2237 host target gene. TSN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TSN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TSN BINDING SITE, designated SEQ ID:10987, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76728] Another function of VGAM2237 is therefore inhibition of Translin (TSN, Accession NM_004622), a gene which is a DNA binding protein and involved in DNA repair, replication, or recombination. Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSN. The function of TSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM98.Vinculin (VCL, Accession NM_003373) is another VGAM2237 host target gene. VCL BINDING SITE1 and VCL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by VCL, corresponding to HOST TARGET binding sites such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VCL BINDING SITE1 and VCL BINDING SITE2, designated SEQ ID:9406 and SEQ ID:15195 respectively, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76729] Another function of VGAM2237 is therefore inhibition of Vinculin (VCL, Accession NM_003373). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VCL. CASPR3 (Accession NM_024879) is another VGAM2237 host target gene. CASPR3 BINDING SITE1 and CASPR3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CASPR3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASPR3 BINDING SITE1 and CASPR3 BINDING SITE2, designated SEQ ID:24317 and SEQ ID:27388 respectively, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76730] Another function of VGAM2237 is therefore inhibition of

CASPR3 (Accession NM_024879). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASPR3. Death Associated Transcription Factor 1 (DATF1, Accession NM_022105) is another VGAM2237 host target gene. DATF1 BINDING SITE1 and DATF1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DATF1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DATF1 BINDING SITE1 and DATF1 BINDING SITE2, designated SEQ ID:22652 and SEQ ID:25991 respectively, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76731] Another function of VGAM2237 is therefore inhibition of Death Associated Transcription Factor 1 (DATF1, Accession NM_022105). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DATF1. FLJ12529 (Accession NM_024811) is another VGAM2237 host target gene. FLJ12529 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by FLJ12529, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12529 BINDING SITE, designated SEQ ID:24190, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76732] Another function of VGAM2237 is therefore inhibition of FLJ12529 (Accession NM_024811). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12529. KIAA0408 (Accession NM_014702) is another VGAM2237 host target gene. KIAA0408 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0408, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0408 BINDING SITE, designated SEQ ID:16228, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76733] Another function of VGAM2237 is therefore inhibition of KIAA0408 (Accession NM_014702). Accordingly, utilities

of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0408. KIAA0618 (Accession NM_014833) is another VGAM2237 host target gene. KIAA0618 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0618, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0618 BINDING SITE, designated SEQ ID:16831, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76734] Another function of VGAM2237 is therefore inhibition of KIAA0618 (Accession NM_014833). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0618. KIAA1191 (Accession NM_020444) is another VGAM2237 host target gene. KIAA1191 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1191, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1191 BINDING SITE, designated SEQ ID:21683, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76735] Another function of VGAM2237 is therefore inhibition of KIAA1191 (Accession NM_020444). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1191. KIAA1944 (Accession XM_062545) is another VGAM2237 host target gene. KIAA1944 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1944, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1944 BINDING SITE, designated SEQ ID:37232, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76736] Another function of VGAM2237 is therefore inhibition of KIAA1944 (Accession XM_062545). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1944. MGC2668 (Accession XM_026968) is another VGAM2237 host target gene. MGC2668 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2668, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2668 BINDING SITE, designated SEQ ID:30379, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76737] Another function of VGAM2237 is therefore inhibition of MGC2668 (Accession XM_026968). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2668. NIN283 (Accession NM_032268) is another VGAM2237 host target gene. NIN283 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NIN283, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NIN283 BINDING SITE, designated SEQ ID:26013, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76738] Another function of VGAM2237 is therefore inhibition of

NIN283 (Accession NM_032268). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NIN283. TRABID (Accession XM_043669) is another VGAM2237 host target gene. TRABID BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TRABID, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRABID BINDING SITE, designated SEQ ID:33992, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76739] Another function of VGAM2237 is therefore inhibition of TRABID (Accession XM_043669). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRABID. LOC139770 (Accession XM_060053) is another VGAM2237 host target gene. LOC139770 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC139770, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC139770 BINDING SITE, designated SEQ ID:37150, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76740] Another function of VGAM2237 is therefore inhibition of LOC139770 (Accession XM_060053). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139770. LOC146268 (Accession XM_085397) is another VGAM2237 host target gene. LOC146268 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146268, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146268 BINDING SITE, designated SEQ ID:38124, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76741] Another function of VGAM2237 is therefore inhibition of LOC146268 (Accession XM_085397). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146268. LOC147136 (Accession XM_085716) is an-

other VGAM2237 host target gene. LOC147136 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147136, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147136 BINDING SITE, designated SEQ ID:38298, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76742] Another function of VGAM2237 is therefore inhibition of LOC147136 (Accession XM_085716). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147136. LOC219793 (Accession XM_166127) is another VGAM2237 host target gene. LOC219793 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219793, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219793 BINDING SITE, designated SEQ ID:43915, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76743] Another function of VGAM2237 is therefore inhibition of LOC219793 (Accession XM_166127). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219793. LOC219920 (Accession XM_167787) is another VGAM2237 host target gene. LOC219920 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219920, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219920 BINDING SITE, designated SEQ ID:44812, to the nucleotide sequence of VGAM2237 RNA, herein designated VGAM RNA, also designated SEQ ID:4948.

[76744] Another function of VGAM2237 is therefore inhibition of LOC219920 (Accession XM_167787). Accordingly, utilities of VGAM2237 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219920. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2238 (VGAM2238) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[76745] VGAM2238 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2238 was detected is described hereinabove with reference to Figs. 1-8.

[76746] VGAM2238 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2238 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76747] VGAM2238 gene encodes a VGAM2238 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2238 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2238 precursor RNA is designated SEQ ID:2224, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2224 is located at position 7462 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76748] VGAM2238 precursor RNA folds onto itself, forming VGAM2238 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76749] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2238 folded precursor RNA into VGAM2238 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2238 RNA is designated SEQ ID:4949, and is provided hereinbelow with reference to the sequence listing part.

[76750] VGAM2238 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2238 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2238 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76751] VGAM2238 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2238 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2238 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2238 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2238 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76752] The complementary binding of VGAM2238 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2238 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2238 host target RNA into VGAM2238 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76753] It is appreciated that VGAM2238 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2238 host target genes. The mRNA of each one of this plurality of VGAM2238 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2238 RNA, herein designated VGAM RNA, and which when bound by VGAM2238 RNA causes inhibition of translation of respective one or more VGAM2238 host target proteins.

[76754] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2238 gene, herein designated VGAM GENE, on one or more VGAM2238 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76755] It is yet further appreciated that a function of VGAM2238 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGAM2238 correlate with, and may be deduced from, the identity of the host target genes which VGAM2238 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[76756] Nucleotide sequences of the VGAM2238 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2238 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2238 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2238 are further described hereinbelow with reference to Table 1.

[76757] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2238 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2238 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76758] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2238 gene, herein designated VGAM is inhibition of expression of VGAM2238 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2238 correlate with, and may be deduced from, the identity of the target genes which VGAM2238 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76759] Adenylate Cyclase 7 (ADCY7, Accession NM_001114) is a VGAM2238 host target gene. ADCY7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADCY7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADCY7 BINDING SITE, designated SEQ ID:6784, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76760] A function of VGAM2238 is therefore inhibition of Adenylate Cyclase 7 (ADCY7, Accession NM_001114), a gene which this a membrane-bound, ca(2+)-inhibitable adenylyl cyclase. Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY7. The function of ADCY7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM108.ATPase, Aminophospholipid Transporter-like, Class I, Type 8A, Member 2 (ATP8A2, Accession XM_167916) is another VGAM2238 host target gene. ATP8A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by ATP8A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP8A2 BINDING SITE, designated SEQ ID:44921, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76761] Another function of VGAM2238 is therefore inhibition of ATPase, Aminophospholipid Transporter-like, Class I, Type 8A, Member 2 (ATP8A2, Accession XM_167916). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8A2. B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6, Accession NM_001706) is another VGAM2238 host target gene. BCL6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BCL6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL6 BINDING SITE, designated SEQ ID:7431, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76762] Another function of VGAM2238 is therefore inhibition of B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6, Accession NM_001706), a gene which is involved in the generation and maintenance of both T and B cells during immune responses. Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL6. The function of BCL6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM481.Myeloid/lymphoid Or Mixed-lineage Leukemia (trithorax homolog, Drosophila); Translocated To, 4 (MLLT4, Accession XM_051832) is another VGAM2238 host target gene. MLLT4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MLLT4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MLLT4 BINDING SITE, designated SEQ ID:35887, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76763] Another function of VGAM2238 is therefore inhibition of

Myeloid/lymphoid Or Mixed-lineage Leukemia (trithorax homolog, Drosophila); Translocated To, 4 (MLLT4, Accession XM_051832), a gene which may act as an intracellular signaling component. Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLLT4. The function of MLLT4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1608.Proteasome (prosome, macropain) Activator Subunit 3 (PA28 gamma; Ki) (PSME3, Accession NM_005789) is another VGAM2238 host target gene. PSME3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PSME3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSME3 BINDING SITE, designated SEQ ID:12371, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76764] Another function of VGAM2238 is therefore inhibition of Proteasome (prosome, macropain) Activator Subunit 3

(PA28 gamma; Ki) (PSME3, Accession NM_005789), a gene which is the activator subunit of the proteasome (prosome macropain). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSME3. The function of PSME3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1498.RAB23, Member RAS Oncogene Family (RAB23, Accession NM_016277) is another VGAM2238 host target gene. RAB23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB23 BINDING SITE, designated SEQ ID:18400, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76765] Another function of VGAM2238 is therefore inhibition of RAB23, Member RAS Oncogene Family (RAB23, Accession NM_016277), a gene which is involved in the regulation of intracellular membrane trafficking. Accordingly, utilities of

VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB23. The function of RAB23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM340.Solute Carrier Family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), Member 1 (SLC1A1, Accession NM_004170) is another VGAM2238 host target gene. SLC1A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC1A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC1A1 BINDING SITE, designated SEQ ID:10377, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76766] Another function of VGAM2238 is therefore inhibition of Solute Carrier Family 1 (neuronal/epithelial high affinity glutamate transporter, system Xag), Member 1 (SLC1A1, Accession NM_004170), a gene which is a glutamate transporter, essential for terminating the postsynaptic action of glutamate by rapidly removing it from the synaptic

cleft. Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC1A1. The function of SLC1A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.ATPase, Class II, Type 9A (ATP9A, Accession XM_030577) is another VGAM2238 host target gene. ATP9A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP9A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP9A BINDING SITE, designated SEQ ID:31085, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76767] Another function of VGAM2238 is therefore inhibition of ATPase, Class II, Type 9A (ATP9A, Accession XM_030577). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP9A. Diacylglycerol Kinase, Delta 130kDa (DGKD, Accession XM_002384) is another VGAM2238 host target gene. DGKD BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by DGKD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGKD BINDING SITE, designated SEQ ID:29883, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76768] Another function of VGAM2238 is therefore inhibition of Diacylglycerol Kinase, Delta 130kDa (DGKD, Accession XM_002384). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGKD. FLJ10520 (Accession NM_018124) is another VGAM2238 host target gene. FLJ10520 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10520, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10520 BINDING SITE, designated SEQ ID:19905, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76769] Another function of VGAM2238 is therefore inhibition of FLJ10520 (Accession NM_018124). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10520. FLJ20618 (Accession NM_017903) is another VGAM2238 host target gene. FLJ20618 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20618, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20618 BINDING SITE, designated SEQ ID:19569, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76770] Another function of VGAM2238 is therefore inhibition of FLJ20618 (Accession NM_017903). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20618. Glutamate Receptor, Ionotropic, N-methyl-D-aspartate 3A (GRIN3A, Accession NM_133445) is another VGAM2238 host target gene. GRIN3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRIN3A, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRIN3A BINDING SITE, designated SEQ ID:28536, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76771] Another function of VGAM2238 is therefore inhibition of Glutamate Receptor, Ionotropic, N-methyl-D-aspartate 3A (GRIN3A, Accession NM_133445). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIN3A. H2A Histone Family, Member J (H2AFJ, Accession NM_018267) is another VGAM2238 host target gene. H2AFJ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by H2AFJ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H2AFJ BINDING SITE, designated SEQ ID:20237, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76772] Another function of VGAM2238 is therefore inhibition of

H2A Histone Family, Member J (H2AFJ, Accession NM_018267). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H2AFJ. KIAA0565 (Accession XM_039912) is another VGAM2238 host target gene. KIAA0565 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0565, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0565 BINDING SITE, designated SEQ ID:33216, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76773] Another function of VGAM2238 is therefore inhibition of KIAA0565 (Accession XM_039912). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0565. KIAA0677 (Accession NM_014663) is another VGAM2238 host target gene. KIAA0677 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0677, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0677 BINDING SITE, designated SEQ ID:16110, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76774] Another function of VGAM2238 is therefore inhibition of KIAA0677 (Accession NM_014663). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0677. KIAA0794 (Accession XM_087353) is another VGAM2238 host target gene. KIAA0794 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0794 BINDING SITE, designated SEQ ID:39177, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76775] Another function of VGAM2238 is therefore inhibition of KIAA0794 (Accession XM_087353). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0794. KIAA0979 (Accession NM_015032) is another VGAM2238 host target gene. KIAA0979 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0979, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0979 BINDING SITE, designated SEQ ID:17387, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76776] Another function of VGAM2238 is therefore inhibition of KIAA0979 (Accession NM_015032). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0979. Lipoma HMGIC Fusion Partner (LHFP, Accession NM_005780) is another VGAM2238 host target gene. LHFP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LHFP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LHFP BINDING SITE, designated SEQ ID:12356, to the nucleotide sequence of VGAM2238 RNA, herein designated

VGAM RNA, also designated SEQ ID:4949.

[76777] Another function of VGAM2238 is therefore inhibition of Lipoma HMGIC Fusion Partner (LHFP, Accession NM_005780). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHFP. MKP-7 (Accession XM_039106) is another VGAM2238 host target gene. MKP-7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MKP-7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MKP-7 BINDING SITE, designated SEQ ID:33007, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76778] Another function of VGAM2238 is therefore inhibition of MKP-7 (Accession XM_039106). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKP-7. PORIMIN (Accession NM_052932) is another VGAM2238 host target gene. PORIMIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by PORIMIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PORIMIN BINDING SITE, designated SEQ ID:27491, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76779] Another function of VGAM2238 is therefore inhibition of PORIMIN (Accession NM_052932). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PORIMIN. Protein Tyrosine Kinase 9 (PTK9, Accession NM_002822) is another VGAM2238 host target gene. PTK9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTK9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTK9 BINDING SITE, designated SEQ ID:8691, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76780] Another function of VGAM2238 is therefore inhibition of Protein Tyrosine Kinase 9 (PTK9, Accession NM_002822).

Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTK9. Syntaphilin (SNPH, Accession NM_014723) is another VGAM2238 host target gene. SNPH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNPH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNPH BINDING SITE, designated SEQ ID:16295, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76781] Another function of VGAM2238 is therefore inhibition of Syntaphilin (SNPH, Accession NM_014723). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNPH. LOC115509 (Accession XM_056092) is another VGAM2238 host target gene. LOC115509 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115509, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC115509 BINDING SITE, designated SEQ ID:36364, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76782] Another function of VGAM2238 is therefore inhibition of LOC115509 (Accession XM_056092). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115509. LOC134266 (Accession XM_059701) is another VGAM2238 host target gene. LOC134266 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC134266, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC134266 BINDING SITE, designated SEQ ID:37068, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76783] Another function of VGAM2238 is therefore inhibition of LOC134266 (Accession XM_059701). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC134266. LOC145439 (Accession XM_085144) is another VGAM2238 host target gene. LOC145439 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145439, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145439 BINDING SITE, designated SEQ ID:37865, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76784] Another function of VGAM2238 is therefore inhibition of LOC145439 (Accession XM_085144). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145439. LOC146819 (Accession XM_085605) is another VGAM2238 host target gene. LOC146819 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146819, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146819 BINDING SITE, designated SEQ ID:38254, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76785] Another function of VGAM2238 is therefore inhibition of

LOC146819 (Accession XM_085605). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146819. LOC146821 (Accession XM_085597) is another VGAM2238 host target gene. LOC146821 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146821, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146821 BINDING SITE, designated SEQ ID:38252, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76786] Another function of VGAM2238 is therefore inhibition of LOC146821 (Accession XM_085597). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146821. LOC150142 (Accession XM_086791) is another VGAM2238 host target gene. LOC150142 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150142, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC150142 BINDING SITE, designated SEQ ID:38853, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76787] Another function of VGAM2238 is therefore inhibition of LOC150142 (Accession XM_086791). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150142. LOC201287 (Accession XM_113947) is another VGAM2238 host target gene. LOC201287 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201287, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201287 BINDING SITE, designated SEQ ID:42559, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76788] Another function of VGAM2238 is therefore inhibition of LOC201287 (Accession XM_113947). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201287. LOC219627 (Accession XM_166402) is an-

other VGAM2238 host target gene. LOC219627 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219627, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219627 BINDING SITE, designated SEQ ID:44271, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76789] Another function of VGAM2238 is therefore inhibition of LOC219627 (Accession XM_166402). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219627. LOC220705 (Accession XM_166000) is another VGAM2238 host target gene. LOC220705 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220705, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220705 BINDING SITE, designated SEQ ID:43834, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76790] Another function of VGAM2238 is therefore inhibition of LOC220705 (Accession XM_166000). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220705. LOC221895 (Accession XM_166511) is another VGAM2238 host target gene. LOC221895 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221895, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221895 BINDING SITE, designated SEQ ID:44442, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76791] Another function of VGAM2238 is therefore inhibition of LOC221895 (Accession XM_166511). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221895. LOC222060 (Accession XM_168427) is another VGAM2238 host target gene. LOC222060 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222060, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222060 BINDING SITE, designated SEQ ID:45160, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76792] Another function of VGAM2238 is therefore inhibition of LOC222060 (Accession XM_168427). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222060. LOC256207 (Accession XM_170837) is another VGAM2238 host target gene. LOC256207 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256207, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256207 BINDING SITE, designated SEQ ID:45617, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76793] Another function of VGAM2238 is therefore inhibition of LOC256207 (Accession XM_170837). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC256207. LOC86651 (Accession XM_044052) is another VGAM2238 host target gene. LOC86651 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC86651, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC86651 BINDING SITE, designated SEQ ID:34098, to the nucleotide sequence of VGAM2238 RNA, herein designated VGAM RNA, also designated SEQ ID:4949.

[76794] Another function of VGAM2238 is therefore inhibition of LOC86651 (Accession XM_044052). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC86651. LOC91151 (Accession NM_033208) is another VGAM2238 host target gene. LOC91151 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91151, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91151 BINDING SITE, designated SEQ ID:27053, to the nucleotide sequence of VGAM2238 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4949.

[76795] Another function of VGAM2238 is therefore inhibition of LOC91151 (Accession NM_033208). Accordingly, utilities of VGAM2238 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91151. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2239 (VGAM2239) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76796] VGAM2239 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2239 was detected is described hereinabove with reference to Figs. 1-8.

[76797] VGAM2239 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2239 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76798] VGAM2239 gene encodes a VGAM2239 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2239 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2239 precursor RNA is designated SEQ ID:2225, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2225 is located at position 11663 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76799] VGAM2239 precursor RNA folds onto itself, forming VGAM2239 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76800] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2239 folded precursor RNA into VGAM2239 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of VGAM2239 RNA is designated SEQ ID:4950, and is provided hereinbelow with reference to the sequence listing part.

[76801] VGAM2239 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2239 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2239 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76802] VGAM2239 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2239 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2239 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2239 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2239 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76803] The complementary binding of VGAM2239 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2239 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2239 host target RNA into VGAM2239 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76804] It is appreciated that VGAM2239 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2239 host target genes. The mRNA of

each one of this plurality of VGAM2239 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2239 RNA, herein designated VGAM RNA, and which when bound by VGAM2239 RNA causes inhibition of translation of respective one or more VGAM2239 host target proteins.

[76805] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2239 gene, herein designated VGAM GENE, on one or more VGAM2239 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[76806] It is yet further appreciated that a function of VGAM2239 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGAM2239 correlate with, and may be deduced from, the identity of the host target genes which VGAM2239 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76807] Nucleotide sequences of the VGAM2239 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2239 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2239 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2239 are further described hereinbelow with reference to Table 1.

[76808] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2239 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2239 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76809] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2239 gene, herein designated VGAM is inhibition of expression of VGAM2239 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2239 correlate with, and may be deduced from, the identity of the target genes which VGAM2239 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76810] ATP-binding Cassette, Sub-family A (ABC1), Member 1 (ABCA1, Accession NM_005502) is a VGAM2239 host target gene. ABCA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCA1 BINDING SITE, designated SEQ ID:12015, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76811] A function of VGAM2239 is therefore inhibition of ATP-binding Cassette, Sub-family A (ABC1), Member 1 (ABCA1,

Accession NM_005502), a gene which camp-dependent and sulfonylurea-sensitive anion transporter. Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCA1. The function of ABCA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1956.Eukaryotic Translation Initiation Factor 1A (EIF1A, Accession XM_114147) is another VGAM2239 host target gene. EIF1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF1A BINDING SITE, designated SEQ ID:42719, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76812] Another function of VGAM2239 is therefore inhibition of Eukaryotic Translation Initiation Factor 1A (EIF1A, Accession XM_114147), a gene which seems to be required for maximal rate of protein biosynthesis. Accordingly, utilities of VGAM2239 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with EIF1A. The function of EIF1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM120.Protocadherin 12 (PCDH12, Accession NM_016580) is another VGAM2239 host target gene. PCDH12 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PCDH12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH12 BINDING SITE, designated SEQ ID:18658, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76813] Another function of VGAM2239 is therefore inhibition of Protocadherin 12 (PCDH12, Accession NM_016580), a gene which is a member of a family of nonclassical cadherins. Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH12. The function of PCDH12 has been established by previous studies. Murine vascular endothelial cadherin-2 is a cellular adhesion

molecule that is distinct from vascular endothelial cadherin-1 (CDH5; 601120) in that it does not interact with catenins and does not appear to affect cell migration or growth (Telo et al., 1998). By sequence database searching, Wu and Maniatis (2000) identified a human VE-cadherin-2 homolog, which they called protocadherin-12 (OMIM Ref. No. PCDH12), encoding a deduced 1,184-amino acid protein that shares 81% sequence identity with the mouse protein. PCDH12 contains 4 exons; a single large exon encodes the extracellular and transmembrane domains, and 3 small exons encode the cytoplasmic domain. Wu and Maniatis (2000) concluded that the presence of unusually large exons is a characteristic feature of protocadherin. Using the mouse Pcdh12 cDNA sequence and RACE-PCR reactions, Ludwig et al. (2000) cloned a full-length PCDH12 cDNA from a human fetal kidney cDNA library. Northern blot analysis detected expression of a 5-kb PCHD12 transcript chiefly in highly vascularized tissues including the heart and placenta, but most tissues contained a low level of expression. Prominent expression was also detected in the spleen. Some tissues, including skeletal muscle and peripheral blood leukocytes, possessed transcripts of a larger size.

[76814] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[76815] Wu, Q.; Maniatis, T. : Large exons encoding multiple ectodomains are a characteristic feature of protocadherin genes. Proc. Nat. Acad. Sci. 97: 3124-3129, 2000. ; and

[76816] Ludwig, D.; Lorenz, J.; Dejana, E.; Bohlen, P.; Hicklin, D. J.; Witte, L.; Pytowski, B. : cDNA cloning, chromosomal mapping, and expression analysis of human VE-cadherin-2. Mammalian Ge.

[76817] Further studies establishing the function and utilities of PCDH12 are found in John Hopkins OMIM database record ID 605622, and in sited publications numbered 6956-695 and 7438 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Ribonucleotide Reductase M2 B (TP53 inducible) (RRM2B, Accession XM_042096) is another VGAM2239 host target gene. RRM2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RRM2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RRM2B BINDING SITE, des-

ignated SEQ ID:33689, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76818] Another function of VGAM2239 is therefore inhibition of Ribonucleotide Reductase M2 B (TP53 inducible) (RRM2B, Accession XM_042096). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RRM2B. V-akt Murine Thymoma Viral Oncogene Homolog 3 (protein kinase B, gamma) (AKT3, Accession NM_005465) is another VGAM2239 host target gene. AKT3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKT3 BINDING SITE, designated SEQ ID:11957, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76819] Another function of VGAM2239 is therefore inhibition of V-akt Murine Thymoma Viral Oncogene Homolog 3 (protein kinase B, gamma) (AKT3, Accession NM_005465). Accordingly, utilities of VGAM2239 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with AKT3. DnaJ (Hsp40) Homolog, Subfamily C, Member 6 (DNAJC6, Accession NM_014787) is another VGAM2239 host target gene. DNAJC6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DNAJC6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNAJC6 BINDING SITE, designated SEQ ID:16661, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76820] Another function of VGAM2239 is therefore inhibition of DnaJ (Hsp40) Homolog, Subfamily C, Member 6 (DNAJC6, Accession NM_014787). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAJC6. KIAA0694 (Accession XM_051970) is another VGAM2239 host target gene. KIAA0694 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0694, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0694 BINDING SITE, designated SEQ ID:35928, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76821] Another function of VGAM2239 is therefore inhibition of KIAA0694 (Accession XM_051970). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0694. KIAA0892 (Accession XM_048457) is another VGAM2239 host target gene. KIAA0892 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0892, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0892 BINDING SITE, designated SEQ ID:35169, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76822] Another function of VGAM2239 is therefore inhibition of KIAA0892 (Accession XM_048457). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0892. Low Density Lipoprotein-related Protein 1B

(deleted in tumors) (LRP1B, Accession NM_018557) is another VGAM2239 host target gene. LRP1B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LRP1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRP1B BINDING SITE, designated SEQ ID:20639, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76823] Another function of VGAM2239 is therefore inhibition of Low Density Lipoprotein-related Protein 1B (deleted in tumors) (LRP1B, Accession NM_018557). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRP1B. Nuclear Receptor Subfamily 6, Group A, Member 1 (NR6A1, Accession NM_033334) is another VGAM2239 host target gene. NR6A1 BINDING SITE1 through NR6A1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NR6A1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of NR6A1 BINDING SITE1 through NR6A1 BINDING SITE3, designated SEQ ID:27181, SEQ ID:27187 and SEQ ID:7233 respectively, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76824] Another function of VGAM2239 is therefore inhibition of Nuclear Receptor Subfamily 6, Group A, Member 1 (NR6A1, Accession NM_033334). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR6A1. LOC147632 (Accession NM_138478) is another VGAM2239 host target gene. LOC147632 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147632, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147632 BINDING SITE, designated SEQ ID:28826, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76825] Another function of VGAM2239 is therefore inhibition of LOC147632 (Accession NM_138478). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC147632. LOC148894 (Accession XM_097542) is another VGAM2239 host target gene. LOC148894 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148894, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148894 BINDING SITE, designated SEQ ID:40919, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76826] Another function of VGAM2239 is therefore inhibition of LOC148894 (Accession XM_097542). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148894. LOC151473 (Accession XM_087215) is another VGAM2239 host target gene. LOC151473 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151473, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151473 BINDING SITE, designated SEQ ID:39120, to

the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76827] Another function of VGAM2239 is therefore inhibition of LOC151473 (Accession XM_087215). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151473. LOC151521 (Accession XM_098076) is another VGAM2239 host target gene. LOC151521 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151521, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151521 BINDING SITE, designated SEQ ID:41370, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76828] Another function of VGAM2239 is therefore inhibition of LOC151521 (Accession XM_098076). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151521. LOC157349 (Accession XM_088298) is another VGAM2239 host target gene. LOC157349 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC157349, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157349 BINDING SITE, designated SEQ ID:39594, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76829] Another function of VGAM2239 is therefore inhibition of LOC157349 (Accession XM_088298). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157349. LOC200150 (Accession XM_114131) is another VGAM2239 host target gene. LOC200150 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200150, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200150 BINDING SITE, designated SEQ ID:42713, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76830] Another function of VGAM2239 is therefore inhibition of LOC200150 (Accession XM_114131). Accordingly, utilities

of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200150. LOC51185 (Accession NM_016302) is another VGAM2239 host target gene. LOC51185 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51185, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51185 BINDING SITE, designated SEQ ID:18424, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76831] Another function of VGAM2239 is therefore inhibition of LOC51185 (Accession NM_016302). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51185. LOC56906 (Accession NM_020147) is another VGAM2239 host target gene. LOC56906 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC56906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC56906 BINDING SITE, designated SEQ ID:21343, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76832] Another function of VGAM2239 is therefore inhibition of LOC56906 (Accession NM_020147). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56906. LOC92539 (Accession XM_045632) is another VGAM2239 host target gene. LOC92539 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92539, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92539 BINDING SITE, designated SEQ ID:34500, to the nucleotide sequence of VGAM2239 RNA, herein designated VGAM RNA, also designated SEQ ID:4950.

[76833] Another function of VGAM2239 is therefore inhibition of LOC92539 (Accession XM_045632). Accordingly, utilities of VGAM2239 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92539. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2240 (VGAM2240) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76834] VGAM2240 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2240 was detected is described hereinabove with reference to Figs. 1-8.

[76835] VGAM2240 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2240 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76836] VGAM2240 gene encodes a VGAM2240 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2240 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2240 precursor RNA is designated SEQ ID:2226, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2226 is located at position 27326 relative to the

genome of Porcine Epidemic Diarrhea Virus.

[76837] VGAM2240 precursor RNA folds onto itself, forming VGAM2240 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76838] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2240 folded precursor RNA into VGAM2240 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2240 RNA is designated SEQ ID:4951, and is provided hereinbelow with reference to the sequence listing part.

[76839] VGAM2240 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2240 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2240 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76840] VGAM2240 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2240 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2240 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2240 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2240 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76841] The complementary binding of VGAM2240 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2240 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2240 host target RNA into VGAM2240 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76842] It is appreciated that VGAM2240 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2240 host target genes. The mRNA of each one of this plurality of VGAM2240 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2240 RNA, herein designated VGAM RNA, and which when bound by VGAM2240 RNA causes inhibition of translation of respective one or more VGAM2240 host target proteins.

[76843] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2240 gene, herein designated VGAM GENE, on one or more VGAM2240 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76844] It is yet further appreciated that a function of VGAM2240 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2240 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of

VGAM2240 correlate with, and may be deduced from, the identity of the host target genes which VGAM2240 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76845] Nucleotide sequences of the VGAM2240 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2240 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2240 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2240 are further described hereinbelow with reference to Table 1.

[76846] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2240 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2240 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76847] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2240 gene, herein designated VGAM is inhibition of expression of VGAM2240 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2240 correlate with, and may be deduced

from, the identity of the target genes which VGAM2240 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76848] Solute Carrier Family 39 (zinc transporter), Member 1 (SLC39A1, Accession NM_014437) is a VGAM2240 host target gene. SLC39A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC39A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC39A1 BINDING SITE, designated SEQ ID:15794, to the nucleotide sequence of VGAM2240 RNA, herein designated VGAM RNA, also designated SEQ ID:4951.

[76849] A function of VGAM2240 is therefore inhibition of Solute Carrier Family 39 (zinc transporter), Member 1 (SLC39A1, Accession NM_014437), a gene which is a divalent (zinc/iron) metal ion transporter. Accordingly, utilities of VGAM2240 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC39A1. The function of SLC39A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to VGAM1049.SRY (sex determining region Y)-box 12 (SOX12, Accession NM_006943) is another VGAM2240 host target gene. SOX12 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SOX12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX12 BINDING SITE, designated SEQ ID:13828, to the nucleotide sequence of VGAM2240 RNA, herein designated VGAM RNA, also designated SEQ ID:4951.

[76850] Another function of VGAM2240 is therefore inhibition of SRY (sex determining region Y)-box 12 (SOX12, Accession NM_006943). Accordingly, utilities of VGAM2240 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX12. Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2, Accession NM_014737) is another VGAM2240 host target gene. RASSF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RASSF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of RASSF2 BINDING SITE, designated SEQ ID:16391, to the nucleotide sequence of VGAM2240 RNA, herein designated VGAM RNA, also designated SEQ ID:4951.

[76851] Another function of VGAM2240 is therefore inhibition of Ras Association (RalGDS/AF-6) Domain Family 2 (RASSF2, Accession NM_014737). Accordingly, utilities of VGAM2240 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RASSF2. Signal Sequence Receptor, Gamma (translocon-associated protein gamma) (SSR3, Accession NM_007107) is another VGAM2240 host target gene. SSR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SSR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SSR3 BINDING SITE, designated SEQ ID:13973, to the nucleotide sequence of VGAM2240 RNA, herein designated VGAM RNA, also designated SEQ ID:4951.

[76852] Another function of VGAM2240 is therefore inhibition of Signal Sequence Receptor, Gamma (translocon-associated protein gamma) (SSR3, Accession NM_007107). Accord-

ingly, utilities of VGAM2240 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSR3. LOC152200 (Accession XM_098174) is another VGAM2240 host target gene. LOC152200 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152200, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152200 BINDING SITE, designated SEQ ID:41436, to the nucleotide sequence of VGAM2240 RNA, herein designated VGAM RNA, also designated SEQ ID:4951.

[76853] Another function of VGAM2240 is therefore inhibition of LOC152200 (Accession XM_098174). Accordingly, utilities of VGAM2240 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152200. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2241 (VGAM2241) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76854] VGAM2241 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2241 was detected is described hereinabove with reference to Figs. 1-8.

[76855] VGAM2241 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2241 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76856] VGAM2241 gene encodes a VGAM2241 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2241 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2241 precursor RNA is designated SEQ ID:2227, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2227 is located at position 14383 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76857] VGAM2241 precursor RNA folds onto itself, forming VGAM2241 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76858] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2241 folded precursor RNA into VGAM2241 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2241 RNA is designated SEQ ID:4952, and is provided hereinbelow with reference to the sequence listing part.

[76859] VGAM2241 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2241 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2241 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[76860] VGAM2241 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2241 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2241 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2241 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2241 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76861] The complementary binding of VGAM2241 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2241 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2241 host target RNA into VGAM2241 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76862] It is appreciated that VGAM2241 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2241 host target genes. The mRNA of each one of this plurality of VGAM2241 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2241 RNA, herein designated VGAM RNA, and which when bound by VGAM2241 RNA causes inhibition of translation of respective one or more VGAM2241 host target proteins.

[76863] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2241 gene, herein designated VGAM GENE, on one or more VGAM2241 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76864] It is yet further appreciated that a function of VGAM2241 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2241 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGAM2241 correlate with, and may be deduced from, the identity of the host target genes which VGAM2241 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76865] Nucleotide sequences of the VGAM2241 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2241 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2241 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2241 are further described hereinbelow with reference to Table 1.

[76866] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2241 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2241 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76867] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2241 gene, herein designated VGAM is inhibition of expression of VGAM2241 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2241 correlate with, and may be deduced from, the identity of the target genes which VGAM2241 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76868] POPX1 (Accession NM_014906) is a VGAM2241 host target gene. POPX1 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by POPX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POPX1 BINDING SITE, designated SEQ ID:17117, to the nucleotide sequence of VGAM2241 RNA, herein designated VGAM RNA, also designated SEQ ID:4952.

[76869] A function of VGAM2241 is therefore inhibition of POPX1 (Accession NM_014906). Accordingly, utilities of VGAM2241 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POPX1. PRO2714 (Accession NM_018534) is another VGAM2241 host target gene. PRO2714 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2714, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2714 BINDING SITE, designated SEQ ID:20603, to the nucleotide sequence of VGAM2241 RNA, herein designated VGAM RNA, also designated SEQ ID:4952.

[76870] Another function of VGAM2241 is therefore inhibition of

PRO2714 (Accession NM_018534). Accordingly, utilities of VGAM2241 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2714. Solute Carrier Family 11 (proton-coupled divalent metal ion transporters), Member 2 (SLC11A2, Accession NM_000617) is another VGAM2241 host target gene. SLC11A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC11A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC11A2 BINDING SITE, designated SEQ ID:6223, to the nucleotide sequence of VGAM2241 RNA, herein designated VGAM RNA, also designated SEQ ID:4952.

[76871] Another function of VGAM2241 is therefore inhibition of Solute Carrier Family 11 (proton-coupled divalent metal ion transporters), Member 2 (SLC11A2, Accession NM_000617). Accordingly, utilities of VGAM2241 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC11A2. LOC254228 (Accession XM_171123) is another VGAM2241 host target gene. LOC254228 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by LOC254228, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254228 BINDING SITE, designated SEQ ID:45918, to the nucleotide sequence of VGAM2241 RNA, herein designated VGAM RNA, also designated SEQ ID:4952.

[76872] Another function of VGAM2241 is therefore inhibition of LOC254228 (Accession XM_171123). Accordingly, utilities of VGAM2241 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254228. LOC90736 (Accession XM_033811) is another VGAM2241 host target gene. LOC90736 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90736, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90736 BINDING SITE, designated SEQ ID:31959, to the nucleotide sequence of VGAM2241 RNA, herein designated VGAM RNA, also designated SEQ ID:4952.

[76873] Another function of VGAM2241 is therefore inhibition of

LOC90736 (Accession XM_033811). Accordingly, utilities of VGAM2241 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90736. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2242 (VGAM2242) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76874] VGAM2242 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2242 was detected is described hereinabove with reference to Figs. 1-8.

[76875] VGAM2242 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2242 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76876] VGAM2242 gene encodes a VGAM2242 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2242 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2242 precursor RNA is designated SEQ ID:2228, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2228 is located at position 2414 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76877] VGAM2242 precursor RNA folds onto itself, forming VGAM2242 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76878] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2242 folded precursor RNA into VGAM2242 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide se-

quence of VGAM2242 RNA is designated SEQ ID:4953, and is provided hereinbelow with reference to the sequence listing part.

[76879] VGAM2242 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2242 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2242 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76880] VGAM2242 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2242 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2242 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2242 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2242 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76881] The complementary binding of VGAM2242 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2242 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2242 host target RNA into VGAM2242 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76882] It is appreciated that VGAM2242 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2242 host target genes. The mRNA of each one of this plurality of VGAM2242 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2242 RNA, herein designated VGAM RNA, and which when bound by VGAM2242 RNA causes inhibition of translation of respective one or more VGAM2242 host target proteins.

[76883] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2242 gene, herein designated VGAM GENE, on one or more VGAM2242 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76884] It is yet further appreciated that a function of VGAM2242

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2242 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGAM2242 correlate with, and may be deduced from, the identity of the host target genes which VGAM2242 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76885] Nucleotide sequences of the VGAM2242 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2242 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2242 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2242 are further described hereinbelow with reference to Table 1.

[76886] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2242 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2242 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76887] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2242 gene, herein designated VGAM is inhibition of expression of VGAM2242 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2242 correlate with, and may be deduced from, the identity of the target genes which VGAM2242 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76888] Aldehyde Dehydrogenase 1 Family, Member A3 (ALDH1A3, Accession NM_000693) is a VGAM2242 host target gene. ALDH1A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALDH1A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALDH1A3 BINDING SITE, designated SEQ ID:6354, to the nucleotide sequence of VGAM2242 RNA, herein designated VGAM RNA, also designated SEQ ID:4953.

[76889] A function of VGAM2242 is therefore inhibition of Aldehyde Dehydrogenase 1 Family, Member A3 (ALDH1A3, Accession NM_000693), a gene which plays a major role in the detoxification of aldehydes generated by alcohol

metabolism and lipid peroxidation. Accordingly, utilities of VGAM2242 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH1A3. The function of ALDH1A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM565.Annexin A9 (ANXA9, Accession NM_003568) is another VGAM2242 host target gene. ANXA9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ANXA9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANXA9 BINDING SITE, designated SEQ ID:9622, to the nucleotide sequence of VGAM2242 RNA, herein designated VGAM RNA, also designated SEQ ID:4953.

[76890] Another function of VGAM2242 is therefore inhibition of Annexin A9 (ANXA9, Accession NM_003568), a gene which aggregates and cooperatively binds anionic phospholipids and extracellular matrix proteins. Accordingly, utilities of VGAM2242 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with ANXA9. The function of ANXA9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1485.Caspase Recruitment Domain Family, Member 6 (CARD6, Accession NM_032587) is another VGAM2242 host target gene. CARD6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CARD6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CARD6 BINDING SITE, designated SEQ ID:26321, to the nucleotide sequence of VGAM2242 RNA, herein designated VGAM RNA, also designated SEQ ID:4953.

[76891] Another function of VGAM2242 is therefore inhibition of Caspase Recruitment Domain Family, Member 6 (CARD6, Accession NM_032587). Accordingly, utilities of VGAM2242 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD6. DKFZp434C0923 (Accession NM_017598) is another VGAM2242 host target gene. DKFZp434C0923 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434C0923,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434C0923 BINDING SITE, designated SEQ ID:19062, to the nucleotide sequence of VGAM2242 RNA, herein designated VGAM RNA, also designated SEQ ID:4953.

[76892] Another function of VGAM2242 is therefore inhibition of DKFZp434C0923 (Accession NM_017598). Accordingly, utilities of VGAM2242 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434C0923. FLJ13491 (Accession NM_024623) is another VGAM2242 host target gene. FLJ13491 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13491, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13491 BINDING SITE, designated SEQ ID:23886, to the nucleotide sequence of VGAM2242 RNA, herein designated VGAM RNA, also designated SEQ ID:4953.

[76893] Another function of VGAM2242 is therefore inhibition of FLJ13491 (Accession NM_024623). Accordingly, utilities of

VGAM2242 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13491. KIAA1229 (Accession XM_030665) is another VGAM2242 host target gene. KIAA1229 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1229 BINDING SITE, designated SEQ ID:31096, to the nucleotide sequence of VGAM2242 RNA, herein designated VGAM RNA, also designated SEQ ID:4953.

[76894] Another function of VGAM2242 is therefore inhibition of KIAA1229 (Accession XM_030665). Accordingly, utilities of VGAM2242 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1229. LOC157798 (Accession XM_098827) is another VGAM2242 host target gene. LOC157798 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157798, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC157798 BINDING SITE, designated SEQ ID:41853, to the nucleotide sequence of VGAM2242 RNA, herein designated VGAM RNA, also designated SEQ ID:4953.

[76895] Another function of VGAM2242 is therefore inhibition of LOC157798 (Accession XM_098827). Accordingly, utilities of VGAM2242 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157798. LOC92912 (Accession XM_047970) is another VGAM2242 host target gene. LOC92912 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92912, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92912 BINDING SITE, designated SEQ ID:35083, to the nucleotide sequence of VGAM2242 RNA, herein designated VGAM RNA, also designated SEQ ID:4953.

[76896] Another function of VGAM2242 is therefore inhibition of LOC92912 (Accession XM_047970). Accordingly, utilities of VGAM2242 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92912. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2243 (VGAM2243) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76897] VGAM2243 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2243 was detected is described hereinabove with reference to Figs. 1-8.

[76898] VGAM2243 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2243 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76899] VGAM2243 gene encodes a VGAM2243 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2243 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2243 precursor RNA is designated SEQ ID:2229, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2229 is located at position 19645 relative to the

genome of Porcine Epidemic Diarrhea Virus.

[76900] VGAM2243 precursor RNA folds onto itself, forming VGAM2243 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76901] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2243 folded precursor RNA into VGAM2243 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2243 RNA is designated SEQ ID:4954, and is provided hereinbelow with reference to the sequence listing part.

[76902] VGAM2243 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2243 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2243 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76903] VGAM2243 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2243 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2243 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2243 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2243 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76904] The complementary binding of VGAM2243 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2243 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2243 host target RNA into VGAM2243 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76905] It is appreciated that VGAM2243 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2243 host target genes. The mRNA of each one of this plurality of VGAM2243 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2243 RNA, herein designated VGAM RNA, and which when bound by VGAM2243 RNA causes inhibition of translation of respective one or more VGAM2243 host target proteins.

[76906] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2243 gene, herein designated VGAM GENE, on one or more VGAM2243 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76907] It is yet further appreciated that a function of VGAM2243 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2243 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of

VGAM2243 correlate with, and may be deduced from, the identity of the host target genes which VGAM2243 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76908] Nucleotide sequences of the VGAM2243 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2243 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2243 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2243 are further described hereinbelow with reference to Table 1.

[76909] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2243 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2243 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76910] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2243 gene, herein designated VGAM is inhibition of expression of VGAM2243 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2243 correlate with, and may be deduced

from, the identity of the target genes which VGAM2243 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76911] Exostoses (multiple)-like 2 (EXTL2, Accession NM_001439) is a VGAM2243 host target gene. EXTL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EXTL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EXTL2 BINDING SITE, designated SEQ ID:7161, to the nucleotide sequence of VGAM2243 RNA, herein designated VGAM RNA, also designated SEQ ID:4954.

[76912] A function of VGAM2243 is therefore inhibition of Exostoses (multiple)-like 2 (EXTL2, Accession NM_001439), a gene which is homologous to the EXT and EXTL genes. Accordingly, utilities of VGAM2243 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EXTL2. The function of EXTL2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM743.Leucine-rich Repeat-containing 2 (LRRC2, Accession NM_024512) is an-

other VGAM2243 host target gene. LRRC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LRRC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRRC2 BINDING SITE, designated SEQ ID:23702, to the nucleotide sequence of VGAM2243 RNA, herein designated VGAM RNA, also designated SEQ ID:4954.

[76913] Another function of VGAM2243 is therefore inhibition of Leucine-rich Repeat-containing 2 (LRRC2, Accession NM_024512). Accordingly, utilities of VGAM2243 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRRC2. Antigen Identified By Monoclonal Antibody Ki-67 (MKI67, Accession NM_002417) is another VGAM2243 host target gene. MKI67 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MKI67, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MKI67 BINDING SITE, designated SEQ ID:8253, to the nucleotide sequence of VGAM2243 RNA, herein

designated VGAM RNA, also designated SEQ ID:4954.

[76914] Another function of VGAM2243 is therefore inhibition of Antigen Identified By Monoclonal Antibody Ki-67 (MKI67, Accession NM_002417), a gene which thought to be required for maintaining cell proliferation. Accordingly, utilities of VGAM2243 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKI67. The function of MKI67 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM786.HML2 (Accession NM_006344) is another VGAM2243 host target gene. HML2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HML2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HML2 BINDING SITE, designated SEQ ID:13041, to the nucleotide sequence of VGAM2243 RNA, herein designated VGAM RNA, also designated SEQ ID:4954.

[76915] Another function of VGAM2243 is therefore inhibition of HML2 (Accession NM_006344). Accordingly, utilities of VGAM2243 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with HML2. KIAA0057 (Accession NM_012288) is another VGAM2243 host target gene. KIAA0057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0057 BINDING SITE, designated SEQ ID:14617, to the nucleotide sequence of VGAM2243 RNA, herein designated VGAM RNA, also designated SEQ ID:4954.

[76916] Another function of VGAM2243 is therefore inhibition of KIAA0057 (Accession NM_012288). Accordingly, utilities of VGAM2243 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0057. LOC145757 (Accession XM_085227) is another VGAM2243 host target gene. LOC145757 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145757, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145757 BINDING SITE, designated SEQ ID:37971, to

the nucleotide sequence of VGAM2243 RNA, herein designated VGAM RNA, also designated SEQ ID:4954.

[76917] Another function of VGAM2243 is therefore inhibition of LOC145757 (Accession XM_085227). Accordingly, utilities of VGAM2243 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145757. LOC149506 (Accession XM_097661) is another VGAM2243 host target gene. LOC149506 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149506, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149506 BINDING SITE, designated SEQ ID:41004, to the nucleotide sequence of VGAM2243 RNA, herein designated VGAM RNA, also designated SEQ ID:4954.

[76918] Another function of VGAM2243 is therefore inhibition of LOC149506 (Accession XM_097661). Accordingly, utilities of VGAM2243 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149506. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2244 (VGAM2244) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76919] VGAM2244 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2244 was detected is described hereinabove with reference to Figs. 1-8.

[76920] VGAM2244 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2244 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76921] VGAM2244 gene encodes a VGAM2244 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2244 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2244 precursor RNA is designated SEQ ID:2230, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2230 is located at position 23117 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76922] VGAM2244 precursor RNA folds onto itself, forming VGAM2244 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76923] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2244 folded precursor RNA into VGAM2244 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2244 RNA is designated SEQ ID:4955, and is provided hereinbelow with reference to the sequence listing part.

[76924] VGAM2244 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2244 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2244 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76925] VGAM2244 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2244 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2244 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2244 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2244 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76926] The complementary binding of VGAM2244 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2244 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2244 host target RNA into VGAM2244 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76927] It is appreciated that VGAM2244 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2244 host target genes. The mRNA of each one of this plurality of VGAM2244 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2244 RNA, herein designated VGAM RNA, and which when bound by VGAM2244 RNA causes inhibition of translation of respective one or more VGAM2244 host target proteins.

[76928] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2244 gene, herein designated VGAM GENE, on one or more VGAM2244 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76929] It is yet further appreciated that a function of VGAM2244 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2244 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea Virus. Specific functions, and accordingly utilities, of VGAM2244 correlate with, and may be deduced from, the

identity of the host target genes which VGAM2244 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76930] Nucleotide sequences of the VGAM2244 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2244 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2244 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2244 are further described hereinbelow with reference to Table 1.

[76931] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2244 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2244 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76932] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2244 gene, herein designated VGAM is inhibition of expression of VGAM2244 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2244 correlate with, and may be deduced from, the identity of the target genes which VGAM2244

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76933] Kell Blood Group Precursor (McLeod phenotype) (XK, Accession NM_021083) is a VGAM2244 host target gene. XK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XK BINDING SITE, designated SEQ ID:22060, to the nucleotide sequence of VGAM2244 RNA, herein designated VGAM RNA, also designated SEQ ID:4955.

[76934] A function of VGAM2244 is therefore inhibition of Kell Blood Group Precursor (McLeod phenotype) (XK, Accession NM_021083). Accordingly, utilities of VGAM2244 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XK. POF1B (Accession NM_024921) is another VGAM2244 host target gene. POF1B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POF1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of POF1B BINDING SITE, designated SEQ ID:24454, to the nucleotide sequence of VGAM2244 RNA, herein designated VGAM RNA, also designated SEQ ID:4955.

[76935] Another function of VGAM2244 is therefore inhibition of POF1B (Accession NM_024921). Accordingly, utilities of VGAM2244 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POF1B. LOC158156 (Accession XM_088496) is another VGAM2244 host target gene. LOC158156 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158156, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158156 BINDING SITE, designated SEQ ID:39738, to the nucleotide sequence of VGAM2244 RNA, herein designated VGAM RNA, also designated SEQ ID:4955.

[76936] Another function of VGAM2244 is therefore inhibition of LOC158156 (Accession XM_088496). Accordingly, utilities of VGAM2244 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158156. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2245 (VGAM2245) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76937] VGAM2245 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2245 was detected is described hereinabove with reference to Figs. 1-8.

[76938] VGAM2245 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Porcine Epidemic Diarrhea Virus. VGAM2245 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76939] VGAM2245 gene encodes a VGAM2245 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2245 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2245 precursor RNA is designated SEQ ID:2231, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2231 is located at position 11817 relative to the genome of Porcine Epidemic Diarrhea Virus.

[76940] VGAM2245 precursor RNA folds onto itself, forming VGAM2245 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76941] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2245 folded precursor RNA into VGAM2245 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2245 RNA is designated SEQ ID:4956, and is provided hereinbelow with reference to the sequence listing part.

[76942] VGAM2245 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2245 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2245 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76943] VGAM2245 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2245 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2245 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2245 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2245 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76944] The complementary binding of VGAM2245 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2245 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2245 host target RNA into VGAM2245 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76945] It is appreciated that VGAM2245 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2245 host target genes. The mRNA of each one of this plurality of VGAM2245 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2245 RNA, herein designated VGAM RNA, and which when bound by VGAM2245 RNA causes inhibition of translation of respective one or more

VGAM2245 host target proteins.

[76946] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2245 gene, herein designated VGAM GENE, on one or more VGAM2245 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76947] It is yet further appreciated that a function of VGAM2245 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2245 include diagnosis, prevention and treatment of viral infection by Porcine Epidemic Diarrhea

Virus. Specific functions, and accordingly utilities, of VGAM2245 correlate with, and may be deduced from, the identity of the host target genes which VGAM2245 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76948] Nucleotide sequences of the VGAM2245 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2245 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2245 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2245 are further described hereinbelow with reference to Table 1.

[76949] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2245 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2245 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76950] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2245 gene, herein designated VGAM is inhibition of expression of VGAM2245 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2245 correlate with, and may be deduced from, the identity of the target genes which VGAM2245 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76951] Ac-like Transposable Element (ALTE, Accession NM_004729) is a VGAM2245 host target gene. ALTE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALTE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALTE BINDING SITE, designated SEQ ID:11106, to the nucleotide sequence of VGAM2245 RNA, herein designated VGAM RNA, also designated SEQ ID:4956.

[76952] A function of VGAM2245 is therefore inhibition of Ac-like Transposable Element (ALTE, Accession NM_004729). Accordingly, utilities of VGAM2245 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALTE. BCL2-associated Athanogene 2 (BAG2, Accession XM_165779) is another VGAM2245 host target gene. BAG2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BAG2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAG2 BINDING SITE, designated SEQ ID:43752, to the nucleotide sequence of VGAM2245 RNA, herein designated VGAM RNA, also designated SEQ ID:4956.

[76953] Another function of VGAM2245 is therefore inhibition of BCL2-associated Athanogene 2 (BAG2, Accession XM_165779). Accordingly, utilities of VGAM2245 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAG2. DKFZp547D155 (Accession XM_046977) is another VGAM2245 host target gene. DKFZp547D155 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp547D155, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547D155 BINDING SITE, designated SEQ ID:34870, to the nucleotide sequence of VGAM2245 RNA, herein designated VGAM RNA, also designated SEQ ID:4956.

[76954] Another function of VGAM2245 is therefore inhibition of DKFZp547D155 (Accession XM_046977). Accordingly,

utilities of VGAM2245 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547D155. DKFZP586A011 (Accession NM_015416) is another VGAM2245 host target gene. DKFZP586A011 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586A011, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586A011 BINDING SITE, designated SEQ ID:17717, to the nucleotide sequence of VGAM2245 RNA, herein designated VGAM RNA, also designated SEQ ID:4956.

[76955] Another function of VGAM2245 is therefore inhibition of DKFZP586A011 (Accession NM_015416). Accordingly, utilities of VGAM2245 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586A011. FLJ10719 (Accession XM_031328) is another VGAM2245 host target gene. FLJ10719 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10719, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of FLJ10719 BINDING SITE, designated SEQ ID:31342, to the nucleotide sequence of VGAM2245 RNA, herein designated VGAM RNA, also designated SEQ ID:4956.

[76956] Another function of VGAM2245 is therefore inhibition of FLJ10719 (Accession XM_031328). Accordingly, utilities of VGAM2245 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10719. KLK15 (Accession NM_023006) is another VGAM2245 host target gene. KLK15 BINDING SITE1 and KLK15 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KLK15, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLK15 BINDING SITE1 and KLK15 BINDING SITE2, designated SEQ ID:23266 and SEQ ID:28864 respectively, to the nucleotide sequence of VGAM2245 RNA, herein designated VGAM RNA, also designated SEQ ID:4956.

[76957] Another function of VGAM2245 is therefore inhibition of KLK15 (Accession NM_023006). Accordingly, utilities of VGAM2245 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with KLK15. Stromal Cell Derived Factor Receptor 1 (SDFR1, Accession NM_012428) is another VGAM2245 host target gene. SDFR1 BINDING SITE1 and SDFR1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SDFR1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDFR1 BINDING SITE1 and SDFR1 BINDING SITE2, designated SEQ ID:14803 and SEQ ID:18930 respectively, to the nucleotide sequence of VGAM2245 RNA, herein designated VGAM RNA, also designated SEQ ID:4956.

[76958] Another function of VGAM2245 is therefore inhibition of Stromal Cell Derived Factor Receptor 1 (SDFR1, Accession NM_012428). Accordingly, utilities of VGAM2245 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDFR1. LOC146540 (Accession XM_085497) is another VGAM2245 host target gene. LOC146540 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146540, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146540 BINDING SITE, designated SEQ ID:38199, to the nucleotide sequence of VGAM2245 RNA, herein designated VGAM RNA, also designated SEQ ID:4956.

[76959] Another function of VGAM2245 is therefore inhibition of LOC146540 (Accession XM_085497). Accordingly, utilities of VGAM2245 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146540. LOC152485 (Accession XM_087479) is another VGAM2245 host target gene. LOC152485 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152485, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152485 BINDING SITE, designated SEQ ID:39280, to the nucleotide sequence of VGAM2245 RNA, herein designated VGAM RNA, also designated SEQ ID:4956.

[76960] Another function of VGAM2245 is therefore inhibition of LOC152485 (Accession XM_087479). Accordingly, utilities of VGAM2245 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC152485. LOC91300 (Accession XM_170568) is another VGAM2245 host target gene. LOC91300 BINDING SITE1 and LOC91300 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC91300, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91300 BINDING SITE1 and LOC91300 BINDING SITE2, designated SEQ ID:45385 and SEQ ID:29004 respectively, to the nucleotide sequence of VGAM2245 RNA, herein designated VGAM RNA, also designated SEQ ID:4956.

[76961] Another function of VGAM2245 is therefore inhibition of LOC91300 (Accession XM_170568). Accordingly, utilities of VGAM2245 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91300. Paired Basic Amino Acid Cleaving System 4 (PACE4, Accession NM_002570) is another VGAM2246 host target gene. PACE4 BINDING SITE1 and PACE4 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PACE4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of PACE4 BINDING SITE1 and PACE4 BINDING SITE2, designated SEQ ID:8429 and SEQ ID:28718 respectively, to the nucleotide sequence of VGAM2246 RNA, herein designated VGAM RNA, also designated SEQ ID:4957.

[76962] Another function of VGAM2246 is therefore inhibition of Paired Basic Amino Acid Cleaving System 4 (PACE4, Accession NM_002570), a gene which processes hormone precursors by cleaving paired basic amino acids. Accordingly, utilities of VGAM2246 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PACE4. The function of PACE4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1194.Tissue Inhibitor of Metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3, Accession NM_000362) is another VGAM2246 host target gene. TIMP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIMP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIMP3 BINDING SITE,

designated SEQ ID:5929, to the nucleotide sequence of VGAM2246 RNA, herein designated VGAM RNA, also designated SEQ ID:4957.

[76963] Another function of VGAM2246 is therefore inhibition of Tissue Inhibitor of Metalloproteinase 3 (Sorsby fundus dystrophy, pseudoinflammatory) (TIMP3, Accession NM_000362). Accordingly, utilities of VGAM2246 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIMP3. FLJ10620 (Accession NM_018157) is another VGAM2246 host target gene. FLJ10620 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10620, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10620 BINDING SITE, designated SEQ ID:19974, to the nucleotide sequence of VGAM2246 RNA, herein designated VGAM RNA, also designated SEQ ID:4957.

[76964] Another function of VGAM2246 is therefore inhibition of FLJ10620 (Accession NM_018157). Accordingly, utilities of VGAM2246 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ10620. FLJ12355 (Accession NM_024988) is another VGAM2246 host target gene. FLJ12355 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12355, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12355 BINDING SITE, designated SEQ ID:24544, to the nucleotide sequence of VGAM2246 RNA, herein designated VGAM RNA, also designated SEQ ID:4957.

[76965] Another function of VGAM2246 is therefore inhibition of FLJ12355 (Accession NM_024988). Accordingly, utilities of VGAM2246 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12355. KIAA0515 (Accession XM_033380) is another VGAM2246 host target gene. KIAA0515 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0515, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0515 BINDING SITE, designated SEQ ID:31917, to the nucleotide sequence of VGAM2246 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4957.

[76966] Another function of VGAM2246 is therefore inhibition of KIAA0515 (Accession XM_033380). Accordingly, utilities of VGAM2246 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0515. KIAA1165 (Accession XM_041162) is another VGAM2246 host target gene. KIAA1165 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1165, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1165 BINDING SITE, designated SEQ ID:33476, to the nucleotide sequence of VGAM2246 RNA, herein designated VGAM RNA, also designated SEQ ID:4957.

[76967] Another function of VGAM2246 is therefore inhibition of KIAA1165 (Accession XM_041162). Accordingly, utilities of VGAM2246 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1165. LOC137964 (Accession XM_059933) is another VGAM2246 host target gene. LOC137964 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC137964, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC137964 BINDING SITE, designated SEQ ID:37109, to the nucleotide sequence of VGAM2246 RNA, herein designated VGAM RNA, also designated SEQ ID:4957.

[76968] Another function of VGAM2246 is therefore inhibition of LOC137964 (Accession XM_059933). Accordingly, utilities of VGAM2246 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137964. LOC145474 (Accession XM_085147) is another VGAM2246 host target gene. LOC145474 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145474, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145474 BINDING SITE, designated SEQ ID:37868, to the nucleotide sequence of VGAM2246 RNA, herein designated VGAM RNA, also designated SEQ ID:4957.

[76969] Another function of VGAM2246 is therefore inhibition of LOC145474 (Accession XM_085147). Accordingly, utilities of VGAM2246 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC145474. LOC158654 (Accession XM_088632) is another VGAM2246 host target gene. LOC158654 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158654, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158654 BINDING SITE, designated SEQ ID:39873, to the nucleotide sequence of VGAM2246 RNA, herein designated VGAM RNA, also designated SEQ ID:4957.

[76970] Another function of VGAM2246 is therefore inhibition of LOC158654 (Accession XM_088632). Accordingly, utilities of VGAM2246 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158654. LOC253897 (Accession XM_171187) is another VGAM2246 host target gene. LOC253897 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253897, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253897 BINDING SITE, designated SEQ ID:45966, to

the nucleotide sequence of VGAM2246 RNA, herein designated VGAM RNA, also designated SEQ ID:4957.

[76971] Another function of VGAM2246 is therefore inhibition of LOC253897 (Accession XM_171187). Accordingly, utilities of VGAM2246 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253897. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2247 (VGAM2247) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76972] VGAM2247 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2247 was detected is described hereinabove with reference to Figs. 1-8.

[76973] VGAM2247 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible Gastroenteritis Virus. VGAM2247 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76974] VGAM2247 gene encodes a VGAM2247 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2247 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2247 precursor RNA is designated SEQ ID:2233, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2233 is located at position 6648 relative to the genome of Transmissible Gastroenteritis Virus.

[76975] VGAM2247 precursor RNA folds onto itself, forming VGAM2247 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76976] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2247 folded precursor RNA into VGAM2247 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2247 RNA is designated SEQ ID:4958, and is provided hereinbelow with reference to the sequence listing part.

[76977] VGAM2247 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2247 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2247 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76978] VGAM2247 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2247 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2247 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2247 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2247 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76979] The complementary binding of VGAM2247 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2247 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2247 host target RNA into VGAM2247 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76980] It is appreciated that VGAM2247 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2247 host target genes. The mRNA of each one of this plurality of VGAM2247 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2247 RNA, herein designated VGAM RNA, and which when bound by VGAM2247 RNA causes inhibition of translation of respective one or more VGAM2247 host target proteins.

[76981] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2247 gene, herein designated VGAM GENE, on one or more VGAM2247 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[76982] It is yet further appreciated that a function of VGAM2247 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2247 include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGAM2247 correlate with, and may be deduced from, the identity of the host target genes which VGAM2247 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[76983] Nucleotide sequences of the VGAM2247 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2247 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2247 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2247 are further described hereinbelow with reference to Table 1.

[76984] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2247 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2247 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[76985] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2247 gene, herein designated VGAM is inhibition of expression of VGAM2247 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2247 correlate with, and may be deduced from, the identity of the target genes which VGAM2247 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[76986] Synaptojanin 2 (SYNJ2, Accession XM_029746) is a VGAM2247 host target gene. SYNJ2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYNJ2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYNJ2 BINDING SITE, designated SEQ ID:30943, to the nucleotide sequence of VGAM2247 RNA, herein designated VGAM RNA, also designated SEQ ID:4958.

[76987] A function of VGAM2247 is therefore inhibition of Synaptojanin 2 (SYNJ2, Accession XM_029746). Accordingly,

utilities of VGAM2247 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYNJ2. LOC125704 (Accession XM_058931) is another VGAM2247 host target gene. LOC125704 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC125704, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC125704 BINDING SITE, designated SEQ ID:36797, to the nucleotide sequence of VGAM2247 RNA, herein designated VGAM RNA, also designated SEQ ID:4958.

[76988] Another function of VGAM2247 is therefore inhibition of LOC125704 (Accession XM_058931). Accordingly, utilities of VGAM2247 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC125704. LOC132321 (Accession XM_059585) is another VGAM2247 host target gene. LOC132321 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC132321, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC132321 BINDING SITE, designated SEQ ID:37025, to the nucleotide sequence of VGAM2247 RNA, herein designated VGAM RNA, also designated SEQ ID:4958.

[76989] Another function of VGAM2247 is therefore inhibition of LOC132321 (Accession XM_059585). Accordingly, utilities of VGAM2247 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132321. LOC219894 (Accession XM_167782) is another VGAM2247 host target gene. LOC219894 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219894, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219894 BINDING SITE, designated SEQ ID:44793, to the nucleotide sequence of VGAM2247 RNA, herein designated VGAM RNA, also designated SEQ ID:4958.

[76990] Another function of VGAM2247 is therefore inhibition of LOC219894 (Accession XM_167782). Accordingly, utilities of VGAM2247 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219894. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2248 (VGAM2248) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[76991] VGAM2248 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2248 was detected is described hereinabove with reference to Figs. 1-8.

[76992] VGAM2248 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible Gastroenteritis Virus. VGAM2248 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[76993] VGAM2248 gene encodes a VGAM2248 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2248 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2248 precursor RNA is designated SEQ ID:2234, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2234 is located at position 10637 relative to the

genome of Transmissible Gastroenteritis Virus.

[76994] VGAM2248 precursor RNA folds onto itself, forming VGAM2248 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[76995] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2248 folded precursor RNA into VGAM2248 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2248 RNA is designated SEQ ID:4959, and is provided hereinbelow with reference to the sequence listing part.

[76996] VGAM2248 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2248 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2248 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[76997] VGAM2248 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2248 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2248 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2248 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2248 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[76998] The complementary binding of VGAM2248 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2248 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2248 host target RNA into VGAM2248 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[76999] It is appreciated that VGAM2248 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2248 host target genes. The mRNA of each one of this plurality of VGAM2248 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2248 RNA, herein designated VGAM RNA, and which when bound by VGAM2248 RNA causes inhibition of translation of respective one or more VGAM2248 host target proteins.

[77000] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2248 gene, herein designated VGAM GENE, on one or more VGAM2248 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77001] It is yet further appreciated that a function of VGAM2248 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2248 include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of

VGAM2248 correlate with, and may be deduced from, the identity of the host target genes which VGAM2248 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77002] Nucleotide sequences of the VGAM2248 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2248 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2248 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2248 are further described hereinbelow with reference to Table 1.

[77003] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2248 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2248 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77004] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2248 gene, herein designated VGAM is inhibition of expression of VGAM2248 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2248 correlate with, and may be deduced

from, the identity of the target genes which VGAM2248 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77005] KIAA0731 (Accession XM_039975) is a VGAM2248 host target gene. KIAA0731 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0731, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0731 BINDING SITE, designated SEQ ID:33238, to the nucleotide sequence of VGAM2248 RNA, herein designated VGAM RNA, also designated SEQ ID:4959.

[77006] A function of VGAM2248 is therefore inhibition of KIAA0731 (Accession XM_039975). Accordingly, utilities of VGAM2248 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0731. LOC256112 (Accession XM_172829) is another VGAM2248 host target gene. LOC256112 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256112, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC256112 BINDING SITE, designated SEQ ID:46104, to the nucleotide sequence of VGAM2248 RNA, herein designated VGAM RNA, also designated SEQ ID:4959.

[77007] Another function of VGAM2248 is therefore inhibition of LOC256112 (Accession XM_172829). Accordingly, utilities of VGAM2248 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256112. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2249 (VGAM2249) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77008] VGAM2249 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2249 was detected is described hereinabove with reference to Figs. 1-8.

[77009] VGAM2249 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible Gastroenteritis Virus. VGAM2249 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene con-

tained in the human genome.

[77010] VGAM2249 gene encodes a VGAM2249 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2249 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2249 precursor RNA is designated SEQ ID:2235, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2235 is located at position 7046 relative to the genome of Transmissible Gastroenteritis Virus.

[77011] VGAM2249 precursor RNA folds onto itself, forming VGAM2249 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77012] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2249 folded precursor RNA into VGAM2249 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2249 RNA is designated SEQ ID:4960, and is provided hereinbelow with reference to the sequence listing part.

[77013] VGAM2249 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2249 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2249 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77014] VGAM2249 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2249 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2249 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2249 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2249 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77015] The complementary binding of VGAM2249 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2249 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2249 host target RNA into VGAM2249 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77016] It is appreciated that VGAM2249 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2249 host target genes. The mRNA of each one of this plurality of VGAM2249 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2249 RNA, herein designated VGAM RNA, and which when bound by VGAM2249 RNA causes inhibition of translation of respective one or more VGAM2249 host target proteins.

[77017] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2249 gene, herein designated VGAM GENE, on one or more VGAM2249 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77018] It is yet further appreciated that a function of VGAM2249 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGAM2249 correlate with, and may be deduced from, the identity of the host target genes which VGAM2249 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77019] Nucleotide sequences of the VGAM2249 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2249 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2249 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2249 are further described hereinbelow with reference to Table 1.

[77020] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2249 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2249 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77021] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2249 gene, herein designated VGAM is inhibition of expression of VGAM2249 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2249 correlate with, and may be deduced from, the identity of the target genes which VGAM2249 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77022] ATPase, Cu++ Transporting, Alpha Polypeptide (Menkes syndrome) (ATP7A, Accession NM_000052) is a VGAM2249 host target gene. ATP7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:5499, to the nucleotide sequence of VGAM2249 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4960.

[77023] A function of VGAM2249 is therefore inhibition of ATPase, Cu++ Transporting, Alpha Polypeptide (Menkes syndrome) (ATP7A, Accession NM_000052). Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7A. EPB72 (Accession NM_004099) is another VGAM2249 host target gene. EPB72 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPB72, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPB72 BINDING SITE, designated SEQ ID:10306, to the nucleotide sequence of VGAM2249 RNA, herein designated VGAM RNA, also designated SEQ ID:4960.

[77024] Another function of VGAM2249 is therefore inhibition of EPB72 (Accession NM_004099), a gene which may regulate cation conductance. Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPB72. The function of EPB72 and its association with various diseases and clinical conditions, has been established by previous

studies, as described hereinabove with reference to VGAM1560.Four and A Half LIM Domains 1 (FHL1, Accession NM_001449) is another VGAM2249 host target gene. FHL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FHL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FHL1 BINDING SITE, designated SEQ ID:7180, to the nucleotide sequence of VGAM2249 RNA, herein designated VGAM RNA, also designated SEQ ID:4960.

[77025] Another function of VGAM2249 is therefore inhibition of Four and A Half LIM Domains 1 (FHL1, Accession NM_001449), a gene which may have an involvement in muscle development or hypertrophy. Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHL1. The function of FHL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1816.V-kit Hardy-Zuckerman 4 Feline Sarcoma Viral Oncogene Homolog (KIT, Accession NM_000222) is another VGAM2249 host target gene. KIT

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIT BINDING SITE, designated SEQ ID:5733, to the nucleotide sequence of VGAM2249 RNA, herein designated VGAM RNA, also designated SEQ ID:4960.

[77026] Another function of VGAM2249 is therefore inhibition of V-kit Hardy-Zuckerman 4 Feline Sarcoma Viral Oncogene Homolog (KIT, Accession NM_000222), a gene which is the receptor for stem cell factor (mast cell growth factor) and has a tyrosine-protein kinase activity. Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIT. The function of KIT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM173.Crn, Crooked Neck-like 1 (Drosophila) (CRNKL1, Accession NM_016652) is another VGAM2249 host target gene. CRNKL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRNKL1, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRNKL1 BINDING SITE, designated SEQ ID:18773, to the nucleotide sequence of VGAM2249 RNA, herein designated VGAM RNA, also designated SEQ ID:4960.

[77027] Another function of VGAM2249 is therefore inhibition of Crn, Crooked Neck-like 1 (Drosophila) (CRNKL1, Accession NM_016652). Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRNKL1. DKFZp434E2220 (Accession NM_017612) is another VGAM2249 host target gene. DKFZp434E2220 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434E2220, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434E2220 BINDING SITE, designated SEQ ID:19114, to the nucleotide sequence of VGAM2249 RNA, herein designated VGAM RNA, also designated SEQ ID:4960.

[77028] Another function of VGAM2249 is therefore inhibition of

DKFZp434E2220 (Accession NM_017612). Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E2220. FLJ11259 (Accession NM_018370) is another VGAM2249 host target gene. FLJ11259 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11259 BINDING SITE, designated SEQ ID:20382, to the nucleotide sequence of VGAM2249 RNA, herein designated VGAM RNA, also designated SEQ ID:4960.

[77029] Another function of VGAM2249 is therefore inhibition of FLJ11259 (Accession NM_018370). Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11259. FLJ14775 (Accession NM_032837) is another VGAM2249 host target gene. FLJ14775 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14775, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ14775 BINDING SITE, designated SEQ ID:26619, to the nucleotide sequence of VGAM2249 RNA, herein designated VGAM RNA, also designated SEQ ID:4960.

[77030] Another function of VGAM2249 is therefore inhibition of FLJ14775 (Accession NM_032837). Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14775. LOC131873 (Accession XM_067585) is another VGAM2249 host target gene. LOC131873 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC131873, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC131873 BINDING SITE, designated SEQ ID:37367, to the nucleotide sequence of VGAM2249 RNA, herein designated VGAM RNA, also designated SEQ ID:4960.

[77031] Another function of VGAM2249 is therefore inhibition of LOC131873 (Accession XM_067585). Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC131873. LOC255798 (Accession XM_173087) is an-

other VGAM2249 host target gene. LOC255798 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255798, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255798 BINDING SITE, designated SEQ ID:46352, to the nucleotide sequence of VGAM2249 RNA, herein designated VGAM RNA, also designated SEQ ID:4960.

[77032] Another function of VGAM2249 is therefore inhibition of LOC255798 (Accession XM_173087). Accordingly, utilities of VGAM2249 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255798. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2250 (VGAM2250) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77033] VGAM2250 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2250 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[77034] VGAM2250 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible Gastroenteritis Virus. VGAM2250 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77035] VGAM2250 gene encodes a VGAM2250 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2250 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2250 precursor RNA is designated SEQ ID:2236, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2236 is located at position 14152 relative to the genome of Transmissible Gastroenteritis Virus.

[77036] VGAM2250 precursor RNA folds onto itself, forming VGAM2250 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77037] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2250 folded precursor RNA into VGAM2250 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2250 RNA is designated SEQ ID:4961, and is provided hereinbelow with reference to the sequence listing part.

[77038] VGAM2250 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2250 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2250 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77039] VGAM2250 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2250 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2250 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2250 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2250 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77040] The complementary binding of VGAM2250 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2250 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2250 host target RNA into VGAM2250 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77041] It is appreciated that VGAM2250 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2250 host target genes. The mRNA of each one of this plurality of VGAM2250 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2250 RNA, herein designated VGAM RNA, and which when bound by VGAM2250 RNA causes inhibition of translation of respective one or more VGAM2250 host target proteins.

[77042] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2250 gene, herein designated VGAM GENE, on one or more VGAM2250 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77043] It is yet further appreciated that a function of VGAM2250 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2250 include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGAM2250 correlate with, and may be deduced from, the identity of the host target genes which VGAM2250 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77044] Nucleotide sequences of the VGAM2250 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2250 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2250 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2250 are further described hereinbelow with reference to Table 1.

[77045] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2250 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2250 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77046] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2250 gene, herein designated VGAM is inhibition of expression of VGAM2250 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2250 correlate with, and may be deduced from, the identity of the target genes which VGAM2250 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77047] Optic Atrophy 1 (autosomal dominant) (OPA1, Accession NM_130833) is a VGAM2250 host target gene. OPA1 BINDING SITE1 through OPA1 BINDING SITE5 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by OPA1, corresponding to HOST TARGET

binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OPA1 BINDING SITE1 through OPA1 BINDING SITE5, designated SEQ ID:28319, SEQ ID:28327, SEQ ID:28335, SEQ ID:28343 and SEQ ID:28351 respectively, to the nucleotide sequence of VGAM2250 RNA, herein designated VGAM RNA, also designated SEQ ID:4961.

[77048] A function of VGAM2250 is therefore inhibition of Optic Atrophy 1 (autosomal dominant) (OPA1, Accession NM_130833). Accordingly, utilities of VGAM2250 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OPA1. KIAA1096 (Accession XM_043678) is another VGAM2250 host target gene. KIAA1096 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1096, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1096 BINDING SITE, designated SEQ ID:33996, to the nucleotide sequence of VGAM2250 RNA, herein designated VGAM RNA, also designated SEQ ID:4961.

[77049] Another function of VGAM2250 is therefore inhibition of KIAA1096 (Accession XM_043678). Accordingly, utilities of VGAM2250 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1096. MGC16142 (Accession NM_032763) is another VGAM2250 host target gene. MGC16142 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC16142, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16142 BINDING SITE, designated SEQ ID:26506, to the nucleotide sequence of VGAM2250 RNA, herein designated VGAM RNA, also designated SEQ ID:4961.

[77050] Another function of VGAM2250 is therefore inhibition of MGC16142 (Accession NM_032763). Accordingly, utilities of VGAM2250 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16142. Protocadherin 19 (PCDH19, Accession XM_033173) is another VGAM2250 host target gene. PCDH19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDH19, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH19 BINDING SITE, designated SEQ ID:31858, to the nucleotide sequence of VGAM2250 RNA, herein designated VGAM RNA, also designated SEQ ID:4961.

[77051] Another function of VGAM2250 is therefore inhibition of Protocadherin 19 (PCDH19, Accession XM_033173). Accordingly, utilities of VGAM2250 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH19. RODH-4 (Accession NM_003708) is another VGAM2250 host target gene. RODH-4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RODH-4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RODH-4 BINDING SITE, designated SEQ ID:9807, to the nucleotide sequence of VGAM2250 RNA, herein designated VGAM RNA, also designated SEQ ID:4961.

[77052] Another function of VGAM2250 is therefore inhibition of RODH-4 (Accession NM_003708). Accordingly, utilities of VGAM2250 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with RODH-4. LOC145123 (Accession XM_041473) is another VGAM2250 host target gene. LOC145123 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145123, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145123 BINDING SITE, designated SEQ ID:33532, to the nucleotide sequence of VGAM2250 RNA, herein designated VGAM RNA, also designated SEQ ID:4961.

[77053] Another function of VGAM2250 is therefore inhibition of LOC145123 (Accession XM_041473). Accordingly, utilities of VGAM2250 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145123. LOC147791 (Accession XM_097293) is another VGAM2250 host target gene. LOC147791 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147791, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147791 BINDING SITE, designated SEQ ID:40857, to

the nucleotide sequence of VGAM2250 RNA, herein designated VGAM RNA, also designated SEQ ID:4961.

[77054] Another function of VGAM2250 is therefore inhibition of LOC147791 (Accession XM_097293). Accordingly, utilities of VGAM2250 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147791. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2251 (VGAM2251) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77055] VGAM2251 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2251 was detected is described hereinabove with reference to Figs. 1-8.

[77056] VGAM2251 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible Gastroenteritis Virus. VGAM2251 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77057] VGAM2251 gene encodes a VGAM2251 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2251 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2251 precursor RNA is designated SEQ ID:2237, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2237 is located at position 4728 relative to the genome of Transmissible Gastroenteritis Virus.

[77058] VGAM2251 precursor RNA folds onto itself, forming VGAM2251 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77059] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2251 folded precursor RNA into VGAM2251 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2251 RNA is designated SEQ ID:4962, and is provided hereinbelow with reference to the sequence listing part.

[77060] VGAM2251 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2251 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2251 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77061] VGAM2251 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2251 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2251 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2251 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2251 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77062] The complementary binding of VGAM2251 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2251 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2251 host target RNA into VGAM2251 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77063] It is appreciated that VGAM2251 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2251 host target genes. The mRNA of each one of this plurality of VGAM2251 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2251 RNA, herein designated VGAM RNA, and which when bound by VGAM2251 RNA causes inhibition of translation of respective one or more VGAM2251 host target proteins.

[77064] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2251 gene, herein designated VGAM GENE, on one or more VGAM2251 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77065] It is yet further appreciated that a function of VGAM2251 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGAM2251 correlate with, and may be deduced from, the identity of the host target genes which VGAM2251 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77066] Nucleotide sequences of the VGAM2251 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2251 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2251 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2251 are further described hereinbelow with reference to Table 1.

[77067] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2251 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2251 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77068] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2251 gene, herein designated VGAM is inhibition of expression of VGAM2251 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2251 correlate with, and may be deduced from, the identity of the target genes which VGAM2251 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77069] Alcohol Dehydrogenase 5 (class III), Chi Polypeptide (ADH5, Accession NM_000671) is a VGAM2251 host target gene. ADH5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADH5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADH5 BINDING SITE, designated SEQ ID:6324, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77070] A function of VGAM2251 is therefore inhibition of Alcohol Dehydrogenase 5 (class III), Chi Polypeptide (ADH5, Ac-

cession NM_000671), a gene which oxidizes ethanol and activated by fatty acids.It oxidizes ethanol very poorly. Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADH5. The function of ADH5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM438.Fibronectin Leucine Rich Transmembrane Protein 2 (FLRT2, Accession NM_013231) is another VGAM2251 host target gene. FLRT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLRT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLRT2 BINDING SITE, designated SEQ ID:14886, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77071] Another function of VGAM2251 is therefore inhibition of Fibronectin Leucine Rich Transmembrane Protein 2 (FLRT2, Accession NM_013231), a gene which may have a function in cell adhesion and/or receptor signaling. Ac-

cordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLRT2. The function of FLRT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM247.FBJ Murine Osteosarcoma Viral Oncogene Homolog B (FOSB, Accession NM_006732) is another VGAM2251 host target gene. FOSB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FOSB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOSB BINDING SITE, designated SEQ ID:13583, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77072] Another function of VGAM2251 is therefore inhibition of FBJ Murine Osteosarcoma Viral Oncogene Homolog B (FOSB, Accession NM_006732), a gene which interacts with jun proteins enhancing their dna binding activity. Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOSB. The function of FOSB and its associ-

ation with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM747.IRTA2 (Accession NM_031281) is another VGAM2251 host target gene. IRTA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IRTA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRTA2 BINDING SITE, designated SEQ ID:25297, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77073] Another function of VGAM2251 is therefore inhibition of IRTA2 (Accession NM_031281), a gene which binds to the fc region of immunoglobulins gamma low affinity receptor. Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRTA2. The function of IRTA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Membrane Metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME, Accession NM_007289) is an-

other VGAM2251 host target gene. MME BINDING SITE1 through MME BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MME, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MME BINDING SITE1 through MME BINDING SITE4, designated SEQ ID:14160, SEQ ID:14155, SEQ ID:14151 and SEQ ID:6603 respectively, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77074] Another function of VGAM2251 is therefore inhibition of Membrane Metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME, Accession NM_007289), a gene which is thermolysin-like specificity. Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MME. The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1332.Polymerase (DNA directed), Theta (POLQ, Accession NM_006596) is another VGAM2251 host target gene. POLQ BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POLQ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POLQ BINDING SITE, designated SEQ ID:13367, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77075] Another function of VGAM2251 is therefore inhibition of Polymerase (DNA directed), Theta (POLQ, Accession NM_006596), a gene which enhances untargeted mutagenesis. Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLQ. The function of POLQ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM922.Roundabout, Axon Guidance Receptor, Homolog 1 (Drosophila) (ROBO1, Accession NM_133631) is another VGAM2251 host target gene. ROBO1 BINDING SITE1 and ROBO1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ROBO1, corresponding to HOST TARGET binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ROBO1 BINDING SITE1 and ROBO1 BINDING SITE2, designated SEQ ID:28585 and SEQ ID:8849 respectively, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77076] Another function of VGAM2251 is therefore inhibition of Roundabout, Axon Guidance Receptor, Homolog 1 (Drosophila) (ROBO1, Accession NM_133631), a gene which is an axon guidance receptor. Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ROBO1. The function of ROBO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM37.Synuclein, Alpha (non A4 component of amyloid precursor) (SNCA, Accession NM_000345) is another VGAM2251 host target gene. SNCA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNCA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates

the complementarity of the nucleotide sequences of SNCA BINDING SITE, designated SEQ ID:5897, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77077] Another function of VGAM2251 is therefore inhibition of Synuclein, Alpha (non A4 component of amyloid precursor) (SNCA, Accession NM_000345). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNCA. Supervillin (SVIL, Accession NM_003174) is another VGAM2251 host target gene. SVIL BINDING SITE1 and SVIL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SVIL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SVIL BINDING SITE1 and SVIL BINDING SITE2, designated SEQ ID:9150 and SEQ ID:22347 respectively, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77078] Another function of VGAM2251 is therefore inhibition of Supervillin (SVIL, Accession NM_003174), a gene which binds actin, links filamentous actin with the plasma mem-

brane; and contains putative nuclear localization signals. Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SVIL. The function of SVIL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1459.Visinin-like 1 (VSNL1, Accession NM_003385) is another VGAM2251 host target gene. VSNL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VSNL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VSNL1 BINDING SITE, designated SEQ ID:9417, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77079] Another function of VGAM2251 is therefore inhibition of Visinin-like 1 (VSNL1, Accession NM_003385). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VSNL1. ARPP-19 (Accession NM_006628) is another VGAM2251 host target gene. ARPP-19 BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARPP-19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARPP-19 BINDING SITE, designated SEQ ID:13424, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77080] Another function of VGAM2251 is therefore inhibition of ARPP-19 (Accession NM_006628). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARPP-19. Chromosome 21 Open Reading Frame 7 (C21orf7, Accession NM_020152) is another VGAM2251 host target gene. C21orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C21orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C21orf7 BINDING SITE, designated SEQ ID:21362, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77081] Another function of VGAM2251 is therefore inhibition of Chromosome 21 Open Reading Frame 7 (C21orf7, Accession NM_020152). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf7. DKFZP586J0619 (Accession XM_088280) is another VGAM2251 host target gene. DKFZP586J0619 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586J0619, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586J0619 BINDING SITE, designated SEQ ID:39582, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77082] Another function of VGAM2251 is therefore inhibition of DKFZP586J0619 (Accession XM_088280). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586J0619. FKSG42 (Accession NM_032032) is another VGAM2251 host target gene. FKSG42 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by FKSG42, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FKSG42 BINDING SITE, designated SEQ ID:25733, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77083] Another function of VGAM2251 is therefore inhibition of FKSG42 (Accession NM_032032). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKSG42. FLJ10352 (Accession NM_032142) is another VGAM2251 host target gene. FLJ10352 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10352, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10352 BINDING SITE, designated SEQ ID:25830, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77084] Another function of VGAM2251 is therefore inhibition of FLJ10352 (Accession NM_032142). Accordingly, utilities of

VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10352. FLJ20275 (Accession NM_017737) is another VGAM2251 host target gene. FLJ20275 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20275, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20275 BINDING SITE, designated SEQ ID:19321, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77085] Another function of VGAM2251 is therefore inhibition of FLJ20275 (Accession NM_017737). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20275. FLJ23074 (Accession NM_025052) is another VGAM2251 host target gene. FLJ23074 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23074, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23074

BINDING SITE, designated SEQ ID:24649, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77086] Another function of VGAM2251 is therefore inhibition of FLJ23074 (Accession NM_025052). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23074. IL22R (Accession NM_021258) is another VGAM2251 host target gene. IL22R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL22R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL22R BINDING SITE, designated SEQ ID:22235, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77087] Another function of VGAM2251 is therefore inhibition of IL22R (Accession NM_021258). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL22R. KIAA0296 (Accession NM_014699) is another VGAM2251 host target gene. KIAA0296 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by KIAA0296, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0296 BINDING SITE, designated SEQ ID:16223, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77088] Another function of VGAM2251 is therefore inhibition of KIAA0296 (Accession NM_014699). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0296. KIAA0376 (Accession XM_037759) is another VGAM2251 host target gene. KIAA0376 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0376, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0376 BINDING SITE, designated SEQ ID:32676, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77089] Another function of VGAM2251 is therefore inhibition of

KIAA0376 (Accession XM_037759). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0376. M96 (Accession NM_007358) is another VGAM2251 host target gene. M96 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by M96, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of M96 BINDING SITE, designated SEQ ID:14287, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77090] Another function of VGAM2251 is therefore inhibition of M96 (Accession NM_007358). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with M96. mPA-PLA1 (Accession NM_139248) is another VGAM2251 host target gene. mPA-PLA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by mPA-PLA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of mPA-PLA1 BINDING SITE, designated SEQ ID:29251, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77091] Another function of VGAM2251 is therefore inhibition of mPA-PLA1 (Accession NM_139248). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with mPA-PLA1. LOC149910 (Accession XM_086699) is another VGAM2251 host target gene. LOC149910 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149910, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149910 BINDING SITE, designated SEQ ID:38829, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77092] Another function of VGAM2251 is therefore inhibition of LOC149910 (Accession XM_086699). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149910. LOC206426 (Accession XM_116505) is an-

other VGAM2251 host target gene. LOC206426 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC206426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC206426 BINDING SITE, designated SEQ ID:43121, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77093] Another function of VGAM2251 is therefore inhibition of LOC206426 (Accession XM_116505). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC206426. LOC220963 (Accession XM_166145) is another VGAM2251 host target gene. LOC220963 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220963, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220963 BINDING SITE, designated SEQ ID:43957, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77094] Another function of VGAM2251 is therefore inhibition of LOC220963 (Accession XM_166145). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220963. LOC91012 (Accession XM_035503) is another VGAM2251 host target gene. LOC91012 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91012, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91012 BINDING SITE, designated SEQ ID:32281, to the nucleotide sequence of VGAM2251 RNA, herein designated VGAM RNA, also designated SEQ ID:4962.

[77095] Another function of VGAM2251 is therefore inhibition of LOC91012 (Accession XM_035503). Accordingly, utilities of VGAM2251 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91012. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2252 (VGAM2252) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[77096] VGAM2252 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2252 was detected is described hereinabove with reference to Figs. 1-8.

[77097] VGAM2252 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible Gastroenteritis Virus. VGAM2252 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77098] VGAM2252 gene encodes a VGAM2252 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2252 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2252 precursor RNA is designated SEQ ID:2238, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2238 is located at position 9049 relative to the genome of Transmissible Gastroenteritis Virus.

[77099] VGAM2252 precursor RNA folds onto itself, forming VGAM2252 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77100] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2252 folded precursor RNA into VGAM2252 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 87%) nucleotide sequence of VGAM2252 RNA is designated SEQ ID:4963, and is provided hereinbelow with reference to the sequence listing part.

[77101] VGAM2252 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2252 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2252 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77102] VGAM2252 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2252 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2252 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2252 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2252 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77103] The complementary binding of VGAM2252 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2252 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2252 host target RNA into VGAM2252 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77104] It is appreciated that VGAM2252 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2252 host target genes. The mRNA of each one of this plurality of VGAM2252 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2252 RNA, herein designated VGAM RNA, and which when bound by VGAM2252 RNA causes inhibition of translation of respective one or more VGAM2252 host target proteins.

[77105] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2252 gene, herein designated VGAM GENE, on one or more VGAM2252 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77106] It is yet further appreciated that a function of VGAM2252 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2252 include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGAM2252 correlate with, and may be deduced from, the identity of the host target genes which VGAM2252 binds and inhibits, and the function of these host target genes,

as elaborated hereinbelow.

[77107] Nucleotide sequences of the VGAM2252 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2252 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2252 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2252 are further described hereinbelow with reference to Table 1.

[77108] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2252 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2252 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77109] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2252 gene, herein designated VGAM is inhibition of expression of VGAM2252 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2252 correlate with, and may be deduced from, the identity of the target genes which VGAM2252 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77110] Carnitine Acetyltransferase (CRAT, Accession NM_000755) is a VGAM2252 host target gene. CRAT BINDING SITE1 and CRAT BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CRAT, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRAT BINDING SITE1 and CRAT BINDING SITE2, designated SEQ ID:6408 and SEQ ID:10153 respectively, to the nucleotide sequence of VGAM2252 RNA, herein designated VGAM RNA, also designated SEQ ID:4963.

[77111] A function of VGAM2252 is therefore inhibition of Carnitine Acetyltransferase (CRAT, Accession NM_000755), a gene which catalyzes the reversible transfer of acyl groups from an acyl-CoA thioester to carnitine. Accordingly, utilities of VGAM2252 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRAT. The function of CRAT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1189.A Disintegrin and Metalloproteinase Domain 9 (meltrin gamma) (ADAM9, Accession NM_003816) is another VGAM2252 host target gene.

ADAM9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADAM9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAM9 BINDING SITE, designated SEQ ID:9906, to the nucleotide sequence of VGAM2252 RNA, herein designated VGAM RNA, also designated SEQ ID:4963.

[77112] Another function of VGAM2252 is therefore inhibition of A Disintegrin and Metalloproteinase Domain 9 (meltrin gamma) (ADAM9, Accession NM_003816). Accordingly, utilities of VGAM2252 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAM9. CDV-1 (Accession NM_031473) is another VGAM2252 host target gene. CDV-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDV-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDV-1 BINDING SITE, designated SEQ ID:25540, to the nucleotide sequence of VGAM2252 RNA, herein designated VGAM RNA,

also designated SEQ ID:4963.

[77113] Another function of VGAM2252 is therefore inhibition of CDV-1 (Accession NM_031473). Accordingly, utilities of VGAM2252 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDV-1. Mitogen-activated Protein Kinase 8 Interacting Protein 2 (MAPK8IP2, Accession NM_139124) is another VGAM2252 host target gene. MAPK8IP2 BINDING SITE1 through MAPK8IP2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MAPK8IP2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPK8IP2 BINDING SITE1 through MAPK8IP2 BINDING SITE3, designated SEQ ID:29156, SEQ ID:14705 and SEQ ID:18553 respectively, to the nucleotide sequence of VGAM2252 RNA, herein designated VGAM RNA, also designated SEQ ID:4963.

[77114] Another function of VGAM2252 is therefore inhibition of Mitogen-activated Protein Kinase 8 Interacting Protein 2 (MAPK8IP2, Accession NM_139124). Accordingly, utilities of VGAM2252 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MAPK8IP2. LOC221641 (Accession XM_168090) is another VGAM2252 host target gene. LOC221641 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221641, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221641 BINDING SITE, designated SEQ ID:45008, to the nucleotide sequence of VGAM2252 RNA, herein designated VGAM RNA, also designated SEQ ID:4963.

[77115] Another function of VGAM2252 is therefore inhibition of LOC221641 (Accession XM_168090). Accordingly, utilities of VGAM2252 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221641. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2253 (VGAM2253) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77116] VGAM2253 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2253 was detected is described hereinabove with reference to Figs. 1-8.

[77117] VGAM2253 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible Gastroenteritis Virus. VGAM2253 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77118] VGAM2253 gene encodes a VGAM2253 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2253 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2253 precursor RNA is designated SEQ ID:2239, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2239 is located at position 2988 relative to the genome of Transmissible Gastroenteritis Virus.

[77119] VGAM2253 precursor RNA folds onto itself, forming VGAM2253 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77120] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2253 folded precursor RNA into VGAM2253 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM2253 RNA is designated SEQ ID:4964, and is provided hereinbelow with reference to the sequence listing part.

[77121] VGAM2253 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2253 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2253 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77122] VGAM2253 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2253 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2253 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2253 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2253 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77123] The complementary binding of VGAM2253 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2253 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2253 host target RNA into VGAM2253 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77124] It is appreciated that VGAM2253 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2253 host target genes. The mRNA of each one of this plurality of VGAM2253 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2253 RNA, herein designated VGAM RNA, and which when bound by VGAM2253 RNA causes inhibition of translation of respective one or more VGAM2253 host target proteins.

[77125] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2253 gene, herein designated VGAM GENE, on one or more VGAM2253 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77126] It is yet further appreciated that a function of VGAM2253 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGAM2253 correlate with, and may be deduced from, the identity of the host target genes which VGAM2253 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77127] Nucleotide sequences of the VGAM2253 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2253 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2253 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2253 are further described hereinbelow with reference to Table 1.

[77128] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2253 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2253 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77129] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2253 gene, herein designated VGAM is inhibition of expression of VGAM2253 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2253 correlate with, and may be deduced from, the identity of the target genes which VGAM2253 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77130] A Kinase (PRKA) Anchor Protein 2 (AKAP2, Accession NM_007203) is a VGAM2253 host target gene. AKAP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKAP2, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP2 BINDING SITE, designated SEQ ID:14064, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77131] A function of VGAM2253 is therefore inhibition of A Kinase (PRKA) Anchor Protein 2 (AKAP2, Accession NM_007203), a gene which binds to regulatory subunit (rii) of protein kinase a. Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP2. The function of AKAP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM18.Dual-specificity tyrosine-(Y)-phosphorylation Regulated Kinase 1A (DYRK1A, Accession NM_001396) is another VGAM2253 host target gene. DYRK1A BINDING SITE1 through DYRK1A BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DYRK1A, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the

nucleotide sequences of DYRK1A BINDING SITE1 through DYRK1A BINDING SITE3, designated SEQ ID:7095, SEQ ID:28167 and SEQ ID:28190 respectively, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77132] Another function of VGAM2253 is therefore inhibition of Dual-specificity tyrosine-(Y)-phosphorylation Regulated Kinase 1A (DYRK1A, Accession NM_001396), a gene which regulates cell proliferation and may be involved in brain development . Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DYRK1A. The function of DYRK1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM42.Integrin, Alpha 1 (ITGA1, Accession XM_032902) is another VGAM2253 host target gene. ITGA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA1 BINDING SITE, designated SEQ ID:31791, to the nu-

cleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77133] Another function of VGAM2253 is therefore inhibition of Integrin, Alpha 1 (ITGA1, Accession XM_032902). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA1. Latrophilin 1 (LPHH1, Accession NM_012302) is another VGAM2253 host target gene. LPHH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LPHH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LPHH1 BINDING SITE, designated SEQ ID:14670, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77134] Another function of VGAM2253 is therefore inhibition of Latrophilin 1 (LPHH1, Accession NM_012302), a gene which probably involved in cell adhesion within tissues and receptor signalling. Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPHH1.

The function of LPHH1 has been established by previous studies. In a study of breast tumor samples, Hoggard et al. (1995) reported a region, 1p31.1, with a high frequency of loss of heterozygosity (LOH). In order to identify candidate sequences, mutation of which might contribute to the development of breast cancer, White et al. (1998) carried out mapping studies of ESTs localized to 1p31.1. They identified and characterized a novel gene, LPHH1 (latrophilin homolog-1), located adjacent to the smallest region of overlapping loss seen in tumors. The 4,209-bp open reading frame of the 7-kb LPHH1 transcript encoded a peptide that showed approximately 65% identity to rat latrophilin, a G-coupled, 7-span transmembrane protein that binds alpha-latrotoxin. Surprisingly, while expression of the rat gene was strictly restricted to neurologic and perhaps some endocrine cells, the human sequence appeared to be expressed very widely in all normal tissues tested. The range of transcripts encoded in a breast tumor cell line, compared to normal breast, suggested that gene product variability was higher in the tumor

[77135] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[77136] Hoggard, N.; Brintell, B.; Howell, A.; Weissenbach, J.; Varley, J. : Allelic imbalance on chromosome 1 in human breast cancer. II. Microsatellite repeat analysis. Genes Chromosomes Cancer 12: 24-31, 1995. ; and

[77137] White, G. R. M.; Varley, J. M.; Heighway, J. : Isolation and characterization of a human homologue of the latrophilin gene from a region of 1p31.1 implicated in breast cancer. Oncogene 17:.

[77138] Further studies establishing the function and utilities of LPHH1 are found in John Hopkins OMIM database record ID 607018, and in sited publications numbered 5377-5378 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Mitogen-activated Protein Kinase Kinase Kinase 7 Interacting Protein 2 (MAP3K7IP2, Accession NM_015093) is another VGAM2253 host target gene. MAP3K7IP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K7IP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K7IP2 BINDING SITE, designated SEQ ID:17487, to the nucleotide sequence of VGAM2253 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4964.

[77139] Another function of VGAM2253 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 7 Interacting Protein 2 (MAP3K7IP2, Accession NM_015093). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K7IP2. AD-020 (Accession XM_002161) is another VGAM2253 host target gene. AD-020 BINDING SITE1 and AD-020 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AD-020, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AD-020 BINDING SITE1 and AD-020 BINDING SITE2, designated SEQ ID:29871 and SEQ ID:21341 respectively, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77140] Another function of VGAM2253 is therefore inhibition of AD-020 (Accession XM_002161). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AD-020. FLJ11101 (Accession NM_018322) is another

VGAM2253 host target gene. FLJ11101 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11101, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11101 BINDING SITE, designated SEQ ID:20314, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77141] Another function of VGAM2253 is therefore inhibition of FLJ11101 (Accession NM_018322). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11101. FLJ21144 (Accession NM_022774) is another VGAM2253 host target gene. FLJ21144 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21144, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21144 BINDING SITE, designated SEQ ID:23038, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77142] Another function of VGAM2253 is therefore inhibition of FLJ21144 (Accession NM_022774). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21144. UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6) (GALNT6, Accession NM_007210) is another VGAM2253 host target gene. GALNT6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GALNT6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALNT6 BINDING SITE, designated SEQ ID:14073, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77143] Another function of VGAM2253 is therefore inhibition of UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 6 (GalNAc-T6) (GALNT6, Accession NM_007210). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

GALNT6. KIAA1240 (Accession XM_039676) is another VGAM2253 host target gene. KIAA1240 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1240, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1240 BINDING SITE, designated SEQ ID:33144, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77144] Another function of VGAM2253 is therefore inhibition of KIAA1240 (Accession XM_039676). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1240. MGC22014 (Accession XM_035307) is another VGAM2253 host target gene. MGC22014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC22014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC22014 BINDING SITE, designated SEQ ID:32224, to the nucleotide sequence of VGAM2253 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4964.

[77145] Another function of VGAM2253 is therefore inhibition of MGC22014 (Accession XM_035307). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC22014. LOC143173 (Accession XM_016685) is another VGAM2253 host target gene. LOC143173 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143173, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143173 BINDING SITE, designated SEQ ID:30272, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77146] Another function of VGAM2253 is therefore inhibition of LOC143173 (Accession XM_016685). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143173. LOC149722 (Accession XM_097709) is another VGAM2253 host target gene. LOC149722 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149722, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149722 BINDING SITE, designated SEQ ID:41043, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77147] Another function of VGAM2253 is therefore inhibition of LOC149722 (Accession XM_097709). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149722. LOC152627 (Accession XM_087495) is another VGAM2253 host target gene. LOC152627 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152627, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152627 BINDING SITE, designated SEQ ID:39295, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77148] Another function of VGAM2253 is therefore inhibition of LOC152627 (Accession XM_087495). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC152627. LOC257482 (Accession XM_168544) is another VGAM2253 host target gene. LOC257482 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257482, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257482 BINDING SITE, designated SEQ ID:45233, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77149] Another function of VGAM2253 is therefore inhibition of LOC257482 (Accession XM_168544). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257482. LOC257485 (Accession XM_037746) is another VGAM2253 host target gene. LOC257485 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257485, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257485 BINDING SITE, designated SEQ ID:32670, to

the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77150] Another function of VGAM2253 is therefore inhibition of LOC257485 (Accession XM_037746). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257485. LOC90670 (Accession XM_033352) is another VGAM2253 host target gene. LOC90670 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90670, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90670 BINDING SITE, designated SEQ ID:31883, to the nucleotide sequence of VGAM2253 RNA, herein designated VGAM RNA, also designated SEQ ID:4964.

[77151] Another function of VGAM2253 is therefore inhibition of LOC90670 (Accession XM_033352). Accordingly, utilities of VGAM2253 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90670. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2254 (VGAM2254) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77152] VGAM2254 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2254 was detected is described hereinabove with reference to Figs. 1-8.

[77153] VGAM2254 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible Gastroenteritis Virus. VGAM2254 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77154] VGAM2254 gene encodes a VGAM2254 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2254 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2254 precursor RNA is designated SEQ ID:2240, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2240 is located at position 9818 relative to the genome of Transmissible Gastroenteritis Virus.

[77155] VGAM2254 precursor RNA folds onto itself, forming VGAM2254 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77156] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2254 folded precursor RNA into VGAM2254 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2254 RNA is designated SEQ ID:4965, and is provided hereinbelow with reference to the sequence listing part.

[77157] VGAM2254 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2254 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2254 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77158] VGAM2254 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2254 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2254 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2254 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2254 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77159] The complementary binding of VGAM2254 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2254 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2254 host target RNA into VGAM2254 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77160] It is appreciated that VGAM2254 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2254 host target genes. The mRNA of each one of this plurality of VGAM2254 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2254 RNA, herein designated VGAM RNA, and which when bound by VGAM2254 RNA causes inhibition of translation of respective one or more VGAM2254 host target proteins.

[77161] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2254 gene, herein designated VGAM GENE, on one or more VGAM2254 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77162] It is yet further appreciated that a function of VGAM2254 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGAM2254 correlate with, and may be deduced from, the

identity of the host target genes which VGAM2254 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77163] Nucleotide sequences of the VGAM2254 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2254 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2254 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2254 are further described hereinbelow with reference to Table 1.

[77164] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2254 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2254 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77165] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2254 gene, herein designated VGAM is inhibition of expression of VGAM2254 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2254 correlate with, and may be deduced from, the identity of the target genes which VGAM2254

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77166] Acid Phosphatase, Testicular (ACPT, Accession NM_080789) is a VGAM2254 host target gene. ACPT BINDING SITE1 and ACPT BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ACPT, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACPT BINDING SITE1 and ACPT BINDING SITE2, designated SEQ ID:28045 and SEQ ID:28048 respectively, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77167] A function of VGAM2254 is therefore inhibition of Acid Phosphatase, Testicular (ACPT, Accession NM_080789). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACPT. Capping Protein (actin filament) Muscle Z-line, Alpha 1 (CAPZA1, Accession XM_052116) is another VGAM2254 host target gene. CAPZA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

CAPZA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAPZA1 BINDING SITE, designated SEQ ID:35951, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77168] Another function of VGAM2254 is therefore inhibition of Capping Protein (actin filament) Muscle Z-line, Alpha 1 (CAPZA1, Accession XM_052116), a gene which is alpha 1 subunit of actin filament capping protein; binds actin, has roles in cell motility and actin assembly. Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPZA1. The function of CAPZA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM547.V-erb-a Erythroblastic Leukemia Viral Oncogene Homolog 4 (avian) (ERBB4, Accession NM_005235) is another VGAM2254 host target gene. ERBB4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERBB4, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERBB4 BINDING SITE, designated SEQ ID:11745, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77169] Another function of VGAM2254 is therefore inhibition of V-erb-a Erythroblastic Leukemia Viral Oncogene Homolog 4 (avian) (ERBB4, Accession NM_005235), a gene which may function in growth/differentiation of normal and transformed cells. Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERBB4. The function of ERBB4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Fibronectin Leucine Rich Transmembrane Protein 2 (FLRT2, Accession NM_013231) is another VGAM2254 host target gene. FLRT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLRT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of FLRT2 BINDING SITE, designated SEQ ID:14885, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77170] Another function of VGAM2254 is therefore inhibition of Fibronectin Leucine Rich Transmembrane Protein 2 (FLRT2, Accession NM_013231), a gene which may have a function in cell adhesion and/or receptor signaling. Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLRT2. The function of FLRT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM247.Nitric Oxide Synthase 1 (neuronal) (NOS1, Accession NM_000620) is another VGAM2254 host target gene. NOS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NOS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NOS1 BINDING SITE, designated SEQ ID:6235, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4965.

[77171] Another function of VGAM2254 is therefore inhibition of Nitric Oxide Synthase 1 (neuronal) (NOS1, Accession NM_000620), a gene which produces nitric oxide (no) which is a messenger molecule with diverse functions throughout the body. Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOS1. The function of NOS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM323.Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 7 (SLC4A7, Accession NM_003615) is another VGAM2254 host target gene. SLC4A7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC4A7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC4A7 BINDING SITE, designated SEQ ID:9670, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77172] Another function of VGAM2254 is therefore inhibition of Solute Carrier Family 4, Sodium Bicarbonate Cotransporter, Member 7 (SLC4A7, Accession NM_003615), a gene which mediates the coupled movement of sodium and bicarbonate ions across the plasma membrane. Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC4A7. The function of SLC4A7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM66.Chromosome 21 Open Reading Frame 108 (C21orf108, Accession XM_114191) is another VGAM2254 host target gene. C21orf108 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C21orf108, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C21orf108 BINDING SITE, designated SEQ ID:42769, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77173] Another function of VGAM2254 is therefore inhibition of

Chromosome 21 Open Reading Frame 108 (C21orf108, Accession XM_114191). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf108. DKFZp434C0328 (Accession NM_017577) is another VGAM2254 host target gene. DKFZp434C0328 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp434C0328, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434C0328 BINDING SITE, designated SEQ ID:19011, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77174] Another function of VGAM2254 is therefore inhibition of DKFZp434C0328 (Accession NM_017577). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434C0328. FLJ10971 (Accession NM_018287) is another VGAM2254 host target gene. FLJ10971 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10971, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10971 BINDING SITE, designated SEQ ID:20280, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77175] Another function of VGAM2254 is therefore inhibition of FLJ10971 (Accession NM_018287). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10971. FLJ13397 (Accession NM_024948) is another VGAM2254 host target gene. FLJ13397 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13397, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13397 BINDING SITE, designated SEQ ID:24500, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77176] Another function of VGAM2254 is therefore inhibition of FLJ13397 (Accession NM_024948). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ13397. FLJ14249 (Accession NM_106552) is another VGAM2254 host target gene. FLJ14249 BINDING SITE1 and FLJ14249 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ14249, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14249 BINDING SITE1 and FLJ14249 BINDING SITE2, designated SEQ ID:28171 and SEQ ID:22801 respectively, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77177] Another function of VGAM2254 is therefore inhibition of FLJ14249 (Accession NM_106552). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14249. KIAA1361 (Accession XM_030845) is another VGAM2254 host target gene. KIAA1361 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1361, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1361 BINDING SITE, designated SEQ ID:31168, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77178] Another function of VGAM2254 is therefore inhibition of KIAA1361 (Accession XM_030845). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1361. Karyopherin Alpha 6 (importin alpha 7) (KPNA6, Accession NM_012316) is another VGAM2254 host target gene. KPNA6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KPNA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KPNA6 BINDING SITE, designated SEQ ID:14689, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77179] Another function of VGAM2254 is therefore inhibition of Karyopherin Alpha 6 (importin alpha 7) (KPNA6, Accession NM_012316). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with KPNA6. Neuromedin U Receptor 2 (NMU2R, Accession NM_020167) is another VGAM2254 host target gene. NMU2R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NMU2R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NMU2R BINDING SITE, designated SEQ ID:21385, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77180] Another function of VGAM2254 is therefore inhibition of Neuromedin U Receptor 2 (NMU2R, Accession NM_020167). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NMU2R. RAB14, Member RAS Oncogene Family (RAB14, Accession NM_016322) is another VGAM2254 host target gene. RAB14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB14 BIND-

ING SITE, designated SEQ ID:18447, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77181] Another function of VGAM2254 is therefore inhibition of RAB14, Member RAS Oncogene Family (RAB14, Accession NM_016322). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB14. T-box 19 (TBX19, Accession NM_005149) is another VGAM2254 host target gene. TBX19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBX19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBX19 BINDING SITE, designated SEQ ID:11624, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77182] Another function of VGAM2254 is therefore inhibition of T-box 19 (TBX19, Accession NM_005149). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBX19. LOC129831 (Accession XM_059376) is an-

other VGAM2254 host target gene. LOC129831 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC129831, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC129831 BINDING SITE, designated SEQ ID:36981, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77183] Another function of VGAM2254 is therefore inhibition of LOC129831 (Accession XM_059376). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129831. LOC146545 (Accession XM_085501) is another VGAM2254 host target gene. LOC146545 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146545, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146545 BINDING SITE, designated SEQ ID:38201, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77184] Another function of VGAM2254 is therefore inhibition of LOC146545 (Accession XM_085501). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146545. LOC149111 (Accession XM_086429) is another VGAM2254 host target gene. LOC149111 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149111, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149111 BINDING SITE, designated SEQ ID:38648, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77185] Another function of VGAM2254 is therefore inhibition of LOC149111 (Accession XM_086429). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149111. LOC152897 (Accession XM_087555) is another VGAM2254 host target gene. LOC152897 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152897, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152897 BINDING SITE, designated SEQ ID:39327, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77186] Another function of VGAM2254 is therefore inhibition of LOC152897 (Accession XM_087555). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152897. LOC199676 (Accession XM_117107) is another VGAM2254 host target gene. LOC199676 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC199676, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199676 BINDING SITE, designated SEQ ID:43225, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77187] Another function of VGAM2254 is therefore inhibition of LOC199676 (Accession XM_117107). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC199676. LOC221814 (Accession XM_168226) is another VGAM2254 host target gene. LOC221814 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221814, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221814 BINDING SITE, designated SEQ ID:45093, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77188] Another function of VGAM2254 is therefore inhibition of LOC221814 (Accession XM_168226). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221814. LOC253868 (Accession XM_170975) is another VGAM2254 host target gene. LOC253868 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253868, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253868 BINDING SITE, designated SEQ ID:45750, to the nucleotide sequence of VGAM2254 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4965.

[77189] Another function of VGAM2254 is therefore inhibition of LOC253868 (Accession XM_170975). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253868. LOC255515 (Accession XM_171185) is another VGAM2254 host target gene. LOC255515 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255515, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255515 BINDING SITE, designated SEQ ID:45961, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77190] Another function of VGAM2254 is therefore inhibition of LOC255515 (Accession XM_171185). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255515. LOC56181 (Accession XM_170954) is another VGAM2254 host target gene. LOC56181 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC56181, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56181 BINDING SITE, designated SEQ ID:45740, to the nucleotide sequence of VGAM2254 RNA, herein designated VGAM RNA, also designated SEQ ID:4965.

[77191] Another function of VGAM2254 is therefore inhibition of LOC56181 (Accession XM_170954). Accordingly, utilities of VGAM2254 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56181. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2255 (VGAM2255) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77192] VGAM2255 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2255 was detected is described hereinabove with reference to Figs. 1-8.

[77193] VGAM2255 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Transmissible Gastroen-

teritis Virus. VGAM2255 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77194] VGAM2255 gene encodes a VGAM2255 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2255 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2255 precursor RNA is designated SEQ ID:2241, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2241 is located at position 11215 relative to the genome of Transmissible Gastroenteritis Virus.

[77195] VGAM2255 precursor RNA folds onto itself, forming VGAM2255 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77196] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2255 folded precursor RNA into VGAM2255 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2255 RNA is designated SEQ ID:4966, and is provided hereinbelow with reference to the sequence listing part.

[77197] VGAM2255 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2255 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2255 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77198] VGAM2255 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2255 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2255 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2255 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2255 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77199] The complementary binding of VGAM2255 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2255 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2255 host target RNA into VGAM2255 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77200] It is appreciated that VGAM2255 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2255 host target genes. The mRNA of each one of this plurality of VGAM2255 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2255 RNA, herein designated VGAM RNA, and which when bound by VGAM2255 RNA causes inhibition of translation of respective one or more VGAM2255 host target proteins.

[77201] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2255 gene, herein designated VGAM GENE, on one or more VGAM2255 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77202] It is yet further appreciated that a function of VGAM2255 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2255 include diagnosis, prevention and treatment of viral infection by Transmissible Gastroenteritis Virus. Specific functions, and accordingly utilities, of VGAM2255 correlate with, and may be deduced from, the identity of the host target genes which VGAM2255 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77203] Nucleotide sequences of the VGAM2255 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2255 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2255 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2255 are further described hereinbelow with reference to Table 1.

[77204] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2255 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2255 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77205] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2255 gene, herein designated VGAM is inhibition of expression of VGAM2255 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2255 correlate with, and may be deduced from, the identity of the target genes which VGAM2255 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77206] Neurotrophic Tyrosine Kinase, Receptor, Type 2 (NTRK2, Accession NM_006180) is a VGAM2255 host target gene. NTRK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NTRK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NTRK2 BINDING SITE, designated SEQ

ID:12849, to the nucleotide sequence of VGAM2255 RNA, herein designated VGAM RNA, also designated SEQ ID:4966.

[77207] A function of VGAM2255 is therefore inhibition of Neurotrophic Tyrosine Kinase, Receptor, Type 2 (NTRK2, Accession NM_006180), a gene which is involved in the development and/or maintenance of the nervous system. Accordingly, utilities of VGAM2255 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTRK2. The function of NTRK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM341.Tumor Necrosis Factor (ligand) Superfamily, Member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF4, Accession NM_003326) is another VGAM2255 host target gene. TNFSF4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFSF4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFSF4 BINDING SITE, designated SEQ ID:9329, to the nucleotide sequence of

VGAM2255 RNA, herein designated VGAM RNA, also designated SEQ ID:4966.

[77208] Another function of VGAM2255 is therefore inhibition of Tumor Necrosis Factor (ligand) Superfamily, Member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF4, Accession NM_003326), a gene which co-stimulates t cell proliferation and cytokine production. Accordingly, utilities of VGAM2255 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFSF4. The function of TNFSF4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM463.FLJ10352 (Accession NM_032142) is another VGAM2255 host target gene. FLJ10352 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10352, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10352 BINDING SITE, designated SEQ ID:25829, to the nucleotide sequence of VGAM2255 RNA, herein designated VGAM RNA, also designated SEQ ID:4966.

[77209] Another function of VGAM2255 is therefore inhibition of FLJ10352 (Accession NM_032142). Accordingly, utilities of VGAM2255 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10352. JIK (Accession NM_016281) is another VGAM2255 host target gene. JIK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by JIK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JIK BINDING SITE, designated SEQ ID:18407, to the nucleotide sequence of VGAM2255 RNA, herein designated VGAM RNA, also designated SEQ ID:4966.

[77210] Another function of VGAM2255 is therefore inhibition of JIK (Accession NM_016281). Accordingly, utilities of VGAM2255 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JIK. LOC115574 (Accession XM_056240) is another VGAM2255 host target gene. LOC115574 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115574, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115574 BINDING SITE, designated SEQ ID:36366, to the nucleotide sequence of VGAM2255 RNA, herein designated VGAM RNA, also designated SEQ ID:4966.

[77211] Another function of VGAM2255 is therefore inhibition of LOC115574 (Accession XM_056240). Accordingly, utilities of VGAM2255 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115574. LOC149711 (Accession XM_097720) is another VGAM2255 host target gene. LOC149711 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149711, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149711 BINDING SITE, designated SEQ ID:41072, to the nucleotide sequence of VGAM2255 RNA, herein designated VGAM RNA, also designated SEQ ID:4966.

[77212] Another function of VGAM2255 is therefore inhibition of LOC149711 (Accession XM_097720). Accordingly, utilities of VGAM2255 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC149711. LOC149837 (Accession XM_097747) is another VGAM2255 host target gene. LOC149837 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149837, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149837 BINDING SITE, designated SEQ ID:41100, to the nucleotide sequence of VGAM2255 RNA, herein designated VGAM RNA, also designated SEQ ID:4966.

[77213] Another function of VGAM2255 is therefore inhibition of LOC149837 (Accession XM_097747). Accordingly, utilities of VGAM2255 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149837. LOC220766 (Accession XM_165471) is another VGAM2255 host target gene. LOC220766 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220766, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220766 BINDING SITE, designated SEQ ID:43650, to the nucleotide sequence of VGAM2255 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4966.

[77214] Another function of VGAM2255 is therefore inhibition of LOC220766 (Accession XM_165471). Accordingly, utilities of VGAM2255 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220766. LOC221272 (Accession XM_168050) is another VGAM2255 host target gene. LOC221272 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221272, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221272 BINDING SITE, designated SEQ ID:44965, to the nucleotide sequence of VGAM2255 RNA, herein designated VGAM RNA, also designated SEQ ID:4966.

[77215] Another function of VGAM2255 is therefore inhibition of LOC221272 (Accession XM_168050). Accordingly, utilities of VGAM2255 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221272. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2256 (VGAM2256) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77216] VGAM2256 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2256 was detected is described hereinabove with reference to Figs. 1-8.

[77217] VGAM2256 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Oat Chlorotic Stunt Virus. VGAM2256 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77218] VGAM2256 gene encodes a VGAM2256 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2256 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2256 precursor RNA is designated SEQ ID:2242, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2242 is located at position 1813 relative to the genome of Oat Chlorotic Stunt Virus.

[77219] VGAM2256 precursor RNA folds onto itself, forming

VGAM2256 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77220] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2256 folded precursor RNA into VGAM2256 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2256 RNA is designated SEQ ID:4967, and is provided hereinbelow with reference to the sequence listing part.

[77221] VGAM2256 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2256 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2256 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77222] VGAM2256 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2256 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2256 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2256 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2256 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77223] The complementary binding of VGAM2256 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2256 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2256 host target RNA into VGAM2256 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77224] It is appreciated that VGAM2256 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2256 host target genes. The mRNA of each one of this plurality of VGAM2256 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2256 RNA, herein designated VGAM RNA, and which when bound by VGAM2256 RNA causes inhibition of translation of respective one or more VGAM2256 host target proteins.

[77225] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2256 gene, herein designated VGAM GENE, on one or more VGAM2256 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77226] It is yet further appreciated that a function of VGAM2256 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2256 include diagnosis, prevention and treatment of viral infection by Oat Chlorotic Stunt Virus. Specific functions, and accordingly utilities, of VGAM2256 correlate with, and may be deduced from, the identity of the host target genes which VGAM2256 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[77227] Nucleotide sequences of the VGAM2256 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2256 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2256 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2256 are further described hereinbelow with reference to Table 1.

[77228] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2256 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2256 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77229] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2256 gene, herein designated VGAM is inhibition of expression of VGAM2256 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2256 correlate with, and may be deduced from, the identity of the target genes which VGAM2256 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[77230] FAT Tumor Suppressor Homolog 2 (Drosophila) (FAT2, Accession NM_001447) is a VGAM2256 host target gene. FAT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FAT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FAT2 BINDING SITE, designated SEQ ID:7172, to the nucleotide sequence of VGAM2256 RNA, herein designated VGAM RNA, also designated SEQ ID:4967.

[77231] A function of VGAM2256 is therefore inhibition of FAT Tumor Suppressor Homolog 2 (Drosophila) (FAT2, Accession NM_001447), a gene which could function as a cell-adhesion protein. Accordingly, utilities of VGAM2256 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FAT2. The function of FAT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM949.KIAA0930 (Accession XM_047214) is another VGAM2256 host target gene. KIAA0930 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA0930, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0930 BINDING SITE, designated SEQ ID:34913, to the nucleotide sequence of VGAM2256 RNA, herein designated VGAM RNA, also designated SEQ ID:4967.

[77232] Another function of VGAM2256 is therefore inhibition of KIAA0930 (Accession XM_047214). Accordingly, utilities of VGAM2256 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0930. Peptidyl Arginine Deiminase, Type I (PADI1, Accession XM_030498) is another VGAM2256 host target gene. PADI1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PADI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PADI1 BINDING SITE, designated SEQ ID:31054, to the nucleotide sequence of VGAM2256 RNA, herein designated VGAM RNA, also designated SEQ ID:4967.

[77233] Another function of VGAM2256 is therefore inhibition of

Peptidyl Arginine Deiminase, Type I (PADI1, Accession XM_030498). Accordingly, utilities of VGAM2256 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PADI1. LOC144600 (Accession XM_096639) is another VGAM2256 host target gene. LOC144600 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144600, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144600 BINDING SITE, designated SEQ ID:40446, to the nucleotide sequence of VGAM2256 RNA, herein designated VGAM RNA, also designated SEQ ID:4967.

[77234] Another function of VGAM2256 is therefore inhibition of LOC144600 (Accession XM_096639). Accordingly, utilities of VGAM2256 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144600. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2257 (VGAM2257) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[77235] VGAM2257 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2257 was detected is described hereinabove with reference to Figs. 1-8.

[77236] VGAM2257 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Oat Chlorotic Stunt Virus. VGAM2257 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77237] VGAM2257 gene encodes a VGAM2257 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2257 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2257 precursor RNA is designated SEQ ID:2243, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2243 is located at position 987 relative to the genome of Oat Chlorotic Stunt Virus.

[77238] VGAM2257 precursor RNA folds onto itself, forming VGAM2257 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77239] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2257 folded precursor RNA into VGAM2257 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2257 RNA is designated SEQ ID:4968, and is provided hereinbelow with reference to the sequence listing part.

[77240] VGAM2257 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2257 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2257 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77241] VGAM2257 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2257 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2257 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2257 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2257 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77242] The complementary binding of VGAM2257 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2257 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2257 host target RNA into VGAM2257 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77243] It is appreciated that VGAM2257 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2257 host target genes. The mRNA of each one of this plurality of VGAM2257 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2257 RNA, herein designated VGAM RNA, and which when bound by VGAM2257 RNA causes inhibition of translation of respective one or more VGAM2257 host target proteins.

[77244] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2257 gene, herein designated VGAM GENE, on one or more VGAM2257 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77245] It is yet further appreciated that a function of VGAM2257 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of viral infection by Oat Chlorotic Stunt Virus. Specific functions, and accordingly utilities, of VGAM2257 correlate with, and may be deduced from, the identity of the host target genes which VGAM2257 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[77246] Nucleotide sequences of the VGAM2257 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2257 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2257 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2257 are further described hereinbelow with reference to Table 1.

[77247] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2257 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2257 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77248] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2257 gene, herein designated VGAM is inhibition of expression of VGAM2257 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2257 correlate with, and may be deduced from, the identity of the target genes which VGAM2257 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77249] Cholinergic Receptor, Muscarinic 1 (CHRM1, Accession XM_170669) is a VGAM2257 host target gene. CHRM1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CHRM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHRM1 BINDING SITE, designated SEQ ID:45441, to the nucleotide sequence of VGAM2257 RNA, herein designated VGAM RNA, also designated SEQ ID:4968.

[77250] A function of VGAM2257 is therefore inhibition of Cholinergic Receptor, Muscarinic 1 (CHRM1, Accession XM_170669), a gene which mediates various cellular responses. Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRM1. The function of CHRM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM302.Ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2, Accession NM_015839) is another VGAM2257 host target gene. FCN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FCN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FCN2 BINDING SITE, designated SEQ ID:17954, to the nucleotide sequence of VGAM2257 RNA, herein designated VGAM RNA, also designated SEQ ID:4968.

[77251] Another function of VGAM2257 is therefore inhibition of Ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2, Accession NM_015839), a gene which is involved in phagocytosis of pathogens. Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCN2. The function of FCN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM493.Mitogen-activated Protein Kinase Kinase Kinase 8 (MAP3K8, Accession NM_005204) is another VGAM2257 host target gene. MAP3K8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAP3K8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of MAP3K8 BINDING SITE, designated SEQ ID:11706, to the nucleotide sequence of VGAM2257 RNA, herein designated VGAM RNA, also designated SEQ ID:4968.

[77252] Another function of VGAM2257 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 8 (MAP3K8, Accession NM_005204), a gene which is able to activate nf-kappa-b 1 by stimulating proteasome- mediated p. Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K8. The function of MAP3K8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM32.Protocadherin 9 (PCDH9, Accession XM_096054) is another VGAM2257 host target gene. PCDH9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PCDH9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH9 BINDING SITE, designated SEQ ID:40296, to the nucleotide sequence of VGAM2257 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4968.

[77253] Another function of VGAM2257 is therefore inhibition of Protocadherin 9 (PCDH9, Accession XM_096054). Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH9. Serine/threonine Kinase 10 (STK10, Accession NM_005990) is another VGAM2257 host target gene. STK10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STK10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STK10 BINDING SITE, designated SEQ ID:12614, to the nucleotide sequence of VGAM2257 RNA, herein designated VGAM RNA, also designated SEQ ID:4968.

[77254] Another function of VGAM2257 is therefore inhibition of Serine/threonine Kinase 10 (STK10, Accession NM_005990), a gene which can act on substrates such as myelin basic protein and histone iia on serine and threonine residues. Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK10. The function of

STK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.TEA Domain Family Member 3 (TEAD3, Accession NM_003214) is another VGAM2257 host target gene. TEAD3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TEAD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEAD3 BINDING SITE, designated SEQ ID:9210, to the nucleotide sequence of VGAM2257 RNA, herein designated VGAM RNA, also designated SEQ ID:4968.

[77255] Another function of VGAM2257 is therefore inhibition of TEA Domain Family Member 3 (TEAD3, Accession NM_003214), a gene which binds to multiple functional elements of the human chorionic somatomammotropin-b gene enhancer. Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEAD3. The function of TEAD3 and its association with various diseases and clinical conditions, has been established by previous studies,

as described hereinabove with reference to VGAM299.Wolf-Hirschhorn Syndrome Candidate 1-like 1 (WHSC1L1, Accession NM_023034) is another VGAM2257 host target gene. WHSC1L1 BINDING SITE1 and WHSC1L1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WHSC1L1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WHSC1L1 BINDING SITE1 and WHSC1L1 BINDING SITE2, designated SEQ ID:23318 and SEQ ID:19411 respectively, to the nucleotide sequence of VGAM2257 RNA, herein designated VGAM RNA, also designated SEQ ID:4968.

[77256] Another function of VGAM2257 is therefore inhibition of Wolf-Hirschhorn Syndrome Candidate 1-like 1 (WHSC1L1, Accession NM_023034), a gene which restores repair of base-base and single- nucleotide insertion-deletion mismatches, and increases the proficiency to process heteroduplexes with insertion-deletion mismatches. Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WHSC1L1. The function of WHSC1L1 and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to VGAM475.LOC203871 (Accession XM_115029) is another VGAM2257 host target gene. LOC203871 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203871 BINDING SITE, designated SEQ ID:43080, to the nucleotide sequence of VGAM2257 RNA, herein designated VGAM RNA, also designated SEQ ID:4968.

[77257] Another function of VGAM2257 is therefore inhibition of LOC203871 (Accession XM_115029). Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203871. LOC221250 (Accession XM_166301) is another VGAM2257 host target gene. LOC221250 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221250, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC221250 BINDING SITE, designated SEQ ID:44120, to the nucleotide sequence of VGAM2257 RNA, herein designated VGAM RNA, also designated SEQ ID:4968.

[77258] Another function of VGAM2257 is therefore inhibition of LOC221250 (Accession XM_166301). Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221250. LOC253805 (Accession XM_172854) is another VGAM2257 host target gene. LOC253805 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253805, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253805 BINDING SITE, designated SEQ ID:46135, to the nucleotide sequence of VGAM2257 RNA, herein designated VGAM RNA, also designated SEQ ID:4968.

[77259] Another function of VGAM2257 is therefore inhibition of LOC253805 (Accession XM_172854). Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253805. LOC91145 (Accession XM_036454) is another VGAM2257 host target gene. LOC91145 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91145, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91145 BINDING SITE, designated SEQ ID:32451, to the nucleotide sequence of VGAM2257 RNA, herein designated VGAM RNA, also designated SEQ ID:4968.

[77260] Another function of VGAM2257 is therefore inhibition of LOC91145 (Accession XM_036454). Accordingly, utilities of VGAM2257 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91145. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2258 (VGAM2258) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77261] VGAM2258 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2258 was detected is described hereinabove with reference to Figs. 1-8.

[77262] VGAM2258 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Oat Chlorotic Stunt Virus. VGAM2258 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77263] VGAM2258 gene encodes a VGAM2258 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2258 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2258 precursor RNA is designated SEQ ID:2244, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2244 is located at position 1727 relative to the genome of Oat Chlorotic Stunt Virus.

[77264] VGAM2258 precursor RNA folds onto itself, forming VGAM2258 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[77265] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2258 folded precursor RNA into VGAM2258 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2258 RNA is designated SEQ ID:4969, and is provided hereinbelow with reference to the sequence listing part.

[77266] VGAM2258 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2258 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2258 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77267] VGAM2258 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2258 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2258 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2258 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2258 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77268] The complementary binding of VGAM2258 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2258 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2258 host target RNA into VGAM2258 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77269] It is appreciated that VGAM2258 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2258 host target genes. The mRNA of each one of this plurality of VGAM2258 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2258 RNA, herein designated VGAM RNA, and which when bound by VGAM2258 RNA causes inhibition of translation of respective one or more VGAM2258 host target proteins.

[77270] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2258 gene, herein designated VGAM GENE, on one or more VGAM2258 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77271] It is yet further appreciated that a function of VGAM2258 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of viral infection by Oat Chlorotic Stunt Virus. Specific functions, and accordingly utilities, of VGAM2258 correlate with, and may be deduced from, the identity of the host target genes which VGAM2258 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77272] Nucleotide sequences of the VGAM2258 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2258 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2258 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2258 are further described hereinbelow with reference to Table 1.

[77273] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2258 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2258 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77274] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2258 gene, herein designated VGAM is inhibition of expression of VGAM2258 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2258 correlate with, and may be deduced from, the identity of the target genes which VGAM2258 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77275] Ets Variant Gene 5 (ets-related molecule) (ETV5, Accession NM_004454) is a VGAM2258 host target gene. ETV5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ETV5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of ETV5 BINDING SITE, designated SEQ ID:10747, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77276] A function of VGAM2258 is therefore inhibition of Ets Variant Gene 5 (ets-related molecule) (ETV5, Accession NM_004454), a gene which DNA binding protein of the Ets oncoprotein family. Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ETV5. The function of ETV5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1171.Hepatocyte Nuclear Factor 4, Gamma (HNF4G, Accession NM_004133) is another VGAM2258 host target gene. HNF4G BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HNF4G, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNF4G BINDING SITE, designated SEQ ID:10346, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ

ID:4969.

[77277] Another function of VGAM2258 is therefore inhibition of Hepatocyte Nuclear Factor 4, Gamma (HNF4G, Accession NM_004133), a gene which may be involved in differential regulation of HNF4-dependent genes. Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNF4G. The function of HNF4G has been established by previous studies. By screening kidney cDNA libraries with a probe based on frog Hnf4-beta, Drewes et al. (1996) isolated cDNAs encoding HNF4G and variants of HNF4A. Sequence analysis predicted that the 774-amino acid HNF4G protein has a relatively long N-terminal domain compared with that of HNF4A, and nearly identical DNA-binding and ligand-binding domains. The C-terminal F domain of HNF4G is 37% identical to that of HNF4A. Northern blot analysis revealed weak expression of 5.5- and 4.1-kb HNF4G transcripts in pancreas, kidney, small intestine, and testis, with no expression detected in liver or other tissues tested. In contrast, expression of HNF4A was detected in liver as well as in all tissues expressing HNF4G. Cells expressing HNF4G had significantly less transactivation potential compared with those ex-

pressing HNF4A. Drewes et al. (1996) concluded that differential transcriptional regulation of HNF4-dependent genes may be due to differential expression of HNF4 proteins. By PCR analysis of genomic DNA from hybrid cell lines, Drewes et al. (1996) mapped the HNF4G gene to chromosome 8. Taraviras et al. (2000) mapped the mouse Hnf4g gene to chromosome 3A.

[77278] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[77279] Drewes, T.; Senkel, S.; Holewa, B.; Ryffel, G. U. : Human hepatocyte nuclear factor 4 isoforms are encoded by distinct and differentially expressed genes. Molec. Cell. Biol. 16: 925-931, 1996. ; and

[77280] Taraviras, S.; Mantamadiotis, T.; Dong-Si, T.; Mincheva, A.; Lichter, P.; Drewes, T.; Ryffel, G. U.; Monaghan, A. P.; Schutz, G. : Primary structure, chromosomal mapping, expression and tra.

[77281] Further studies establishing the function and utilities of HNF4G are found in John Hopkins OMIM database record ID 605966, and in sited publications numbered 6811-6812 listed in the bibliography section hereinbelow, which are also hereby incorporated by refer-

ence.Intersectin 1 (SH3 domain protein) (ITSN1, Accession NM_003024) is another VGAM2258 host target gene. ITSN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITSN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITSN1 BINDING SITE, designated SEQ ID:8955, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77282] Another function of VGAM2258 is therefore inhibition of Intersectin 1 (SH3 domain protein) (ITSN1, Accession NM_003024), a gene which may be involved in endocytosis and synaptic vesicle recycling. Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITSN1. The function of ITSN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1233.Tumor Necrosis Factor (ligand) Superfamily, Member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF4, Accession NM_003326) is another VGAM2258 host target gene. TNFSF4 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFSF4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFSF4 BINDING SITE, designated SEQ ID:9332, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77283] Another function of VGAM2258 is therefore inhibition of Tumor Necrosis Factor (ligand) Superfamily, Member 4 (tax-transcriptionally activated glycoprotein 1, 34kDa) (TNFSF4, Accession NM_003326), a gene which co-stimulates t cell proliferation and cytokine production. Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFSF4. The function of TNFSF4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM463.Chromosome 20 Open Reading Frame 12 (C20orf12, Accession NM_018152) is another VGAM2258 host target gene. C20orf12 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA

encoded by C20orf12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf12 BINDING SITE, designated SEQ ID:19958, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77284] Another function of VGAM2258 is therefore inhibition of Chromosome 20 Open Reading Frame 12 (C20orf12, Accession NM_018152). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf12. Chloride Intracellular Channel 4 (CLIC4, Accession NM_013943) is another VGAM2258 host target gene. CLIC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLIC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLIC4 BINDING SITE, designated SEQ ID:15129, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77285] Another function of VGAM2258 is therefore inhibition of

Chloride Intracellular Channel 4 (CLIC4, Accession NM_013943). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLIC4. DKFZp434A171 (Accession XM_047716) is another VGAM2258 host target gene. DKFZp434A171 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp434A171, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434A171 BINDING SITE, designated SEQ ID:35037, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77286] Another function of VGAM2258 is therefore inhibition of DKFZp434A171 (Accession XM_047716). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434A171. IPLA2(GAMMA) (Accession XM_027224) is another VGAM2258 host target gene. IPLA2(GAMMA) BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IPLA2(GAMMA), corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IPLA2(GAMMA) BINDING SITE, designated SEQ ID:30445, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77287] Another function of VGAM2258 is therefore inhibition of IPLA2(GAMMA) (Accession XM_027224). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IPLA2(GAMMA). KIAA0171 (Accession NM_014666) is another VGAM2258 host target gene. KIAA0171 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0171, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0171 BINDING SITE, designated SEQ ID:16122, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77288] Another function of VGAM2258 is therefore inhibition of KIAA0171 (Accession NM_014666). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0171. KIAA1879 (Accession XM_056635) is another VGAM2258 host target gene. KIAA1879 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1879, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1879 BINDING SITE, designated SEQ ID:36414, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77289] Another function of VGAM2258 is therefore inhibition of KIAA1879 (Accession XM_056635). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1879. Kelch-like 4 (Drosophila) (KLHL4, Accession NM_019117) is another VGAM2258 host target gene. KLHL4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLHL4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLHL4 BINDING SITE, designated SEQ

ID:21195, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77290] Another function of VGAM2258 is therefore inhibition of Kelch-like 4 (Drosophila) (KLHL4, Accession NM_019117). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLHL4. LanC Lantibiotic Synthetase Component C-like 2 (bacterial) (LANCL2, Accession NM_018697) is another VGAM2258 host target gene. LANCL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LANCL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LANCL2 BINDING SITE, designated SEQ ID:20777, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77291] Another function of VGAM2258 is therefore inhibition of LanC Lantibiotic Synthetase Component C-like 2 (bacterial) (LANCL2, Accession NM_018697). Accordingly, utilities of VGAM2258 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with LANCL2. LEC3 (Accession NM_015236) is another VGAM2258 host target gene. LEC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LEC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LEC3 BINDING SITE, designated SEQ ID:17569, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77292] Another function of VGAM2258 is therefore inhibition of LEC3 (Accession NM_015236). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LEC3. MGC21688 (Accession NM_144635) is another VGAM2258 host target gene. MGC21688 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC21688, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC21688 BINDING SITE, designated SEQ ID:29454, to the nucleotide se-

quence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77293] Another function of VGAM2258 is therefore inhibition of MGC21688 (Accession NM_144635). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21688. MGC5566 (Accession NM_024049) is another VGAM2258 host target gene. MGC5566 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC5566, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5566 BINDING SITE, designated SEQ ID:23486, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77294] Another function of VGAM2258 is therefore inhibition of MGC5566 (Accession NM_024049). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5566. Mitochondrial Ribosomal Protein S21 (MRPS21, Accession NM_018997) is another VGAM2258 host target gene. MRPS21 BINDING SITE is HOST TARGET binding site

found in the 5` untranslated region of mRNA encoded by MRPS21, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPS21 BINDING SITE, designated SEQ ID:21070, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77295] Another function of VGAM2258 is therefore inhibition of Mitochondrial Ribosomal Protein S21 (MRPS21, Accession NM_018997). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS21. Nuclear Receptor Coactivator 2 (NCOA2, Accession NM_006540) is another VGAM2258 host target gene. NCOA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NCOA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOA2 BINDING SITE, designated SEQ ID:13295, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77296] Another function of VGAM2258 is therefore inhibition of Nuclear Receptor Coactivator 2 (NCOA2, Accession NM_006540). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA2. RP4-622L5 (Accession NM_019118) is another VGAM2258 host target gene. RP4-622L5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RP4-622L5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RP4-622L5 BINDING SITE, designated SEQ ID:21201, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77297] Another function of VGAM2258 is therefore inhibition of RP4-622L5 (Accession NM_019118). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RP4-622L5. TACTILE (Accession NM_005816) is another VGAM2258 host target gene. TACTILE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TACTILE, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TACTILE BINDING SITE, designated SEQ ID:12412, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77298] Another function of VGAM2258 is therefore inhibition of TACTILE (Accession NM_005816). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TACTILE. LOC112840 (Accession NM_080666) is another VGAM2258 host target gene. LOC112840 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC112840, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112840 BINDING SITE, designated SEQ ID:27957, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77299] Another function of VGAM2258 is therefore inhibition of LOC112840 (Accession NM_080666). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC112840. LOC127702 (Accession XM_060619) is another VGAM2258 host target gene. LOC127702 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC127702, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127702 BINDING SITE, designated SEQ ID:37181, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77300] Another function of VGAM2258 is therefore inhibition of LOC127702 (Accession XM_060619). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127702. LOC146287 (Accession XM_096967) is another VGAM2258 host target gene. LOC146287 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146287, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146287 BINDING SITE, designated SEQ ID:40689, to

the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77301] Another function of VGAM2258 is therefore inhibition of LOC146287 (Accession XM_096967). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146287. LOC150933 (Accession XM_097971) is another VGAM2258 host target gene. LOC150933 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150933, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150933 BINDING SITE, designated SEQ ID:41271, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77302] Another function of VGAM2258 is therefore inhibition of LOC150933 (Accession XM_097971). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150933. LOC255374 (Accession XM_171171) is another VGAM2258 host target gene. LOC255374 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC255374, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255374 BINDING SITE, designated SEQ ID:45955, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77303] Another function of VGAM2258 is therefore inhibition of LOC255374 (Accession XM_171171). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255374. LOC90906 (Accession XM_034809) is another VGAM2258 host target gene. LOC90906 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90906 BINDING SITE, designated SEQ ID:32150, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77304] Another function of VGAM2258 is therefore inhibition of LOC90906 (Accession XM_034809). Accordingly, utilities

of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90906. LOC92080 (Accession XM_042704) is another VGAM2258 host target gene. LOC92080 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92080, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92080 BINDING SITE, designated SEQ ID:33758, to the nucleotide sequence of VGAM2258 RNA, herein designated VGAM RNA, also designated SEQ ID:4969.

[77305] Another function of VGAM2258 is therefore inhibition of LOC92080 (Accession XM_042704). Accordingly, utilities of VGAM2258 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92080. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2259 (VGAM2259) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77306] VGAM2259 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2259 was detected is described hereinabove with reference to Figs. 1-8.

[77307] VGAM2259 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2259 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77308] VGAM2259 gene encodes a VGAM2259 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2259 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2259 precursor RNA is designated SEQ ID:2245, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2245 is located at position 30401 relative to the genome of Alcelaphine Herpesvirus 1.

[77309] VGAM2259 precursor RNA folds onto itself, forming VGAM2259 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77310] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2259 folded precursor RNA into VGAM2259 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 72%) nucleotide sequence of VGAM2259 RNA is designated SEQ ID:4970, and is provided hereinbelow with reference to the sequence listing part.

[77311] VGAM2259 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2259 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2259 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[77312] VGAM2259 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2259 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2259 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2259 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2259 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77313] The complementary binding of VGAM2259 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2259 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2259 host target RNA into VGAM2259 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77314] It is appreciated that VGAM2259 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2259 host target genes. The mRNA of each one of this plurality of VGAM2259 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2259 RNA, herein designated VGAM RNA, and which when bound by VGAM2259 RNA causes inhibition of translation of respective one or more VGAM2259 host target proteins.

[77315] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2259 gene, herein designated VGAM GENE, on one or more VGAM2259 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77316] It is yet further appreciated that a function of VGAM2259 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2259 correlate with, and may be deduced from, the identity of the host target genes which VGAM2259 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77317] Nucleotide sequences of the VGAM2259 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2259 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2259 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2259 are further described hereinbelow with reference to Table 1.

[77318] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2259 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2259 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77319] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2259 gene, herein designated VGAM is inhibition of expression of VGAM2259 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2259 correlate with, and may be deduced from, the identity of the target genes which VGAM2259 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77320] ADP-ribosyltransferase (NAD+; poly (ADP-ribose) Polymerase) (ADPRT, Accession NM_001618) is a VGAM2259

host target gene. ADPRT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADPRT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADPRT BINDING SITE, designated SEQ ID:7326, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77321] A function of VGAM2259 is therefore inhibition of ADP-ribosyltransferase (NAD+; poly (ADP-ribose) Polymerase) (ADPRT, Accession NM_001618), a gene which catalyzes addition of mono-ADP-ribose to arginine residues of proteins, inhibits Pol II transcription. Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADPRT. The function of ADPRT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM506.Diptheria Toxin Resistance Protein Required For Diphthamide Biosynthesis-like 1 (S. cerevisiae) (DPH2L1, Accession NM_001383) is another VGAM2259 host target gene. DPH2L1 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by DPH2L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DPH2L1 BINDING SITE, designated SEQ ID:7055, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77322] Another function of VGAM2259 is therefore inhibition of Diptheria Toxin Resistance Protein Required For Diphthamide Biosynthesis-like 1 (S. cerevisiae) (DPH2L1, Accession NM_001383), a gene which may be involved in regulating global protein synthesis; has similarity to S. cerevisiae Dph2p. Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPH2L1. The function of DPH2L1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM608.Guanylate Binding Protein 1, Interferon-inducible, 67kDa (GBP1, Accession NM_002053) is another VGAM2259 host target gene. GBP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by GBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GBP1 BINDING SITE, designated SEQ ID:7811, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77323] Another function of VGAM2259 is therefore inhibition of Guanylate Binding Protein 1, Interferon-inducible, 67kDa (GBP1, Accession NM_002053), a gene which specifically binds guanylate nucleotides (GMP, GDP and GTP). Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GBP1. The function of GBP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM46.Neurotrophic Tyrosine Kinase, Receptor, Type 2 (NTRK2, Accession NM_006180) is another VGAM2259 host target gene. NTRK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NTRK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of NTRK2 BINDING SITE, designated SEQ ID:12844, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77324] Another function of VGAM2259 is therefore inhibition of Neurotrophic Tyrosine Kinase, Receptor, Type 2 (NTRK2, Accession NM_006180), a gene which is involved in the development and/or maintenance of the nervous system. Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTRK2. The function of NTRK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM341.Phosphodiesterase 4B, CAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B, Accession NM_002600) is another VGAM2259 host target gene. PDE4B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE4B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE4B BINDING SITE, des-

ignated SEQ ID:8464, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77325] Another function of VGAM2259 is therefore inhibition of Phosphodiesterase 4B, CAMP-specific (phosphodiesterase E4 dunce homolog, Drosophila) (PDE4B, Accession NM_002600), a gene which may be involved in mediating central nervous system effects of therapeutic agents ranging from antidepressants to antiasthmatic and anti-inflammatory agents. Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4B. The function of PDE4B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM51.PRO0149 (Accession NM_014117) is another VGAM2259 host target gene. PRO0149 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0149, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0149 BINDING SITE, designated SEQ ID:15370, to the nucleotide

sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77326] Another function of VGAM2259 is therefore inhibition of PRO0149 (Accession NM_014117). Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0149. PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335) is another VGAM2259 host target gene. PRPF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRPF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRPF8 BINDING SITE, designated SEQ ID:30688, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77327] Another function of VGAM2259 is therefore inhibition of PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335). Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRPF8. LOC127428 (Accession XM_059144) is another

VGAM2259 host target gene. LOC127428 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC127428, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127428 BINDING SITE, designated SEQ ID:36899, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77328] Another function of VGAM2259 is therefore inhibition of LOC127428 (Accession XM_059144). Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127428. LOC149175 (Accession XM_086445) is another VGAM2259 host target gene. LOC149175 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149175, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149175 BINDING SITE, designated SEQ ID:38659, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77329] Another function of VGAM2259 is therefore inhibition of LOC149175 (Accession XM_086445). Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149175. LOC158318 (Accession XM_098925) is another VGAM2259 host target gene. LOC158318 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158318 BINDING SITE, designated SEQ ID:41956, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77330] Another function of VGAM2259 is therefore inhibition of LOC158318 (Accession XM_098925). Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158318. LOC158450 (Accession XM_088580) is another VGAM2259 host target gene. LOC158450 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158450, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158450 BINDING SITE, designated SEQ ID:39845, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77331] Another function of VGAM2259 is therefore inhibition of LOC158450 (Accession XM_088580). Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158450. LOC158504 (Accession XM_088591) is another VGAM2259 host target gene. LOC158504 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158504, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158504 BINDING SITE, designated SEQ ID:39856, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77332] Another function of VGAM2259 is therefore inhibition of LOC158504 (Accession XM_088591). Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC158504. LOC51170 (Accession NM_016245) is another VGAM2259 host target gene. LOC51170 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51170, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51170 BINDING SITE, designated SEQ ID:18364, to the nucleotide sequence of VGAM2259 RNA, herein designated VGAM RNA, also designated SEQ ID:4970.

[77333] Another function of VGAM2259 is therefore inhibition of LOC51170 (Accession NM_016245). Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51170. LOC90249 (Accession XM_030300) is another VGAM2259 host target gene. LOC90249 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90249, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90249 BINDING SITE, designated SEQ ID:31015, to the nucleotide sequence of VGAM2259 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4970.

[77334] Another function of VGAM2259 is therefore inhibition of LOC90249 (Accession XM_030300). Accordingly, utilities of VGAM2259 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90249. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2260 (VGAM2260) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77335] VGAM2260 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2260 was detected is described hereinabove with reference to Figs. 1-8.

[77336] VGAM2260 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2260 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77337] VGAM2260 gene encodes a VGAM2260 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2260 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2260 precursor RNA is designated SEQ ID:2246, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2246 is located at position 26713 relative to the genome of Alcelaphine Herpesvirus 1.

[77338] VGAM2260 precursor RNA folds onto itself, forming VGAM2260 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77339] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2260 folded precursor RNA into VGAM2260 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 62%) nucleotide sequence of VGAM2260 RNA is designated SEQ ID:4971, and is provided hereinbelow with reference to the sequence listing part.

[77340] VGAM2260 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2260 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2260 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77341] VGAM2260 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2260 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2260 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2260 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2260 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77342] The complementary binding of VGAM2260 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2260 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2260 host target RNA into VGAM2260 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77343] It is appreciated that VGAM2260 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2260 host target genes. The mRNA of

each one of this plurality of VGAM2260 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2260 RNA, herein designated VGAM RNA, and which when bound by VGAM2260 RNA causes inhibition of translation of respective one or more VGAM2260 host target proteins.

[77344] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2260 gene, herein designated VGAM GENE, on one or more VGAM2260 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[77345] It is yet further appreciated that a function of VGAM2260 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2260 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2260 correlate with, and may be deduced from, the identity of the host target genes which VGAM2260 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77346] Nucleotide sequences of the VGAM2260 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2260 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2260 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2260 are further described hereinbelow with reference to Table 1.

[77347] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2260 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2260 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77348] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2260 gene, herein designated VGAM is inhibition of expression of VGAM2260 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2260 correlate with, and may be deduced from, the identity of the target genes which VGAM2260 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77349] Secretogranin III (SCG3, Accession NM_013243) is a VGAM2260 host target gene. SCG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCG3 BINDING SITE, designated SEQ ID:14902, to the nucleotide sequence of VGAM2260 RNA, herein designated VGAM RNA, also designated SEQ ID:4971.

[77350] A function of VGAM2260 is therefore inhibition of Secretogranin III (SCG3, Accession NM_013243). Accordingly, utilities of VGAM2260 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with SCG3. Chromosome 11 Open Reading Frame 23 (C11orf23, Accession NM_018312) is another VGAM2260 host target gene. C11orf23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf23 BINDING SITE, designated SEQ ID:20302, to the nucleotide sequence of VGAM2260 RNA, herein designated VGAM RNA, also designated SEQ ID:4971.

[77351] Another function of VGAM2260 is therefore inhibition of Chromosome 11 Open Reading Frame 23 (C11orf23, Accession NM_018312). Accordingly, utilities of VGAM2260 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf23. COAS3 (Accession NM_139020) is another VGAM2260 host target gene. COAS3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COAS3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of COAS3 BINDING SITE, designated SEQ ID:29119, to the nucleotide sequence of VGAM2260 RNA, herein designated VGAM RNA, also designated SEQ ID:4971.

[77352] Another function of VGAM2260 is therefore inhibition of COAS3 (Accession NM_139020). Accordingly, utilities of VGAM2260 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COAS3. FLJ12076 (Accession NM_025187) is another VGAM2260 host target gene. FLJ12076 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12076, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12076 BINDING SITE, designated SEQ ID:24822, to the nucleotide sequence of VGAM2260 RNA, herein designated VGAM RNA, also designated SEQ ID:4971.

[77353] Another function of VGAM2260 is therefore inhibition of FLJ12076 (Accession NM_025187). Accordingly, utilities of VGAM2260 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12076. KIAA1550 (Accession XM_039393) is another

VGAM2260 host target gene. KIAA1550 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1550, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1550 BINDING SITE, designated SEQ ID:33069, to the nucleotide sequence of VGAM2260 RNA, herein designated VGAM RNA, also designated SEQ ID:4971.

[77354] Another function of VGAM2260 is therefore inhibition of KIAA1550 (Accession XM_039393). Accordingly, utilities of VGAM2260 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1550. NRBF-2 (Accession NM_030759) is another VGAM2260 host target gene. NRBF-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NRBF-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NRBF-2 BINDING SITE, designated SEQ ID:25043, to the nucleotide sequence of VGAM2260 RNA, herein designated VGAM RNA, also designated SEQ ID:4971.

[77355] Another function of VGAM2260 is therefore inhibition of NRBF-2 (Accession NM_030759). Accordingly, utilities of VGAM2260 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRBF-2. SE57-1 (Accession NM_025214) is another VGAM2260 host target gene. SE57-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SE57-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SE57-1 BINDING SITE, designated SEQ ID:24887, to the nucleotide sequence of VGAM2260 RNA, herein designated VGAM RNA, also designated SEQ ID:4971.

[77356] Another function of VGAM2260 is therefore inhibition of SE57-1 (Accession NM_025214). Accordingly, utilities of VGAM2260 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SE57-1. WWP1 (Accession XM_087357) is another VGAM2260 host target gene. WWP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by WWP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WWP1 BINDING SITE, designated SEQ ID:39190, to the nucleotide sequence of VGAM2260 RNA, herein designated VGAM RNA, also designated SEQ ID:4971.

[77357] Another function of VGAM2260 is therefore inhibition of WWP1 (Accession XM_087357). Accordingly, utilities of VGAM2260 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WWP1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2261 (VGAM2261) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77358] VGAM2261 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2261 was detected is described hereinabove with reference to Figs. 1-8.

[77359] VGAM2261 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2261 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[77360] VGAM2261 gene encodes a VGAM2261 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2261 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2261 precursor RNA is designated SEQ ID:2247, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2247 is located at position 24763 relative to the genome of Alcelaphine Herpesvirus 1.

[77361] VGAM2261 precursor RNA folds onto itself, forming VGAM2261 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77362] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2261 folded precursor RNA into VGAM2261 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2261 RNA is designated SEQ ID:4972, and is provided hereinbelow with reference to the sequence listing part.

[77363] VGAM2261 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2261 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2261 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77364] VGAM2261 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2261 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2261 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2261 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2261 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77365] The complementary binding of VGAM2261 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2261 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2261 host target RNA into VGAM2261 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77366] It is appreciated that VGAM2261 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2261 host target genes. The mRNA of each one of this plurality of VGAM2261 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2261 RNA, herein designated VGAM RNA, and which when bound by VGAM2261 RNA causes inhibition of translation of respective one or more VGAM2261 host target proteins.

[77367] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2261 gene, herein designated VGAM GENE, on one or more VGAM2261 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77368] It is yet further appreciated that a function of VGAM2261 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2261 correlate with, and may be deduced from, the identity of the host target genes which VGAM2261 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77369] Nucleotide sequences of the VGAM2261 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2261 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2261 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2261 are further described hereinbelow with reference to Table 1.

[77370] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2261 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2261 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77371] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2261 gene, herein designated VGAM is inhibition of expression of VGAM2261 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2261 correlate with, and may be deduced from, the identity of the target genes which VGAM2261 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77372] ATPase, Ca++ Transporting, Ubiquitous (ATP2A3, Accession NM_005173) is a VGAM2261 host target gene. ATP2A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP2A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP2A3 BINDING SITE, designated SEQ ID:11672, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ

ID:4972.

[77373] A function of VGAM2261 is therefore inhibition of ATPase, Ca++ Transporting, Ubiquitous (ATP2A3, Accession NM_005173). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP2A3. Gamma-aminobutyric Acid (GABA) A Receptor, Pi (GABRP, Accession NM_014211) is another VGAM2261 host target gene. GABRP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABRP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABRP BINDING SITE, designated SEQ ID:15478, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77374] Another function of VGAM2261 is therefore inhibition of Gamma-aminobutyric Acid (GABA) A Receptor, Pi (GABRP, Accession NM_014211), a gene which mediates neuronal inhibition by binding to the gaba/benzodiazepine receptor and opening an integral chloride channel. Accordingly, utilities of VGAM2261 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with GABRP. The function of GABRP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM795.N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 (NDST1, Accession NM_001543) is another VGAM2261 host target gene. NDST1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NDST1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDST1 BINDING SITE, designated SEQ ID:7270, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77375] Another function of VGAM2261 is therefore inhibition of N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 1 (NDST1, Accession NM_001543), a gene which catalyses the n-sulfation and n-deacetylation of glucosamine of the glycosaminoglycan in heparan sulfate. Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with NDST1. The function of NDST1 has been established by previous studies. Dixon et al. (1995) cloned a human heparan sulfate N-deacetylase/N-sulfotransferase cDNA from a placental library using a cosmid from the Treacher Collins syndrome (OMIM Ref. No. 154500) candidate region, 5q32-q33.1. They detected 2 different mRNAs, which varied in the length of the 3-prime UTR but encoded the same protein. The sequence predicted an 882-amino acid protein which is 98% identical to the previously reported rat gene (Hashimoto et al., 1995). The Treacher Collins Syndrome Collaborative Group (1996) stated that the most 5-prime exon of HSST lies approximately 150 kb distal to 'TREACLE,' the gene responsible for Treacher Collins syndrome. Gladwin et al. (1996) elucidated the genomic organization of the HSST gene with identification of 14 exons which were tested for Treacher-Collins-specific mutations. Mutations within the coding sequence and adjacent splice junctions of HSST were excluded from a causative role in the pathogenesis of Treacher Collins syndrome.

[77376] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[77377] Dixon, J.; Loftus, S. K.; Gladwin, A. J.; Scambler, P. J.; Wasmuth, J. J.; Dixon, M. J. : Cloning of the human heparan sulfate-N-deacetylase/N-sulfotransferase gene from the Treacher Collins syndrome candidate region at 5q32-q33.1. Genomics 26: 239-244, 1995. ; and

[77378] Gladwin, A. J.; Dixon, J.; Loftus, S. K.; Wasmuth, J. J.; Dixon, M. J. : Genomic organization of the human heparan sulfate-N-deacetylase/N-sulfotransferase gene: exclusion from a causat.

[77379] Further studies establishing the function and utilities of NDST1 are found in John Hopkins OMIM database record ID 600853, and in sited publications numbered 10062-1006 and 3538 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Protein Phosphatase 2 (formerly 2A), Regulatory Subunit B (PR 52), Beta Isoform (PPP2R2B, Accession NM_004576) is another VGAM2261 host target gene. PPP2R2B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PPP2R2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP2R2B BINDING SITE, designated SEQ

ID:10923, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77380] Another function of VGAM2261 is therefore inhibition of Protein Phosphatase 2 (formerly 2A), Regulatory Subunit B (PR 52), Beta Isoform (PPP2R2B, Accession NM_004576). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP2R2B. Ryanodine Receptor 3 (RYR3, Accession NM_001036) is another VGAM2261 host target gene. RYR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RYR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RYR3 BINDING SITE, designated SEQ ID:6700, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77381] Another function of VGAM2261 is therefore inhibition of Ryanodine Receptor 3 (RYR3, Accession NM_001036), a gene which is involved in communication between transverse-tubules and sarcoplasmic reticulum. Accordingly,

utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RYR3. The function of RYR3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2014.Solute Carrier Family 9 (sodium/hydrogen exchanger), Isoform 1 (antiporter, Na+/H+, amiloride sensitive) (SLC9A1, Accession XM_046881) is another VGAM2261 host target gene. SLC9A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC9A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC9A1 BINDING SITE, designated SEQ ID:34857, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77382] Another function of VGAM2261 is therefore inhibition of Solute Carrier Family 9 (sodium/hydrogen exchanger), Isoform 1 (antiporter, Na+/H+, amiloride sensitive) (SLC9A1, Accession XM_046881), a gene which is involved in ph regulation to eliminate acids generated by active

metabolism or to counter adverse environmental conditions. Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC9A1. The function of SLC9A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.TYRO3 Protein Tyrosine Kinase (TYRO3, Accession NM_006293) is another VGAM2261 host target gene. TYRO3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TYRO3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TYRO3 BINDING SITE, designated SEQ ID:12984, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77383] Another function of VGAM2261 is therefore inhibition of TYRO3 Protein Tyrosine Kinase (TYRO3, Accession NM_006293), a gene which may be involved in cell adhesion processes, particularly in the central nervous system. Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with TYRO3. The function of TYRO3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM711.ALK7 (Accession XM_065712) is another VGAM2261 host target gene. ALK7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ALK7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALK7 BINDING SITE, designated SEQ ID:37294, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77384] Another function of VGAM2261 is therefore inhibition of ALK7 (Accession XM_065712). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALK7. Chromosome 6 Open Reading Frame 37 (C6orf37, Accession XM_041375) is another VGAM2261 host target gene. C6orf37 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C6orf37, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of C6orf37 BINDING SITE, designated SEQ ID:33512, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77385] Another function of VGAM2261 is therefore inhibition of Chromosome 6 Open Reading Frame 37 (C6orf37, Accession XM_041375). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6orf37. DC-TM4F2 (Accession NM_030927) is another VGAM2261 host target gene. DC-TM4F2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DC-TM4F2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DC-TM4F2 BINDING SITE, designated SEQ ID:25197, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77386] Another function of VGAM2261 is therefore inhibition of DC-TM4F2 (Accession NM_030927). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with DC-TM4F2. Dynactin 4 (p62) (DCTN4, Accession XM_041993) is another VGAM2261 host target gene. DCTN4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCTN4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCTN4 BINDING SITE, designated SEQ ID:33664, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77387] Another function of VGAM2261 is therefore inhibition of Dynactin 4 (p62) (DCTN4, Accession XM_041993). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCTN4. FLJ22127 (Accession NM_022775) is another VGAM2261 host target gene. FLJ22127 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22127, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

FLJ22127 BINDING SITE, designated SEQ ID:23041, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77388] Another function of VGAM2261 is therefore inhibition of FLJ22127 (Accession NM_022775). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22127. FLJ23447 (Accession NM_024825) is another VGAM2261 host target gene. FLJ23447 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23447, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23447 BINDING SITE, designated SEQ ID:24217, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77389] Another function of VGAM2261 is therefore inhibition of FLJ23447 (Accession NM_024825). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23447. KIAA0323 (Accession XM_032634) is another VGAM2261 host target gene. KIAA0323 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0323 BINDING SITE, designated SEQ ID:31689, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77390] Another function of VGAM2261 is therefore inhibition of KIAA0323 (Accession XM_032634). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0323. KIAA1045 (Accession XM_048592) is another VGAM2261 host target gene. KIAA1045 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1045, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1045 BINDING SITE, designated SEQ ID:35198, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77391] Another function of VGAM2261 is therefore inhibition of

KIAA1045 (Accession XM_048592). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1045. KIAA1509 (Accession XM_029353) is another VGAM2261 host target gene. KIAA1509 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1509, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1509 BINDING SITE, designated SEQ ID:30873, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77392] Another function of VGAM2261 is therefore inhibition of KIAA1509 (Accession XM_029353). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1509. Mesoderm Development Candidate 2 (MESDC2, Accession XM_051854) is another VGAM2261 host target gene. MESDC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MESDC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of MESDC2 BINDING SITE, designated SEQ ID:35890, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77393] Another function of VGAM2261 is therefore inhibition of Mesoderm Development Candidate 2 (MESDC2, Accession XM_051854). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MESDC2. MGC11352 (Accession XM_035941) is another VGAM2261 host target gene. MGC11352 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC11352, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11352 BINDING SITE, designated SEQ ID:32355, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77394] Another function of VGAM2261 is therefore inhibition of MGC11352 (Accession XM_035941). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC11352. LOC147645 (Accession XM_085831) is another VGAM2261 host target gene. LOC147645 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147645, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147645 BINDING SITE, designated SEQ ID:38358, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77395] Another function of VGAM2261 is therefore inhibition of LOC147645 (Accession XM_085831). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147645. LOC151742 (Accession NM_139245) is another VGAM2261 host target gene. LOC151742 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151742, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151742 BINDING SITE, designated SEQ ID:29242, to

the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77396] Another function of VGAM2261 is therefore inhibition of LOC151742 (Accession NM_139245). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151742. LOC154790 (Accession XM_088044) is another VGAM2261 host target gene. LOC154790 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154790, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154790 BINDING SITE, designated SEQ ID:39490, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77397] Another function of VGAM2261 is therefore inhibition of LOC154790 (Accession XM_088044). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154790. LOC219914 (Accession XM_167788) is another VGAM2261 host target gene. LOC219914 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC219914, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219914 BINDING SITE, designated SEQ ID:44815, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77398] Another function of VGAM2261 is therefore inhibition of LOC219914 (Accession XM_167788). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219914. LOC222008 (Accession XM_168361) is another VGAM2261 host target gene. LOC222008 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222008, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222008 BINDING SITE, designated SEQ ID:45123, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77399] Another function of VGAM2261 is therefore inhibition of LOC222008 (Accession XM_168361). Accordingly, utilities

of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222008. LOC256979 (Accession XM_171162) is another VGAM2261 host target gene. LOC256979 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256979, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256979 BINDING SITE, designated SEQ ID:45951, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77400] Another function of VGAM2261 is therefore inhibition of LOC256979 (Accession XM_171162). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256979. LOC56181 (Accession XM_170954) is another VGAM2261 host target gene. LOC56181 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC56181, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC56181 BINDING SITE, designated SEQ ID:45738, to the nucleotide sequence of VGAM2261 RNA, herein designated VGAM RNA, also designated SEQ ID:4972.

[77401] Another function of VGAM2261 is therefore inhibition of LOC56181 (Accession XM_170954). Accordingly, utilities of VGAM2261 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56181. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2262 (VGAM2262) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77402] VGAM2262 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2262 was detected is described hereinabove with reference to Figs. 1-8.

[77403] VGAM2262 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2262 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77404] VGAM2262 gene encodes a VGAM2262 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2262 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2262 precursor RNA is designated SEQ ID:2248, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2248 is located at position 17900 relative to the genome of Alcelaphine Herpesvirus 1.

[77405] VGAM2262 precursor RNA folds onto itself, forming VGAM2262 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77406] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2262 folded precursor RNA into VGAM2262 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2262 RNA is designated SEQ ID:4973, and is provided hereinbelow with reference to the sequence listing part.

[77407] VGAM2262 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2262 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2262 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77408] VGAM2262 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2262 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2262 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2262 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2262 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77409] The complementary binding of VGAM2262 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2262 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2262 host target RNA into VGAM2262 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77410] It is appreciated that VGAM2262 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2262 host target genes. The mRNA of each one of this plurality of VGAM2262 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2262 RNA, herein designated VGAM RNA, and which when bound by VGAM2262 RNA causes inhibition of translation of respective one or more VGAM2262 host target proteins.

[77411] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2262 gene, herein designated VGAM GENE, on one or more VGAM2262 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77412] It is yet further appreciated that a function of VGAM2262 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2262 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2262 correlate with, and may be deduced from, the identity of the host target genes which VGAM2262 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77413] Nucleotide sequences of the VGAM2262 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2262 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2262 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2262 are further described hereinbelow with reference to Table 1.

[77414] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2262 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2262 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77415] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2262 gene, herein designated VGAM is inhibition of expression of VGAM2262 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2262 correlate with, and may be deduced from, the identity of the target genes which VGAM2262 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77416] Caspase 9, Apoptosis-related Cysteine Protease (CASP9, Accession NM_001229) is a VGAM2262 host target gene. CASP9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CASP9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASP9 BINDING SITE, designated SEQ ID:6898, to the nucleotide sequence of VGAM2262 RNA, herein designated VGAM RNA, also designated SEQ ID:4973.

[77417] A function of VGAM2262 is therefore inhibition of Cas-

pase 9, Apoptosis-related Cysteine Protease (CASP9, Accession NM_001229). Accordingly, utilities of VGAM2262 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP9. DKFZP586A011 (Accession NM_015416) is another VGAM2262 host target gene. DKFZP586A011 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586A011, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586A011 BINDING SITE, designated SEQ ID:17716, to the nucleotide sequence of VGAM2262 RNA, herein designated VGAM RNA, also designated SEQ ID:4973.

[77418] Another function of VGAM2262 is therefore inhibition of DKFZP586A011 (Accession NM_015416). Accordingly, utilities of VGAM2262 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586A011. HSU24186 (Accession NM_013347) is another VGAM2262 host target gene. HSU24186 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HSU24186, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSU24186 BINDING SITE, designated SEQ ID:14990, to the nucleotide sequence of VGAM2262 RNA, herein designated VGAM RNA, also designated SEQ ID:4973.

[77419] Another function of VGAM2262 is therefore inhibition of HSU24186 (Accession NM_013347). Accordingly, utilities of VGAM2262 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSU24186. KIAA1497 (Accession XM_041431) is another VGAM2262 host target gene. KIAA1497 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1497, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1497 BINDING SITE, designated SEQ ID:33523, to the nucleotide sequence of VGAM2262 RNA, herein designated VGAM RNA, also designated SEQ ID:4973.

[77420] Another function of VGAM2262 is therefore inhibition of KIAA1497 (Accession XM_041431). Accordingly, utilities of VGAM2262 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1497. Mannosidase, Alpha, Class 1C, Member 1 (MAN1C1, Accession NM_020379) is another VGAM2262 host target gene. MAN1C1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAN1C1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAN1C1 BINDING SITE, designated SEQ ID:21643, to the nucleotide sequence of VGAM2262 RNA, herein designated VGAM RNA, also designated SEQ ID:4973.

[77421] Another function of VGAM2262 is therefore inhibition of Mannosidase, Alpha, Class 1C, Member 1 (MAN1C1, Accession NM_020379). Accordingly, utilities of VGAM2262 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAN1C1. PRO0902 (Accession NM_053057) is another VGAM2262 host target gene. PRO0902 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0902, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of PRO0902 BINDING SITE, designated SEQ ID:27605, to the nucleotide sequence of VGAM2262 RNA, herein designated VGAM RNA, also designated SEQ ID:4973.

[77422] Another function of VGAM2262 is therefore inhibition of PRO0902 (Accession NM_053057). Accordingly, utilities of VGAM2262 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0902. LOC222159 (Accession XM_168421) is another VGAM2262 host target gene. LOC222159 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222159, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222159 BINDING SITE, designated SEQ ID:45147, to the nucleotide sequence of VGAM2262 RNA, herein designated VGAM RNA, also designated SEQ ID:4973.

[77423] Another function of VGAM2262 is therefore inhibition of LOC222159 (Accession XM_168421). Accordingly, utilities of VGAM2262 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222159. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2263 (VGAM2263) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77424] VGAM2263 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2263 was detected is described hereinabove with reference to Figs. 1-8.

[77425] VGAM2263 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2263 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77426] VGAM2263 gene encodes a VGAM2263 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2263 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2263 precursor RNA is designated SEQ ID:2249, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2249 is located at position 27186 relative to the genome of Alcelaphine Herpesvirus 1.

[77427] VGAM2263 precursor RNA folds onto itself, forming VGAM2263 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77428] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2263 folded precursor RNA into VGAM2263 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2263 RNA is designated SEQ ID:4974, and is provided hereinbelow with reference to the sequence listing part.

[77429] VGAM2263 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2263 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2263 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77430] VGAM2263 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2263 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2263 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2263 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2263 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77431] The complementary binding of VGAM2263 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2263 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2263 host target RNA into VGAM2263 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77432] It is appreciated that VGAM2263 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2263 host target genes. The mRNA of each one of this plurality of VGAM2263 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2263 RNA, herein designated VGAM RNA, and which when bound by VGAM2263 RNA causes inhibition of translation of respective one or more

VGAM2263 host target proteins.

[77433] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2263 gene, herein designated VGAM GENE, on one or more VGAM2263 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77434] It is yet further appreciated that a function of VGAM2263 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1.

Specific functions, and accordingly utilities, of VGAM2263 correlate with, and may be deduced from, the identity of the host target genes which VGAM2263 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77435] Nucleotide sequences of the VGAM2263 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2263 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2263 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2263 are further described hereinbelow with reference to Table 1.

[77436] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2263 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2263 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77437] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2263 gene, herein designated VGAM is inhibition of expression of VGAM2263 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2263 correlate with, and may be deduced from, the identity of the target genes which VGAM2263 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77438] GTP Cyclohydrolase 1 (dopa-responsive dystonia) (GCH1, Accession NM_000161) is a VGAM2263 host target gene. GCH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GCH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GCH1 BINDING SITE, designated SEQ ID:5665, to the nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, also designated SEQ ID:4974.

[77439] A function of VGAM2263 is therefore inhibition of GTP Cyclohydrolase 1 (dopa-responsive dystonia) (GCH1, Accession NM_000161). Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GCH1. RAN Binding Protein 2-like 1 (RANBP2L1, Accession NM_032260) is another VGAM2263 host target gene. RANBP2L1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RANBP2L1, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RANBP2L1 BINDING SITE, designated SEQ ID:26004, to the nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, also designated SEQ ID:4974.

[77440] Another function of VGAM2263 is therefore inhibition of RAN Binding Protein 2-like 1 (RANBP2L1, Accession NM_032260). Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RANBP2L1. Single-minded Homolog 1 (Drosophila) (SIM1, Accession NM_005068) is another VGAM2263 host target gene. SIM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIM1 BINDING SITE, designated SEQ ID:11510, to the nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, also designated SEQ ID:4974.

[77441] Another function of VGAM2263 is therefore inhibition of Single-minded Homolog 1 (Drosophila) (SIM1, Accession

NM_005068), a gene which may have pleiotropic effects during embryogenesis and in the adult. Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIM1. The function of SIM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM665.Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 1 (KCNS1, Accession NM_002251) is another VGAM2263 host target gene. KCNS1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCNS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNS1 BINDING SITE, designated SEQ ID:8045, to the nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, also designated SEQ ID:4974.

[77442] Another function of VGAM2263 is therefore inhibition of Potassium Voltage-gated Channel, Delayed-rectifier, Subfamily S, Member 1 (KCNS1, Accession NM_002251). Accordingly, utilities of VGAM2263 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with KCNS1. KIAA0446 (Accession XM_044155) is another VGAM2263 host target gene. KIAA0446 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0446, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0446 BINDING SITE, designated SEQ ID:34155, to the nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, also designated SEQ ID:4974.

[77443] Another function of VGAM2263 is therefore inhibition of KIAA0446 (Accession XM_044155). Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0446. KIAA1828 (Accession XM_057526) is another VGAM2263 host target gene. KIAA1828 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1828, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1828 BINDING SITE, designated SEQ ID:36525, to the

nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, also designated SEQ ID:4974.

[77444] Another function of VGAM2263 is therefore inhibition of KIAA1828 (Accession XM_057526). Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1828. Zinc Finger, DHHC Domain Containing 3 (ZDHHC3, Accession NM_016598) is another VGAM2263 host target gene. ZDHHC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZDHHC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZDHHC3 BINDING SITE, designated SEQ ID:18691, to the nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, also designated SEQ ID:4974.

[77445] Another function of VGAM2263 is therefore inhibition of Zinc Finger, DHHC Domain Containing 3 (ZDHHC3, Accession NM_016598). Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZDHHC3. LOC130813 (Accession XM_065904) is another VGAM2263 host target

gene. LOC130813 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130813, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130813 BINDING SITE, designated SEQ ID:37308, to the nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, also designated SEQ ID:4974.

[77446] Another function of VGAM2263 is therefore inhibition of LOC130813 (Accession XM_065904). Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130813. LOC150759 (Accession XM_086995) is another VGAM2263 host target gene. LOC150759 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150759, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150759 BINDING SITE, designated SEQ ID:39014, to the nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, also designated SEQ ID:4974.

[77447] Another function of VGAM2263 is therefore inhibition of LOC150759 (Accession XM_086995). Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150759. LOC151323 (Accession XM_087168) is another VGAM2263 host target gene. LOC151323 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151323 BINDING SITE, designated SEQ ID:39103, to the nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, also designated SEQ ID:4974.

[77448] Another function of VGAM2263 is therefore inhibition of LOC151323 (Accession XM_087168). Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151323. LOC200399 (Accession XM_114226) is another VGAM2263 host target gene. LOC200399 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200399, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200399 BINDING SITE, designated SEQ ID:42811, to the nucleotide sequence of VGAM2263 RNA, herein designated VGAM RNA, also designated SEQ ID:4974.

[77449] Another function of VGAM2263 is therefore inhibition of LOC200399 (Accession XM_114226). Accordingly, utilities of VGAM2263 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200399. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2264 (VGAM2264) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77450] VGAM2264 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2264 was detected is described hereinabove with reference to Figs. 1-8.

[77451] VGAM2264 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2264 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[77452] VGAM2264 gene encodes a VGAM2264 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2264 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2264 precursor RNA is designated SEQ ID:2250, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2250 is located at position 20319 relative to the genome of Alcelaphine Herpesvirus 1.

[77453] VGAM2264 precursor RNA folds onto itself, forming VGAM2264 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77454] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2264 folded precursor RNA into VGAM2264

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2264 RNA is designated SEQ ID:4975, and is provided hereinbelow with reference to the sequence listing part.

[77455] VGAM2264 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2264 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2264 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77456] VGAM2264 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2264 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2264 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2264 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2264 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77457] The complementary binding of VGAM2264 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2264 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2264 host target RNA into VGAM2264 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[77458] It is appreciated that VGAM2264 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2264 host target genes. The mRNA of each one of this plurality of VGAM2264 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2264 RNA, herein designated VGAM RNA, and which when bound by VGAM2264 RNA causes inhibition of translation of respective one or more VGAM2264 host target proteins.

[77459] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2264 gene, herein designated VGAM GENE, on one or more VGAM2264 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77460] It is yet further appreciated that a function of VGAM2264 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2264 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2264 correlate with, and may be deduced from, the identity of the host target genes which VGAM2264 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77461] Nucleotide sequences of the VGAM2264 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2264 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2264 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2264 are further described hereinbelow with reference to Table 1.

[77462] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2264 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2264 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[77463] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2264 gene, herein designated VGAM is inhibition of expression of VGAM2264 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2264 correlate with, and may be deduced from, the identity of the target genes which VGAM2264 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77464] COX11 Homolog, Cytochrome C Oxidase Assembly Protein (yeast) (COX11, Accession NM_004375) is a VGAM2264 host target gene. COX11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COX11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COX11 BINDING SITE, designated SEQ ID:10593, to the nucleotide sequence of VGAM2264 RNA, herein designated VGAM RNA, also designated SEQ ID:4975.

[77465] A function of VGAM2264 is therefore inhibition of COX11 Homolog, Cytochrome C Oxidase Assembly Protein (yeast) (COX11, Accession NM_004375). Accordingly, utilities of

VGAM2264 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COX11. Chemokine (C-X-C motif) Ligand 13 (B-cell chemoattractant) (CXCL13, Accession NM_006419) is another VGAM2264 host target gene. CXCL13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CXCL13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CXCL13 BINDING SITE, designated SEQ ID:13135, to the nucleotide sequence of VGAM2264 RNA, herein designated VGAM RNA, also designated SEQ ID:4975.

[77466] Another function of VGAM2264 is therefore inhibition of Chemokine (C-X-C motif) Ligand 13 (B-cell chemoattractant) (CXCL13, Accession NM_006419), a gene which plays a role in directing the migration of b lymphocytes to follicles . Accordingly, utilities of VGAM2264 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCL13. The function of CXCL13 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM1276.Myotubularin Related Protein 6 (MTMR6, Accession XM_167970) is another VGAM2264 host target gene. MTMR6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTMR6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTMR6 BINDING SITE, designated SEQ ID:44937, to the nucleotide sequence of VGAM2264 RNA, herein designated VGAM RNA, also designated SEQ ID:4975.

[77467] Another function of VGAM2264 is therefore inhibition of Myotubularin Related Protein 6 (MTMR6, Accession XM_167970). Accordingly, utilities of VGAM2264 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTMR6. Hairy/enhancer-of-split Related with YRPW Motif 2 (HEY2, Accession NM_012259) is another VGAM2264 host target gene. HEY2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HEY2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of HEY2 BINDING SITE, designated SEQ ID:14565, to the nucleotide sequence of VGAM2264 RNA, herein designated VGAM RNA, also designated SEQ ID:4975.

[77468] Another function of VGAM2264 is therefore inhibition of Hairy/enhancer-of-split Related with YRPW Motif 2 (HEY2, Accession NM_012259). Accordingly, utilities of VGAM2264 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEY2. KIAA0546 (Accession XM_049055) is another VGAM2264 host target gene. KIAA0546 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0546, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0546 BINDING SITE, designated SEQ ID:35330, to the nucleotide sequence of VGAM2264 RNA, herein designated VGAM RNA, also designated SEQ ID:4975.

[77469] Another function of VGAM2264 is therefore inhibition of KIAA0546 (Accession XM_049055). Accordingly, utilities of VGAM2264 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0546. KIAA1511 (Accession XM_046581) is another

VGAM2264 host target gene. KIAA1511 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1511, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1511 BINDING SITE, designated SEQ ID:34755, to the nucleotide sequence of VGAM2264 RNA, herein designated VGAM RNA, also designated SEQ ID:4975.

[77470] Another function of VGAM2264 is therefore inhibition of KIAA1511 (Accession XM_046581). Accordingly, utilities of VGAM2264 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1511. Phosphodiesterase 1C, Calmodulin-dependent 70kDa (PDE1C, Accession NM_005020) is another VGAM2264 host target gene. PDE1C BINDING SITE1 and PDE1C BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PDE1C, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE1C BINDING SITE1 and PDE1C BINDING SITE2, designated SEQ ID:11458 and SEQ ID:11459 re-

spectively, to the nucleotide sequence of VGAM2264 RNA, herein designated VGAM RNA, also designated SEQ ID:4975.

[77471] Another function of VGAM2264 is therefore inhibition of Phosphodiesterase 1C, Calmodulin-dependent 70kDa (PDE1C, Accession NM_005020). Accordingly, utilities of VGAM2264 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE1C. LOC169436 (Accession XM_095696) is another VGAM2264 host target gene. LOC169436 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC169436, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169436 BINDING SITE, designated SEQ ID:40277, to the nucleotide sequence of VGAM2264 RNA, herein designated VGAM RNA, also designated SEQ ID:4975.

[77472] Another function of VGAM2264 is therefore inhibition of LOC169436 (Accession XM_095696). Accordingly, utilities of VGAM2264 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169436. LOC92399 (Accession NM_138777) is an-

other VGAM2264 host target gene. LOC92399 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92399, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92399 BINDING SITE, designated SEQ ID:29012, to the nucleotide sequence of VGAM2264 RNA, herein designated VGAM RNA, also designated SEQ ID:4975.

[77473] Another function of VGAM2264 is therefore inhibition of LOC92399 (Accession NM_138777). Accordingly, utilities of VGAM2264 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92399. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2265 (VGAM2265) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77474] VGAM2265 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2265 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[77475] VGAM2265 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2265 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77476] VGAM2265 gene encodes a VGAM2265 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2265 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2265 precursor RNA is designated SEQ ID:2251, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2251 is located at position 27645 relative to the genome of Alcelaphine Herpesvirus 1.

[77477] VGAM2265 precursor RNA folds onto itself, forming VGAM2265 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77478] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2265 folded precursor RNA into VGAM2265 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2265 RNA is designated SEQ ID:4976, and is provided hereinbelow with reference to the sequence listing part.

[77479] VGAM2265 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2265 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2265 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77480] VGAM2265 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2265 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2265 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2265 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2265 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77481] The complementary binding of VGAM2265 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2265 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2265 host target RNA into VGAM2265 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77482] It is appreciated that VGAM2265 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2265 host target genes. The mRNA of each one of this plurality of VGAM2265 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2265 RNA, herein designated VGAM RNA, and which when bound by VGAM2265 RNA causes inhibition of translation of respective one or more VGAM2265 host target proteins.

[77483] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2265 gene, herein designated VGAM GENE, on one or more VGAM2265 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77484] It is yet further appreciated that a function of VGAM2265 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2265 correlate with, and may be deduced from, the identity of the host target genes which VGAM2265 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77485] Nucleotide sequences of the VGAM2265 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2265 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2265 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2265 are further described hereinbelow with reference to Table 1.

[77486] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2265 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2265 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77487] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2265 gene, herein designated VGAM is inhibition of expression of VGAM2265 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2265 correlate with, and may be deduced from, the identity of the target genes which VGAM2265 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77488] Rho GTPase Activating Protein 6 (ARHGAP6, Accession NM_001174) is a VGAM2265 host target gene. ARHGAP6 BINDING SITE1 and ARHGAP6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ARHGAP6, corresponding to HOST

TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGAP6 BINDING SITE1 and ARHGAP6 BINDING SITE2, designated SEQ ID:6839 and SEQ ID:15083 respectively, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77489] A function of VGAM2265 is therefore inhibition of Rho GTPase Activating Protein 6 (ARHGAP6, Accession NM_001174), a gene which activates the rho-type GTPases by converting them to an inactive GTP-bound state. Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP6. The function of ARHGAP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Proteasome (prosome, macropain) Subunit, Beta Type, 9 (large multifunctional protease 2) (PSMB9, Accession NM_002800) is another VGAM2265 host target gene. PSMB9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSMB9, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSMB9 BINDING SITE, designated SEQ ID:8674, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77490] Another function of VGAM2265 is therefore inhibition of Proteasome (prosome, macropain) Subunit, Beta Type, 9 (large multifunctional protease 2) (PSMB9, Accession NM_002800), a gene which is one component of a multicatalytic proteinase complex. Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSMB9. The function of PSMB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1915.CGG Triplet Repeat Binding Protein 1 (CGGBP1, Accession NM_003663) is another VGAM2265 host target gene. CGGBP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CGGBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CGGBP1 BINDING SITE,

designated SEQ ID:9736, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77491] Another function of VGAM2265 is therefore inhibition of CGG Triplet Repeat Binding Protein 1 (CGGBP1, Accession NM_003663). Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGGBP1. Dual Specificity Phosphatase 10 (DUSP10, Accession NM_007207) is another VGAM2265 host target gene. DUSP10 BINDING SITE1 and DUSP10 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DUSP10, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DUSP10 BINDING SITE1 and DUSP10 BINDING SITE2, designated SEQ ID:14070 and SEQ ID:29554 respectively, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77492] Another function of VGAM2265 is therefore inhibition of Dual Specificity Phosphatase 10 (DUSP10, Accession NM_007207). Accordingly, utilities of VGAM2265 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP10. KIAA0140 (Accession NM_014661) is another VGAM2265 host target gene. KIAA0140 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0140 BINDING SITE, designated SEQ ID:16106, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77493] Another function of VGAM2265 is therefore inhibition of KIAA0140 (Accession NM_014661). Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0140. KIAA1211 (Accession XM_044178) is another VGAM2265 host target gene. KIAA1211 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1211, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1211 BINDING SITE, designated SEQ ID:34157, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77494] Another function of VGAM2265 is therefore inhibition of KIAA1211 (Accession XM_044178). Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1211. KIAA1676 (Accession XM_167612) is another VGAM2265 host target gene. KIAA1676 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1676, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1676 BINDING SITE, designated SEQ ID:44723, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77495] Another function of VGAM2265 is therefore inhibition of KIAA1676 (Accession XM_167612). Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1676. Microtubule-actin Crosslinking Factor 1 (MACF1, Accession NM_033044) is another VGAM2265

host target gene. MACF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MACF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MACF1 BINDING SITE, designated SEQ ID:26933, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77496] Another function of VGAM2265 is therefore inhibition of Microtubule-actin Crosslinking Factor 1 (MACF1, Accession NM_033044). Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MACF1. Makorin, Ring Finger Protein, 2 (MKRN2, Accession XM_051580) is another VGAM2265 host target gene. MKRN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MKRN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MKRN2 BINDING SITE, designated SEQ ID:35855, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA,

also designated SEQ ID:4976.

[77497] Another function of VGAM2265 is therefore inhibition of Makorin, Ring Finger Protein, 2 (MKRN2, Accession XM_051580). Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKRN2. POPX1 (Accession NM_014906) is another VGAM2265 host target gene. POPX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POPX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POPX1 BINDING SITE, designated SEQ ID:17114, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77498] Another function of VGAM2265 is therefore inhibition of POPX1 (Accession NM_014906). Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POPX1. TRIP-Br2 (Accession NM_014755) is another VGAM2265 host target gene. TRIP-Br2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by TRIP-Br2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIP-Br2 BINDING SITE, designated SEQ ID:16478, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77499] Another function of VGAM2265 is therefore inhibition of TRIP-Br2 (Accession NM_014755). Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIP-Br2. LOC144997 (Accession XM_096702) is another VGAM2265 host target gene. LOC144997 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144997, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144997 BINDING SITE, designated SEQ ID:40481, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77500] Another function of VGAM2265 is therefore inhibition of LOC144997 (Accession XM_096702). Accordingly, utilities

of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144997. LOC159053 (Accession XM_099021) is another VGAM2265 host target gene. LOC159053 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC159053, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159053 BINDING SITE, designated SEQ ID:42059, to the nucleotide sequence of VGAM2265 RNA, herein designated VGAM RNA, also designated SEQ ID:4976.

[77501] Another function of VGAM2265 is therefore inhibition of LOC159053 (Accession XM_099021). Accordingly, utilities of VGAM2265 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159053. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2266 (VGAM2266) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77502] VGAM2266 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2266 was detected is described hereinabove with reference to Figs. 1-8.

[77503] VGAM2266 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2266 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77504] VGAM2266 gene encodes a VGAM2266 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2266 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2266 precursor RNA is designated SEQ ID:2252, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2252 is located at position 27936 relative to the genome of Alcelaphine Herpesvirus 1.

[77505] VGAM2266 precursor RNA folds onto itself, forming VGAM2266 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77506] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2266 folded precursor RNA into VGAM2266 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2266 RNA is designated SEQ ID:4977, and is provided hereinbelow with reference to the sequence listing part.

[77507] VGAM2266 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2266 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2266 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[77508] VGAM2266 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2266 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2266 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2266 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2266 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77509] The complementary binding of VGAM2266 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2266 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2266 host target RNA into VGAM2266 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77510] It is appreciated that VGAM2266 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2266 host target genes. The mRNA of each one of this plurality of VGAM2266 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2266 RNA, herein designated VGAM RNA, and which when bound by VGAM2266 RNA causes inhibition of translation of respective one or more VGAM2266 host target proteins.

[77511] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2266 gene, herein designated VGAM GENE, on one or more VGAM2266 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77512] It is yet further appreciated that a function of VGAM2266 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2266 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2266 correlate with, and may be deduced from, the identity of the host target genes which VGAM2266 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77513] Nucleotide sequences of the VGAM2266 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2266 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2266 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2266 are further described hereinbelow with reference to Table 1.

[77514] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2266 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2266 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77515] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2266 gene, herein designated VGAM is inhibition of expression of VGAM2266 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2266 correlate with, and may be deduced from, the identity of the target genes which VGAM2266 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77516] Inhibitor of Kappa Light Polypeptide Gene Enhancer In B-cells, Kinase Beta (IKBKB, Accession XM_032491) is a

VGAM2266 host target gene. IKBKB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IKBKB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IKBKB BINDING SITE, designated SEQ ID:31662, to the nucleotide sequence of VGAM2266 RNA, herein designated VGAM RNA, also designated SEQ ID:4977.

[77517] A function of VGAM2266 is therefore inhibition of Inhibitor of Kappa Light Polypeptide Gene Enhancer In B-cells, Kinase Beta (IKBKB, Accession XM_032491), a gene which leads to the dissociation of the inhibitor/nf-kappa-b complex. Accordingly, utilities of VGAM2266 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IKBKB. The function of IKBKB has been established by previous studies. Woronicz et al. (1997) observed that IKK-beta activated NF-kappa-B when overexpressed and phosphorylated serine residues 32 and 36 of I-kappa-B-alpha and 19 and 23 of I-kappa-B-beta. The activity of IKK-beta was stimulated by TNF (OMIM Ref. No. 191160) and IL1. IKK-alpha and IKK-beta formed heterodimers that interacted with

NF-kappa-B-inducing kinase (NIK; 604655). Overexpression of catalytically inactive IKK-beta blocked cytokine-induced NF-kappa-B activation. Thus, the active I-kappa-B kinase complex appears to require 3 distinct protein kinases: IKK-alpha, IKK-beta, and NIK. Mercurio et al. (1997) found that mutations in IKK2 had a more pronounced effect upon NFKB activation than did comparable mutations in IKK1. Ozes et al. (1999) showed that AKT1 (OMIM Ref. No. 164730) is involved in the activation of NFKB1 by TNF, following the activation of phosphatidylinositol 3-kinase (PIK3; OMIM Ref. No. 171834). Constitutively active AKT1 induces NFKB1 activity, mediated by phosphorylation of IKK-alpha at threonine 23, which can be blocked by activated NIK. Conversely, NIK activation of NFKB1, mediated by phosphorylation of IKK-alpha at serine 176, is blocked by an AKT1 mutant lacking kinase activity (i.e., kinase dead AKT), indicating that both AKT1 and NIK are necessary for TNF activation of NFKB1 through the phosphorylation of IKK-alpha. IKK-beta is not phosphorylated by either NIK or AKT1 and is apparently differentially regulated. Tang et al. (2001) reported that IKK-beta is specifically proteolyzed by caspase-3 (OMIM Ref. No. 600636)-related caspases at aspartic acid

residues 78, 242, 373, and 546 during TNF-alpha-induced apoptosis. Proteolysis of IKK-beta eliminated its enzymatic activity, interfered with IKK activation, and promoted TNF-alpha killing. Point mutations that abrogated IKK-beta proteolysis generated a caspase-resistant IKK-beta mutant that suppressed TNF-alpha-induced apoptosis. This study demonstrated that TNF-alpha-induced apoptosis requires caspase-mediated proteolysis of IKK-beta. Rossi et al. (2000) demonstrated a novel mechanism of antiinflammatory activity that was based on the direct inhibition and modification of the IKK-beta subunit of IKK. Since IKK-beta is responsible for the activation of NF-kappa-B by proinflammatory stimuli, Rossi et al. (2000) suggested that their findings explained how cyclopentenone prostaglandins function and can be used to improve the utility of COX2 (OMIM Ref. No. 600262) inhibitors. May et al. (2000) determined that an N-terminal alpha-helical region of NEMO (OMIM Ref. No. 300248) associates with a region of IKKA and IKKB that they termed the NBD for 'NEMO-binding domain.' The NBD is a 6-amino acid C-terminal segment within the region denoted alpha-2 of IKKA and IKKB. Wildtype, but not mutant, NDB peptide inhibited cytokine-induced NFKB ac-

tivation and ameliorated experimental acute inflammation Animal model experiments lend further support to the function of IKBKB. Pasparakis et al. (2002) used Cre/loxP-mediated gene targeting to investigate the function of IKK2 specifically in epidermal keratinocytes. IKK2 deficiency inhibits NFKB activation, but does not lead to cell-autonomous hyperproliferation or impaired differentiation of keratinocytes. Mice with epidermis-specific deletion of IKK2 develop a severe inflammatory skin disease, which is caused by a tumor necrosis factor (OMIM Ref. No. 191160)-mediated, alpha-beta T-cell-independent inflammatory response that develops in the skin shortly after birth. Pasparakis et al. (2002) concluded that the critical function of IKK2-mediated NFKB activity in epidermal keratinocytes is to regulate mechanisms that maintain the immune homeostasis of the skin.

[77518] It is appreciated that the abovementioned animal model for IKBKB is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[77519] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[77520] Pasparakis, M.; Courtois, G.; Hafner, M.; Schmidt-Supprian, M.; Nenci, A.; Toksoy, A.; Krampert, M.; Goebeler, M.; Gillitzer, R.; Israel, A.; Krieg, T.; Rajewsky, K.; Haase, I. : TNF-mediated inflammatory skin disease in mice with epidermis-specific deletion of IKK2. Nature 417: 861-866, 2002. ; and

[77521] May, M. J.; D'Acquisto, F.; Madge, L. A.; Glockner, J.; Pober, J. S.; Ghosh, S. : Selective inhibition of NF-kappa-B activation by a peptide that blocks the interaction of NEMO with the.

[77522] Further studies establishing the function and utilities of IKBKB are found in John Hopkins OMIM database record ID 603258, and in sited publications numbered 8500-8176, 9198, 9201, 12739-850 and 12225 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.NORE1 (Accession NM_031437) is another VGAM2266 host target gene. NORE1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NORE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NORE1 BINDING SITE, designated SEQ ID:25444, to the nucleotide se-

quence of VGAM2266 RNA, herein designated VGAM RNA, also designated SEQ ID:4977.

[77523] Another function of VGAM2266 is therefore inhibition of NORE1 (Accession NM_031437), a gene which may modulate intracellular signal transduction pathways. Accordingly, utilities of VGAM2266 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NORE1. The function of NORE1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM276.Heat Shock 90kDa Protein 1, Alpha-like 3 (HSPCAL3, Accession XM_084514) is another VGAM2266 host target gene. HSPCAL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSPCAL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPCAL3 BINDING SITE, designated SEQ ID:37617, to the nucleotide sequence of VGAM2266 RNA, herein designated VGAM RNA, also designated SEQ ID:4977.

[77524] Another function of VGAM2266 is therefore inhibition of Heat Shock 90kDa Protein 1, Alpha-like 3 (HSPCAL3, Ac-

cession XM_084514). Accordingly, utilities of VGAM2266 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPCAL3. RTBDN (Accession NM_031429) is another VGAM2266 host target gene. RTBDN BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RTBDN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RTBDN BINDING SITE, designated SEQ ID:25424, to the nucleotide sequence of VGAM2266 RNA, herein designated VGAM RNA, also designated SEQ ID:4977.

[77525] Another function of VGAM2266 is therefore inhibition of RTBDN (Accession NM_031429). Accordingly, utilities of VGAM2266 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RTBDN. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2267 (VGAM2267) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77526] VGAM2267 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2267 was detected is described hereinabove with reference to Figs. 1-8.

[77527] VGAM2267 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2267 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77528] VGAM2267 gene encodes a VGAM2267 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2267 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2267 precursor RNA is designated SEQ ID:2253, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2253 is located at position 29434 relative to the genome of Alcelaphine Herpesvirus 1.

[77529] VGAM2267 precursor RNA folds onto itself, forming VGAM2267 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77530] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2267 folded precursor RNA into VGAM2267 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2267 RNA is designated SEQ ID:4978, and is provided hereinbelow with reference to the sequence listing part.

[77531] VGAM2267 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2267 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2267 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[77532] VGAM2267 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2267 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2267 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2267 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2267 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77533] The complementary binding of VGAM2267 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2267 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2267 host target RNA into VGAM2267 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77534] It is appreciated that VGAM2267 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2267 host target genes. The mRNA of each one of this plurality of VGAM2267 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2267 RNA, herein designated VGAM RNA, and which when bound by VGAM2267 RNA causes inhibition of translation of respective one or more VGAM2267 host target proteins.

[77535] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2267 gene, herein designated VGAM GENE, on one or more VGAM2267 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77536] It is yet further appreciated that a function of VGAM2267 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2267 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2267 correlate with, and may be deduced from, the identity of the host target genes which VGAM2267 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77537] Nucleotide sequences of the VGAM2267 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2267 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2267 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2267 are further described hereinbelow with reference to Table 1.

[77538] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2267 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2267 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77539] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2267 gene, herein designated VGAM is inhibition of expression of VGAM2267 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2267 correlate with, and may be deduced from, the identity of the target genes which VGAM2267 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77540] Histamine Receptor H1 (HRH1, Accession NM_000861) is a VGAM2267 host target gene. HRH1 BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by HRH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRH1 BINDING SITE, designated SEQ ID:6524, to the nucleotide sequence of VGAM2267 RNA, herein designated VGAM RNA, also designated SEQ ID:4978.

[77541] A function of VGAM2267 is therefore inhibition of Histamine Receptor H1 (HRH1, Accession NM_000861), a gene which stimulates the synthesis of inositol phosphate. Accordingly, utilities of VGAM2267 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRH1. The function of HRH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM766.DKFZP564I122 (Accession XM_032397) is another VGAM2267 host target gene. DKFZP564I122 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564I122, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of DKFZP564I122 BINDING SITE, designated SEQ ID:31643, to the nucleotide sequence of VGAM2267 RNA, herein designated VGAM RNA, also designated SEQ ID:4978.

[77542] Another function of VGAM2267 is therefore inhibition of DKFZP564I122 (Accession XM_032397). Accordingly, utilities of VGAM2267 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564I122. Integrin, Alpha 10 (ITGA10, Accession XM_002097) is another VGAM2267 host target gene. ITGA10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ITGA10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA10 BINDING SITE, designated SEQ ID:29866, to the nucleotide sequence of VGAM2267 RNA, herein designated VGAM RNA, also designated SEQ ID:4978.

[77543] Another function of VGAM2267 is therefore inhibition of Integrin, Alpha 10 (ITGA10, Accession XM_002097). Accordingly, utilities of VGAM2267 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with ITGA10. YKT6 (Accession NM_006555) is another VGAM2267 host target gene. YKT6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by YKT6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YKT6 BINDING SITE, designated SEQ ID:13321, to the nucleotide sequence of VGAM2267 RNA, herein designated VGAM RNA, also designated SEQ ID:4978.

[77544] Another function of VGAM2267 is therefore inhibition of YKT6 (Accession NM_006555). Accordingly, utilities of VGAM2267 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YKT6. ZFD25 (Accession NM_016220) is another VGAM2267 host target gene. ZFD25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZFD25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZFD25 BINDING SITE, designated SEQ ID:18324, to the nucleotide sequence of VGAM2267 RNA, herein designated VGAM RNA, also designated SEQ

ID:4978.

[77545] Another function of VGAM2267 is therefore inhibition of ZFD25 (Accession NM_016220). Accordingly, utilities of VGAM2267 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFD25. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2268 (VGAM2268) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77546] VGAM2268 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2268 was detected is described hereinabove with reference to Figs. 1-8.

[77547] VGAM2268 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2268 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77548] VGAM2268 gene encodes a VGAM2268 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2268 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2268 precursor RNA is designated SEQ ID:2254, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2254 is located at position 29021 relative to the genome of Alcelaphine Herpesvirus 1.

[77549] VGAM2268 precursor RNA folds onto itself, forming VGAM2268 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77550] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2268 folded precursor RNA into VGAM2268 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2268 RNA is designated SEQ ID:4979, and is provided hereinbelow with reference to the sequence listing part.

[77551] VGAM2268 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2268 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2268 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77552] VGAM2268 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2268 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2268 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2268 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2268 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77553] The complementary binding of VGAM2268 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2268 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2268 host target RNA into VGAM2268 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77554] It is appreciated that VGAM2268 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2268 host target genes. The mRNA of each one of this plurality of VGAM2268 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2268 RNA, herein designated VGAM RNA, and which when bound by VGAM2268 RNA causes inhibition of translation of respective one or more VGAM2268 host target proteins.

[77555] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2268 gene, herein designated VGAM GENE, on one or more VGAM2268 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77556] It is yet further appreciated that a function of VGAM2268 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2268 correlate with, and may be deduced from, the identity of the host target genes which VGAM2268 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77557] Nucleotide sequences of the VGAM2268 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2268 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2268 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2268 are further described hereinbelow with reference to Table 1.

[77558] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2268 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2268 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[77559] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2268 gene, herein designated VGAM is inhibition of expression of VGAM2268 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2268 correlate with, and may be deduced from, the identity of the target genes which VGAM2268 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77560] IRTA1 (Accession NM_031282) is a VGAM2268 host target gene. IRTA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IRTA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRTA1 BINDING SITE, designated SEQ ID:25304, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77561] A function of VGAM2268 is therefore inhibition of IRTA1 (Accession NM_031282). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRTA1. Methylthioadenosine Phosphorylase (MTAP, Accession

NM_002451) is another VGAM2268 host target gene. MTAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTAP BINDING SITE, designated SEQ ID:8288, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77562] Another function of VGAM2268 is therefore inhibition of Methylthioadenosine Phosphorylase (MTAP, Accession NM_002451), a gene which plays a major role in polyamine metabolism. Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTAP. The function of MTAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM68.Prospero-related Homeobox 1 (PROX1, Accession NM_002763) is another VGAM2268 host target gene. PROX1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PROX1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PROX1 BINDING SITE, designated SEQ ID:8652, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77563] Another function of VGAM2268 is therefore inhibition of Prospero-related Homeobox 1 (PROX1, Accession NM_002763), a gene which may regulate gene expression and development of postmitotic undifferentiated young neurons. Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROX1. The function of PROX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM430.Arginyl Aminopeptidase (aminopeptidase B)-like 1 (RNPEPL1, Accession NM_018226) is another VGAM2268 host target gene. RNPEPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNPEPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of RNPEPL1 BINDING SITE, designated SEQ ID:20164, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77564] Another function of VGAM2268 is therefore inhibition of Arginyl Aminopeptidase (aminopeptidase B)-like 1 (RNPEPL1, Accession NM_018226). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNPEPL1. V-akt Murine Thymoma Viral Oncogene Homolog 3 (protein kinase B, gamma) (AKT3, Accession NM_005465) is another VGAM2268 host target gene. AKT3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKT3 BINDING SITE, designated SEQ ID:11961, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77565] Another function of VGAM2268 is therefore inhibition of V-akt Murine Thymoma Viral Oncogene Homolog 3 (protein kinase B, gamma) (AKT3, Accession NM_005465).

Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKT3. Chromosome 20 Open Reading Frame 38 (C20orf38, Accession NM_018327) is another VGAM2268 host target gene. C20orf38 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf38, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf38 BINDING SITE, designated SEQ ID:20324, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77566] Another function of VGAM2268 is therefore inhibition of Chromosome 20 Open Reading Frame 38 (C20orf38, Accession NM_018327). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf38. KIAA1160 (Accession NM_020701) is another VGAM2268 host target gene. KIAA1160 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1160 BINDING SITE, designated SEQ ID:21851, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77567] Another function of VGAM2268 is therefore inhibition of KIAA1160 (Accession NM_020701). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1160. KIAA1198 (Accession XM_032674) is another VGAM2268 host target gene. KIAA1198 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1198, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE, designated SEQ ID:31715, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77568] Another function of VGAM2268 is therefore inhibition of KIAA1198 (Accession XM_032674). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1198. KOC1 (Accession XM_165847) is another VGAM2268 host target gene. KOC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KOC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KOC1 BINDING SITE, designated SEQ ID:43779, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77569] Another function of VGAM2268 is therefore inhibition of KOC1 (Accession XM_165847). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KOC1. Leiomodin 1 (smooth muscle) (LMOD1, Accession NM_012134) is another VGAM2268 host target gene. LMOD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LMOD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LMOD1 BINDING SITE, designated SEQ ID:14445, to the nucleotide sequence of VGAM2268 RNA,

herein designated VGAM RNA, also designated SEQ ID:4979.

[77570] Another function of VGAM2268 is therefore inhibition of Leiomodin 1 (smooth muscle) (LMOD1, Accession NM_012134). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LMOD1. Polymerase (DNA directed), Mu (POLM, Accession XM_165867) is another VGAM2268 host target gene. POLM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POLM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POLM BINDING SITE, designated SEQ ID:43783, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77571] Another function of VGAM2268 is therefore inhibition of Polymerase (DNA directed), Mu (POLM, Accession XM_165867). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLM. PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession

XM_028335) is another VGAM2268 host target gene. PRPF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRPF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRPF8 BINDING SITE, designated SEQ ID:30676, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77572] Another function of VGAM2268 is therefore inhibition of PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRPF8. Regulatory Factor X, 4 (influences HLA class II expression) (RFX4, Accession NM_032491) is another VGAM2268 host target gene. RFX4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RFX4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RFX4 BINDING SITE, designated SEQ

ID:26243, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77573] Another function of VGAM2268 is therefore inhibition of Regulatory Factor X, 4 (influences HLA class II expression) (RFX4, Accession NM_032491). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFX4. Rho-related BTB Domain Containing 3 (RHOBTB3, Accession NM_014899) is another VGAM2268 host target gene. RHOBTB3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RHOBTB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RHOBTB3 BINDING SITE, designated SEQ ID:17077, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77574] Another function of VGAM2268 is therefore inhibition of Rho-related BTB Domain Containing 3 (RHOBTB3, Accession NM_014899). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with RHOBTB3. RLUCL (Accession NM_058192) is another VGAM2268 host target gene. RLUCL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RLUCL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RLUCL BINDING SITE, designated SEQ ID:27753, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77575] Another function of VGAM2268 is therefore inhibition of RLUCL (Accession NM_058192). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RLUCL. Ring Finger Protein (C3HC4 type) 8 (RNF8, Accession NM_003958) is another VGAM2268 host target gene. RNF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF8 BINDING SITE, designated SEQ ID:10102,

to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77576] Another function of VGAM2268 is therefore inhibition of Ring Finger Protein (C3HC4 type) 8 (RNF8, Accession NM_003958). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF8. Ubiquitin Specific Protease 8 (USP8, Accession NM_005154) is another VGAM2268 host target gene. USP8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP8 BINDING SITE, designated SEQ ID:11632, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77577] Another function of VGAM2268 is therefore inhibition of Ubiquitin Specific Protease 8 (USP8, Accession NM_005154). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP8. LOC144438 (Accession XM_084860) is another VGAM2268 host target

gene. LOC144438 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144438, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144438 BINDING SITE, designated SEQ ID:37741, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77578] Another function of VGAM2268 is therefore inhibition of LOC144438 (Accession XM_084860). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144438. LOC196955 (Accession XM_085210) is another VGAM2268 host target gene. LOC196955 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC196955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196955 BINDING SITE, designated SEQ ID:37942, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77579] Another function of VGAM2268 is therefore inhibition of LOC196955 (Accession XM_085210). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196955. LOC200488 (Accession XM_117240) is another VGAM2268 host target gene. LOC200488 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200488, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200488 BINDING SITE, designated SEQ ID:43317, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77580] Another function of VGAM2268 is therefore inhibition of LOC200488 (Accession XM_117240). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200488. LOC200940 (Accession XM_114324) is another VGAM2268 host target gene. LOC200940 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200940, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200940 BINDING SITE, designated SEQ ID:42875, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77581] Another function of VGAM2268 is therefore inhibition of LOC200940 (Accession XM_114324). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200940. LOC255057 (Accession XM_170903) is another VGAM2268 host target gene. LOC255057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255057 BINDING SITE, designated SEQ ID:45662, to the nucleotide sequence of VGAM2268 RNA, herein designated VGAM RNA, also designated SEQ ID:4979.

[77582] Another function of VGAM2268 is therefore inhibition of LOC255057 (Accession XM_170903). Accordingly, utilities of VGAM2268 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC255057. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2269 (VGAM2269) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77583] VGAM2269 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2269 was detected is described hereinabove with reference to Figs. 1-8.

[77584] VGAM2269 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2269 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77585] VGAM2269 gene encodes a VGAM2269 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2269 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2269 precursor RNA is designated SEQ ID:2255, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2255 is located at position 30842 relative to the genome of Alcelaphine Herpesvirus 1.

[77586] VGAM2269 precursor RNA folds onto itself, forming VGAM2269 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77587] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2269 folded precursor RNA into VGAM2269 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2269 RNA is designated SEQ ID:4980, and is provided hereinbelow with reference to the sequence listing part.

[77588] VGAM2269 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2269 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2269 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77589] VGAM2269 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2269 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2269 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2269 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2269 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77590] The complementary binding of VGAM2269 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2269 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2269 host target RNA into VGAM2269 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77591] It is appreciated that VGAM2269 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2269 host target genes. The mRNA of each one of this plurality of VGAM2269 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2269 RNA, herein designated VGAM RNA, and which when bound by VGAM2269 RNA causes

inhibition of translation of respective one or more VGAM2269 host target proteins.

[77592] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2269 gene, herein designated VGAM GENE, on one or more VGAM2269 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77593] It is yet further appreciated that a function of VGAM2269 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2269 include diagnosis, prevention and

treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2269 correlate with, and may be deduced from, the identity of the host target genes which VGAM2269 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77594] Nucleotide sequences of the VGAM2269 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2269 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2269 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2269 are further described hereinbelow with reference to Table 1.

[77595] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2269 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2269 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77596] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2269 gene, herein designated VGAM is inhibition of expression of VGAM2269 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2269 correlate with, and may be deduced from, the identity of the target genes which VGAM2269 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77597] A Kinase (PRKA) Anchor Protein 13 (AKAP13, Accession XM_116974) is a VGAM2269 host target gene. AKAP13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKAP13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP13 BINDING SITE, designated SEQ ID:43180, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77598] A function of VGAM2269 is therefore inhibition of A Kinase (PRKA) Anchor Protein 13 (AKAP13, Accession XM_116974), a gene which regulates subcellular localization of type II cAMP-dependent PKA. Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP13. The function of AKAP13 and its association with various diseases and clinical conditions, has been estab-

lished by previous studies, as described hereinabove with reference to VGAM17.Aldehyde Dehydrogenase 3 Family, Member B1 (ALDH3B1, Accession XM_166190) is another VGAM2269 host target gene. ALDH3B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALDH3B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALDH3B1 BINDING SITE, designated SEQ ID:44000, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77599] Another function of VGAM2269 is therefore inhibition of Aldehyde Dehydrogenase 3 Family, Member B1 (ALDH3B1, Accession XM_166190), a gene which may play a major role in the detoxification of aldehydes generated by alcohol metabolism and lipid peroxidation. Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ALDH3B1. The function of ALDH3B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2007.Branched Chain

Aminotransferase 1, Cytosolic (BCAT1, Accession XM_038659) is another VGAM2269 host target gene. BCAT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCAT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCAT1 BINDING SITE, designated SEQ ID:32897, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77600] Another function of VGAM2269 is therefore inhibition of Branched Chain Aminotransferase 1, Cytosolic (BCAT1, Accession XM_038659), a gene which catalyzes of the essential branched chain leucine, isoleucine, and valine. Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCAT1. The function of BCAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1367.Ret Proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease) (RET, Accession

NM_020630) is another VGAM2269 host target gene. RET BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RET, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RET BINDING SITE, designated SEQ ID:21789, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77601] Another function of VGAM2269 is therefore inhibition of Ret Proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease) (RET, Accession NM_020630), a gene which transduces signals for cell growth and differentiation. Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RET. The function of RET and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Regulator of G-protein Signalling 5 (RGS5, Accession NM_003617) is another VGAM2269 host target gene. RGS5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by RGS5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RGS5 BINDING SITE, designated SEQ ID:9680, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77602] Another function of VGAM2269 is therefore inhibition of Regulator of G-protein Signalling 5 (RGS5, Accession NM_003617). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS5. Roundabout, Axon Guidance Receptor, Homolog 1 (Drosophila) (ROBO1, Accession NM_133631) is another VGAM2269 host target gene. ROBO1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ROBO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ROBO1 BINDING SITE, designated SEQ ID:28588, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77603] Another function of VGAM2269 is therefore inhibition of Roundabout, Axon Guidance Receptor, Homolog 1 (Drosophila) (ROBO1, Accession NM_133631), a gene which is an axon guidance receptor. Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ROBO1. The function of ROBO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM37.Syndecan 4 (amphiglycan, ryudocan) (SDC4, Accession NM_002999) is another VGAM2269 host target gene. SDC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SDC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDC4 BINDING SITE, designated SEQ ID:8894, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77604] Another function of VGAM2269 is therefore inhibition of Syndecan 4 (amphiglycan, ryudocan) (SDC4, Accession NM_002999), a gene which is a cell surface proteoglycan.

Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDC4. The function of SDC4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM552.Solute Carrier Family 21 (prostaglandin transporter), Member 2 (SLC21A2, Accession NM_005630) is another VGAM2269 host target gene. SLC21A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC21A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC21A2 BINDING SITE, designated SEQ ID:12160, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77605] Another function of VGAM2269 is therefore inhibition of Solute Carrier Family 21 (prostaglandin transporter), Member 2 (SLC21A2, Accession NM_005630), a gene which is a Prostaglandin transporter. Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

SLC21A2. The function of SLC21A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM83.T-cell Acute Lymphocytic Leukemia 1 (TAL1, Accession NM_003189) is another VGAM2269 host target gene. TAL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAL1 BINDING SITE, designated SEQ ID:9174, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77606] Another function of VGAM2269 is therefore inhibition of T-cell Acute Lymphocytic Leukemia 1 (TAL1, Accession NM_003189), a gene which may help control cell growth and differentiation. Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAL1. The function of TAL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM172.Ubiquitin-conjugating Enzyme E2L 3 (UBE2L3, Accession NM_003347) is another VGAM2269 host target gene. UBE2L3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UBE2L3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE2L3 BINDING SITE, designated SEQ ID:9362, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77607] Another function of VGAM2269 is therefore inhibition of Ubiquitin-conjugating Enzyme E2L 3 (UBE2L3, Accession NM_003347), a gene which catalyzes the covalent attachment of ubiquitin to other proteins. Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE2L3. The function of UBE2L3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM215.Calsyntenin 1 (CLSTN1, Accession NM_014944) is another VGAM2269 host target gene. CLSTN1 BINDING SITE is HOST TARGET binding site found

in the 5` untranslated region of mRNA encoded by CLSTN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLSTN1 BINDING SITE, designated SEQ ID:17258, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77608] Another function of VGAM2269 is therefore inhibition of Calsyntenin 1 (CLSTN1, Accession NM_014944). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLSTN1. D21S2056E (Accession NM_003683) is another VGAM2269 host target gene. D21S2056E BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by D21S2056E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of D21S2056E BINDING SITE, designated SEQ ID:9790, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77609] Another function of VGAM2269 is therefore inhibition of

D21S2056E (Accession NM_003683). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with D21S2056E. Fatty Acid Desaturase 2 (FADS2, Accession NM_004265) is another VGAM2269 host target gene. FADS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FADS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FADS2 BINDING SITE, designated SEQ ID:10470, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77610] Another function of VGAM2269 is therefore inhibition of Fatty Acid Desaturase 2 (FADS2, Accession NM_004265). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FADS2. FLJ13265 (Accession NM_024877) is another VGAM2269 host target gene. FLJ13265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13265, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13265 BINDING SITE, designated SEQ ID:24314, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77611] Another function of VGAM2269 is therefore inhibition of FLJ13265 (Accession NM_024877). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13265. KIAA1854 (Accession XM_049884) is another VGAM2269 host target gene. KIAA1854 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1854, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1854 BINDING SITE, designated SEQ ID:35538, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77612] Another function of VGAM2269 is therefore inhibition of KIAA1854 (Accession XM_049884). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1854. KIAA1855 (Accession XM_166453) is another VGAM2269 host target gene. KIAA1855 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1855, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1855 BINDING SITE, designated SEQ ID:44363, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77613] Another function of VGAM2269 is therefore inhibition of KIAA1855 (Accession XM_166453). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1855. MGC15854 (Accession NM_145029) is another VGAM2269 host target gene. MGC15854 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC15854, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15854 BINDING SITE, designated SEQ ID:29646, to

the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77614] Another function of VGAM2269 is therefore inhibition of MGC15854 (Accession NM_145029). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15854. Tumor Necrosis Factor, Alpha-induced Protein 3 (TNFAIP3, Accession NM_006290) is another VGAM2269 host target gene. TNFAIP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFAIP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFAIP3 BINDING SITE, designated SEQ ID:12980, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77615] Another function of VGAM2269 is therefore inhibition of Tumor Necrosis Factor, Alpha-induced Protein 3 (TNFAIP3, Accession NM_006290). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFAIP3. TNF Receptor-associated Factor 6 (TRAF6, Acces-

sion NM_004620) is another VGAM2269 host target gene. TRAF6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRAF6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRAF6 BINDING SITE, designated SEQ ID:10970, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77616] Another function of VGAM2269 is therefore inhibition of TNF Receptor-associated Factor 6 (TRAF6, Accession NM_004620). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF6. VPS39 (Accession XM_031720) is another VGAM2269 host target gene. VPS39 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VPS39, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS39 BINDING SITE, designated SEQ ID:31474, to the nucleotide sequence of VGAM2269 RNA,

herein designated VGAM RNA, also designated SEQ ID:4980.

[77617] Another function of VGAM2269 is therefore inhibition of VPS39 (Accession XM_031720). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS39. WIT-1 (Accession NM_015855) is another VGAM2269 host target gene. WIT-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WIT-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WIT-1 BINDING SITE, designated SEQ ID:17992, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77618] Another function of VGAM2269 is therefore inhibition of WIT-1 (Accession NM_015855). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WIT-1. LOC129607 (Accession XM_059368) is another VGAM2269 host target gene. LOC129607 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC129607, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC129607 BINDING SITE, designated SEQ ID:36976, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77619] Another function of VGAM2269 is therefore inhibition of LOC129607 (Accession XM_059368). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129607. LOC144308 (Accession XM_096575) is another VGAM2269 host target gene. LOC144308 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144308 BINDING SITE, designated SEQ ID:40409, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77620] Another function of VGAM2269 is therefore inhibition of LOC144308 (Accession XM_096575). Accordingly, utilities

of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144308. LOC145761 (Accession XM_096855) is another VGAM2269 host target gene. LOC145761 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145761, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145761 BINDING SITE, designated SEQ ID:40586, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77621] Another function of VGAM2269 is therefore inhibition of LOC145761 (Accession XM_096855). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145761. LOC158310 (Accession XM_098919) is another VGAM2269 host target gene. LOC158310 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158310, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC158310 BINDING SITE, designated SEQ ID:41945, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77622] Another function of VGAM2269 is therefore inhibition of LOC158310 (Accession XM_098919). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158310. LOC199986 (Accession XM_117168) is another VGAM2269 host target gene. LOC199986 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC199986, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199986 BINDING SITE, designated SEQ ID:43270, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77623] Another function of VGAM2269 is therefore inhibition of LOC199986 (Accession XM_117168). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199986. LOC201952 (Accession XM_117345) is another VGAM2269 host target gene. LOC201952 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201952, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201952 BINDING SITE, designated SEQ ID:43396, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77624] Another function of VGAM2269 is therefore inhibition of LOC201952 (Accession XM_117345). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201952. LOC219404 (Accession XM_167909) is another VGAM2269 host target gene. LOC219404 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219404, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219404 BINDING SITE, designated SEQ ID:44911, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77625] Another function of VGAM2269 is therefore inhibition of

LOC219404 (Accession XM_167909). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219404. LOC219653 (Accession XM_166093) is another VGAM2269 host target gene. LOC219653 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219653, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219653 BINDING SITE, designated SEQ ID:43868, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77626] Another function of VGAM2269 is therefore inhibition of LOC219653 (Accession XM_166093). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219653. LOC221178 (Accession XM_167936) is another VGAM2269 host target gene. LOC221178 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC221178 BINDING SITE, designated SEQ ID:44927, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77627] Another function of VGAM2269 is therefore inhibition of LOC221178 (Accession XM_167936). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221178. LOC245812 (Accession XM_168296) is another VGAM2269 host target gene. LOC245812 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC245812, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC245812 BINDING SITE, designated SEQ ID:45100, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77628] Another function of VGAM2269 is therefore inhibition of LOC245812 (Accession XM_168296). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC245812. LOC91660 (Accession XM_039902) is an-

other VGAM2269 host target gene. LOC91660 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91660, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91660 BINDING SITE, designated SEQ ID:33208, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77629] Another function of VGAM2269 is therefore inhibition of LOC91660 (Accession XM_039902). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91660. LOC92689 (Accession XM_046663) is another VGAM2269 host target gene. LOC92689 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92689, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92689 BINDING SITE, designated SEQ ID:34785, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77630] Another function of VGAM2269 is therefore inhibition of LOC92689 (Accession XM_046663). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92689. LOC92906 (Accession NM_138394) is another VGAM2269 host target gene. LOC92906 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92906 BINDING SITE, designated SEQ ID:28762, to the nucleotide sequence of VGAM2269 RNA, herein designated VGAM RNA, also designated SEQ ID:4980.

[77631] Another function of VGAM2269 is therefore inhibition of LOC92906 (Accession NM_138394). Accordingly, utilities of VGAM2269 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92906. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2270 (VGAM2270) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[77632] VGAM2270 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2270 was detected is described hereinabove with reference to Figs. 1-8.

[77633] VGAM2270 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2270 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77634] VGAM2270 gene encodes a VGAM2270 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2270 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2270 precursor RNA is designated SEQ ID:2256, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2256 is located at position 26539 relative to the genome of Alcelaphine Herpesvirus 1.

[77635] VGAM2270 precursor RNA folds onto itself, forming VGAM2270 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77636] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2270 folded precursor RNA into VGAM2270 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2270 RNA is designated SEQ ID:4981, and is provided hereinbelow with reference to the sequence listing part.

[77637] VGAM2270 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2270 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2270 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77638] VGAM2270 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2270 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2270 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2270 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2270 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77639] The complementary binding of VGAM2270 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2270 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2270 host target RNA into VGAM2270 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77640] It is appreciated that VGAM2270 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2270 host target genes. The mRNA of each one of this plurality of VGAM2270 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2270 RNA, herein designated VGAM RNA, and which when bound by VGAM2270 RNA causes inhibition of translation of respective one or more VGAM2270 host target proteins.

[77641] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2270 gene, herein designated VGAM GENE, on one or more VGAM2270 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77642] It is yet further appreciated that a function of VGAM2270 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2270 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2270 correlate with, and may be deduced from, the identity of the host target genes which VGAM2270 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[77643] Nucleotide sequences of the VGAM2270 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2270 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2270 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2270 are further described hereinbelow with reference to Table 1.

[77644] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2270 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2270 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77645] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2270 gene, herein designated VGAM is inhibition of expression of VGAM2270 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2270 correlate with, and may be deduced from, the identity of the target genes which VGAM2270 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77646] HEF1 (Accession NM_006403) is a VGAM2270 host target gene. HEF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HEF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HEF1 BINDING SITE, designated SEQ ID:13110, to the nucleotide sequence of VGAM2270 RNA, herein designated VGAM RNA, also designated SEQ ID:4981.

[77647] A function of VGAM2270 is therefore inhibition of HEF1 (Accession NM_006403). Accordingly, utilities of VGAM2270 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEF1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2271 (VGAM2271) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77648] VGAM2271 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2271 was detected is described hereinabove with reference to Figs. 1-8.

[77649] VGAM2271 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2271 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77650] VGAM2271 gene encodes a VGAM2271 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2271 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2271 precursor RNA is designated SEQ ID:2257, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2257 is located at position 29858 relative to the genome of Alcelaphine Herpesvirus 1.

[77651] VGAM2271 precursor RNA folds onto itself, forming VGAM2271 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[77652] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2271 folded precursor RNA into VGAM2271 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2271 RNA is designated SEQ ID:4982, and is provided hereinbelow with reference to the sequence listing part.

[77653] VGAM2271 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2271 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2271 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77654] VGAM2271 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2271 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2271 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2271 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2271 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77655] The complementary binding of VGAM2271 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2271 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2271 host target RNA into VGAM2271 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77656] It is appreciated that VGAM2271 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2271 host target genes. The mRNA of each one of this plurality of VGAM2271 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2271 RNA, herein designated VGAM RNA, and which when bound by VGAM2271 RNA causes inhibition of translation of respective one or more VGAM2271 host target proteins.

[77657] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2271 gene, herein designated VGAM GENE, on one or more VGAM2271 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77658] It is yet further appreciated that a function of VGAM2271 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2271 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2271 correlate with, and may be deduced from, the identity of the host target genes which VGAM2271 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77659] Nucleotide sequences of the VGAM2271 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2271 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2271 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2271 are further described hereinbelow with reference to Table 1.

[77660] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2271 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2271 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77661] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2271 gene, herein designated VGAM is inhibition of expression of VGAM2271 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2271 correlate with, and may be deduced from, the identity of the target genes which VGAM2271 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77662] Protein Phosphatase 3 (formerly 2B), Catalytic Subunit, Alpha Isoform (calcineurin A alpha) (PPP3CA, Accession NM_000944) is a VGAM2271 host target gene. PPP3CA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP3CA, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP3CA BINDING SITE, designated SEQ ID:6642, to the nucleotide sequence of VGAM2271 RNA, herein designated VGAM RNA, also designated SEQ ID:4982.

[77663] A function of VGAM2271 is therefore inhibition of Protein Phosphatase 3 (formerly 2B), Catalytic Subunit, Alpha Isoform (calcineurin A alpha) (PPP3CA, Accession NM_000944), a gene which is the catalytic subunit of calcium-dependent, calmodulin-stimulated protein phosphatase. Accordingly, utilities of VGAM2271 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP3CA. The function of PPP3CA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM497.Ceramide Kinase (cerk, Accession NM_022766) is another VGAM2271 host target gene. cerk BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by cerk, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of cerk BINDING

SITE, designated SEQ ID:23012, to the nucleotide sequence of VGAM2271 RNA, herein designated VGAM RNA, also designated SEQ ID:4982.

[77664] Another function of VGAM2271 is therefore inhibition of Ceramide Kinase (cerk, Accession NM_022766). Accordingly, utilities of VGAM2271 include diagnosis, prevention and treatment of diseases and clinical conditions associated with cerk. DKFZP434P0111 (Accession XM_041116) is another VGAM2271 host target gene. DKFZP434P0111 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434P0111, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434P0111 BINDING SITE, designated SEQ ID:33453, to the nucleotide sequence of VGAM2271 RNA, herein designated VGAM RNA, also designated SEQ ID:4982.

[77665] Another function of VGAM2271 is therefore inhibition of DKFZP434P0111 (Accession XM_041116). Accordingly, utilities of VGAM2271 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434P0111. FLJ11004 (Accession NM_018296)

is another VGAM2271 host target gene. FLJ11004 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ11004, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11004 BINDING SITE, designated SEQ ID:20286, to the nucleotide sequence of VGAM2271 RNA, herein designated VGAM RNA, also designated SEQ ID:4982.

[77666] Another function of VGAM2271 is therefore inhibition of FLJ11004 (Accession NM_018296). Accordingly, utilities of VGAM2271 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11004. FLJ21276 (Accession NM_024633) is another VGAM2271 host target gene. FLJ21276 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21276, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21276 BINDING SITE, designated SEQ ID:23900, to the nucleotide sequence of VGAM2271 RNA, herein designated VGAM RNA, also designated SEQ ID:4982.

[77667] Another function of VGAM2271 is therefore inhibition of FLJ21276 (Accession NM_024633). Accordingly, utilities of VGAM2271 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21276. IDI2 (Accession NM_033261) is another VGAM2271 host target gene. IDI2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IDI2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IDI2 BINDING SITE, designated SEQ ID:27090, to the nucleotide sequence of VGAM2271 RNA, herein designated VGAM RNA, also designated SEQ ID:4982.

[77668] Another function of VGAM2271 is therefore inhibition of IDI2 (Accession NM_033261). Accordingly, utilities of VGAM2271 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IDI2. RAB-R (Accession NM_006076) is another VGAM2271 host target gene. RAB-R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB-R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of RAB-R BINDING SITE, designated SEQ ID:12720, to the nucleotide sequence of VGAM2271 RNA, herein designated VGAM RNA, also designated SEQ ID:4982.

[77669] Another function of VGAM2271 is therefore inhibition of RAB-R (Accession NM_006076). Accordingly, utilities of VGAM2271 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB-R. LOC165693 (Accession XM_093373) is another VGAM2271 host target gene. LOC165693 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC165693, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC165693 BINDING SITE, designated SEQ ID:40186, to the nucleotide sequence of VGAM2271 RNA, herein designated VGAM RNA, also designated SEQ ID:4982.

[77670] Another function of VGAM2271 is therefore inhibition of LOC165693 (Accession XM_093373). Accordingly, utilities of VGAM2271 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC165693. LOC255042 (Accession XM_170896) is another VGAM2271 host target gene. LOC255042 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255042, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255042 BINDING SITE, designated SEQ ID:45649, to the nucleotide sequence of VGAM2271 RNA, herein designated VGAM RNA, also designated SEQ ID:4982.

[77671] Another function of VGAM2271 is therefore inhibition of LOC255042 (Accession XM_170896). Accordingly, utilities of VGAM2271 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255042. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2272 (VGAM2272) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77672] VGAM2272 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2272 was detected is described hereinabove with reference to Figs. 1-8.

[77673] VGAM2272 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2272 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77674] VGAM2272 gene encodes a VGAM2272 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2272 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2272 precursor RNA is designated SEQ ID:2258, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2258 is located at position 18433 relative to the genome of Alcelaphine Herpesvirus 1.

[77675] VGAM2272 precursor RNA folds onto itself, forming VGAM2272 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77676] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2272 folded precursor RNA into VGAM2272 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2272 RNA is designated SEQ ID:4983, and is provided hereinbelow with reference to the sequence listing part.

[77677] VGAM2272 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2272 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2272 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77678] VGAM2272 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2272 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2272 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2272 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2272 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77679] The complementary binding of VGAM2272 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2272 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2272 host target RNA into VGAM2272 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77680] It is appreciated that VGAM2272 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2272 host target genes. The mRNA of each one of this plurality of VGAM2272 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2272 RNA, herein designated VGAM RNA, and which when bound by VGAM2272 RNA causes inhibition of translation of respective one or more VGAM2272 host target proteins.

[77681] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2272 gene, herein designated VGAM GENE, on one or more VGAM2272 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77682] It is yet further appreciated that a function of VGAM2272 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2272 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2272 correlate with, and may be deduced from, the identity of the host target genes which VGAM2272 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77683] Nucleotide sequences of the VGAM2272 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2272 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2272 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2272 are further described hereinbelow with reference to Table 1.

[77684] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2272 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2272 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77685] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2272 gene, herein designated VGAM is inhibition of expression of VGAM2272 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2272 correlate with, and may be deduced from, the identity of the target genes which VGAM2272 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77686] Formyl Peptide Receptor-like 1 (FPRL1, Accession NM_001462) is a VGAM2272 host target gene. FPRL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FPRL1, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FPRL1 BINDING SITE, designated SEQ ID:7195, to the nucleotide sequence of VGAM2272 RNA, herein designated VGAM RNA, also designated SEQ ID:4983.

[77687] A function of VGAM2272 is therefore inhibition of Formyl Peptide Receptor-like 1 (FPRL1, Accession NM_001462). Accordingly, utilities of VGAM2272 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FPRL1. LIM Domain Kinase 1 (LIMK1, Accession NM_016735) is another VGAM2272 host target gene. LIMK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIMK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIMK1 BINDING SITE, designated SEQ ID:18800, to the nucleotide sequence of VGAM2272 RNA, herein designated VGAM RNA, also designated SEQ ID:4983.

[77688] Another function of VGAM2272 is therefore inhibition of LIM Domain Kinase 1 (LIMK1, Accession NM_016735). Ac-

cordingly, utilities of VGAM2272 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIMK1. Myeloid Cell Leukemia Sequence 1 (BCL2-related) (MCL1, Accession NM_021960) is another VGAM2272 host target gene. MCL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MCL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MCL1 BINDING SITE, designated SEQ ID:22486, to the nucleotide sequence of VGAM2272 RNA, herein designated VGAM RNA, also designated SEQ ID:4983.

[77689] Another function of VGAM2272 is therefore inhibition of Myeloid Cell Leukemia Sequence 1 (BCL2-related) (MCL1, Accession NM_021960), a gene which involved in programing of differentiation and concomitant maintenance of viability. Accordingly, utilities of VGAM2272 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCL1. The function of MCL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM1083.Chromosome 5 Open Reading Frame 4 (C5orf4, Accession NM_016348) is another VGAM2272 host target gene. C5orf4 BINDING SITE1 and C5orf4 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by C5orf4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5orf4 BINDING SITE1 and C5orf4 BINDING SITE2, designated SEQ ID:18472 and SEQ ID:26177 respectively, to the nucleotide sequence of VGAM2272 RNA, herein designated VGAM RNA, also designated SEQ ID:4983.

[77690] Another function of VGAM2272 is therefore inhibition of Chromosome 5 Open Reading Frame 4 (C5orf4, Accession NM_016348). Accordingly, utilities of VGAM2272 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf4. DKFZP434C128 (Accession XM_036086) is another VGAM2273 host target gene. DKFZP434C128 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434C128, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of DKFZP434C128 BINDING SITE, designated SEQ ID:32374, to the nucleotide sequence of VGAM2273 RNA, herein designated VGAM RNA, also designated SEQ ID:4984.

[77691] Another function of VGAM2273 is therefore inhibition of DKFZP434C128 (Accession XM_036086). Accordingly, utilities of VGAM2273 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434C128. IMP-2 (Accession NM_006548) is another VGAM2273 host target gene. IMP-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IMP-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IMP-2 BINDING SITE, designated SEQ ID:13302, to the nucleotide sequence of VGAM2273 RNA, herein designated VGAM RNA, also designated SEQ ID:4984.

[77692] Another function of VGAM2273 is therefore inhibition of IMP-2 (Accession NM_006548). Accordingly, utilities of VGAM2273 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMP-2. Transducer of ERBB2, 2 (TOB2, Accession XM_170995) is

another VGAM2273 host target gene. TOB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOB2 BINDING SITE, designated SEQ ID:45764, to the nucleotide sequence of VGAM2273 RNA, herein designated VGAM RNA, also designated SEQ ID:4984.

[77693] Another function of VGAM2273 is therefore inhibition of Transducer of ERBB2, 2 (TOB2, Accession XM_170995). Accordingly, utilities of VGAM2273 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOB2. LOC147671 (Accession XM_085844) is another VGAM2273 host target gene. LOC147671 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147671, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147671 BINDING SITE, designated SEQ ID:38376, to the nucleotide sequence of VGAM2273 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4984.

[77694] Another function of VGAM2273 is therefore inhibition of LOC147671 (Accession XM_085844). Accordingly, utilities of VGAM2273 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147671. LOC158819 (Accession XM_098995) is another VGAM2273 host target gene. LOC158819 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158819, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158819 BINDING SITE, designated SEQ ID:42024, to the nucleotide sequence of VGAM2273 RNA, herein designated VGAM RNA, also designated SEQ ID:4984.

[77695] Another function of VGAM2273 is therefore inhibition of LOC158819 (Accession XM_098995). Accordingly, utilities of VGAM2273 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158819. LOC200014 (Accession XM_114087) is another VGAM2273 host target gene. LOC200014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200014, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200014 BINDING SITE, designated SEQ ID:42693, to the nucleotide sequence of VGAM2273 RNA, herein designated VGAM RNA, also designated SEQ ID:4984.

[77696] Another function of VGAM2273 is therefore inhibition of LOC200014 (Accession XM_114087). Accordingly, utilities of VGAM2273 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200014. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2274 (VGAM2274) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77697] VGAM2274 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2274 was detected is described hereinabove with reference to Figs. 1-8.

[77698] VGAM2274 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus

1. VGAM2274 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77699] VGAM2274 gene encodes a VGAM2274 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2274 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2274 precursor RNA is designated SEQ ID:2260, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2260 is located at position 31577 relative to the genome of Alcelaphine Herpesvirus 1.

[77700] VGAM2274 precursor RNA folds onto itself, forming VGAM2274 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77701] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2274 folded precursor RNA into VGAM2274 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2274 RNA is designated SEQ ID:4985, and is provided hereinbelow with reference to the sequence listing part.

[77702] VGAM2274 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2274 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2274 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77703] VGAM2274 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2274 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2274 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2274 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2274 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77704] The complementary binding of VGAM2274 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2274 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2274 host target RNA into VGAM2274 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77705] It is appreciated that VGAM2274 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2274 host target genes. The mRNA of each one of this plurality of VGAM2274 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2274 RNA, herein designated VGAM RNA, and which when bound by VGAM2274 RNA causes inhibition of translation of respective one or more VGAM2274 host target proteins.

[77706] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2274 gene, herein designated VGAM GENE, on one or more VGAM2274 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77707] It is yet further appreciated that a function of VGAM2274 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2274 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2274 correlate with, and may be deduced from, the identity of the host target genes which VGAM2274 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77708] Nucleotide sequences of the VGAM2274 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2274 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2274 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2274 are further described hereinbelow with reference to Table 1.

[77709] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2274 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2274 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77710] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2274 gene, herein designated VGAM is inhibition of expression of VGAM2274 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2274 correlate with, and may be deduced from, the identity of the target genes which VGAM2274 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77711] Alpha Thalassemia/mental Retardation Syndrome X-linked (RAD54 homolog, S. cerevisiae) (ATRX, Accession NM_000489) is a VGAM2274 host target gene. ATRX BINDING SITE1 and ATRX BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ATRX, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of ATRX BINDING SITE1 and ATRX BINDING SITE2, designated SEQ ID:6094 and SEQ ID:28683 respectively, to the nucleotide sequence of VGAM2274 RNA, herein designated VGAM RNA, also designated SEQ ID:4985.

[77712] A function of VGAM2274 is therefore inhibition of Alpha Thalassemia/mental Retardation Syndrome X-linked (RAD54 homolog, S. cerevisiae) (ATRX, Accession NM_000489). Accordingly, utilities of VGAM2274 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATRX. KIAA1102 (Accession XM_044461) is another VGAM2274 host target gene. KIAA1102 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1102, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1102 BINDING SITE, designated SEQ ID:34211, to the nucleotide sequence of VGAM2274 RNA, herein designated VGAM RNA, also designated SEQ ID:4985.

[77713] Another function of VGAM2274 is therefore inhibition of KIAA1102 (Accession XM_044461). Accordingly, utilities

of VGAM2274 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1102. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2275 (VGAM2275) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77714] VGAM2275 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2275 was detected is described hereinabove with reference to Figs. 1-8.

[77715] VGAM2275 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2275 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77716] VGAM2275 gene encodes a VGAM2275 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2275 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2275 precursor RNA is designated SEQ ID:2261, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2261 is located at position 30158 relative to the genome of Alcelaphine Herpesvirus 1.

[77717] VGAM2275 precursor RNA folds onto itself, forming VGAM2275 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77718] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2275 folded precursor RNA into VGAM2275 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2275 RNA is designated SEQ ID:4986, and

is provided hereinbelow with reference to the sequence listing part.

[77719] VGAM2275 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2275 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2275 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77720] VGAM2275 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2275 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2275 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2275 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2275 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77721] The complementary binding of VGAM2275 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2275 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2275 host target RNA into VGAM2275 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77722] It is appreciated that VGAM2275 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2275 host target genes. The mRNA of each one of this plurality of VGAM2275 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2275 RNA, herein designated VGAM RNA, and which when bound by VGAM2275 RNA causes inhibition of translation of respective one or more VGAM2275 host target proteins.

[77723] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2275 gene, herein designated VGAM GENE, on one or more VGAM2275 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77724] It is yet further appreciated that a function of VGAM2275 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2275 correlate with, and may be deduced from, the identity of the host target genes which VGAM2275 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77725] Nucleotide sequences of the VGAM2275 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2275 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2275 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2275 are further described hereinbelow with reference to Table 1.

[77726] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2275 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2275 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77727] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2275 gene, herein designated VGAM is inhibition of expression of VGAM2275 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2275 correlate with, and may be deduced from, the identity of the target genes which VGAM2275 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77728] Collagen, Type VI, Alpha 2 (COL6A2, Accession NM_058175) is a VGAM2275 host target gene. COL6A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL6A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL6A2 BINDING SITE, designated SEQ ID:27726, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77729] A function of VGAM2275 is therefore inhibition of Collagen, Type VI, Alpha 2 (COL6A2, Accession NM_058175). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A2. DKFZP434H132 (Accession

XM_057020) is another VGAM2275 host target gene. DKFZP434H132 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434H132, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434H132 BINDING SITE, designated SEQ ID:36445, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77730] Another function of VGAM2275 is therefore inhibition of DKFZP434H132 (Accession XM_057020). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434H132. DKFZP586I2223 (Accession NM_080730) is another VGAM2275 host target gene. DKFZP586I2223 BINDING SITE1 through DKFZP586I2223 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DKFZP586I2223, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586I2223 BINDING SITE1

through DKFZP586I2223 BINDING SITE3, designated SEQ ID:28017, SEQ ID:28019 and SEQ ID:17730 respectively, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77731] Another function of VGAM2275 is therefore inhibition of DKFZP586I2223 (Accession NM_080730). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586I2223. FLJ00007 (Accession XM_048928) is another VGAM2275 host target gene. FLJ00007 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00007, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00007 BINDING SITE, designated SEQ ID:35310, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77732] Another function of VGAM2275 is therefore inhibition of FLJ00007 (Accession XM_048928). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00007. FLJ23231 (Accession NM_025079) is another

VGAM2275 host target gene. FLJ23231 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23231 BINDING SITE, designated SEQ ID:24679, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77733] Another function of VGAM2275 is therefore inhibition of FLJ23231 (Accession NM_025079). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23231. MIG2 (Accession XM_051693) is another VGAM2275 host target gene. MIG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MIG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MIG2 BINDING SITE, designated SEQ ID:35863, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77734] Another function of VGAM2275 is therefore inhibition of MIG2 (Accession XM_051693). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIG2. PRO0650 (Accession NM_014137) is another VGAM2275 host target gene. PRO0650 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0650, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0650 BINDING SITE, designated SEQ ID:15403, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77735] Another function of VGAM2275 is therefore inhibition of PRO0650 (Accession NM_014137). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0650. LOC165140 (Accession XM_092406) is another VGAM2275 host target gene. LOC165140 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC165140, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC165140 BINDING SITE, designated SEQ ID:40117, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77736] Another function of VGAM2275 is therefore inhibition of LOC165140 (Accession XM_092406). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC165140. LOC197414 (Accession XM_113880) is another VGAM2275 host target gene. LOC197414 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197414, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197414 BINDING SITE, designated SEQ ID:42514, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77737] Another function of VGAM2275 is therefore inhibition of LOC197414 (Accession XM_113880). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC197414. LOC199923 (Accession XM_114057) is another VGAM2275 host target gene. LOC199923 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199923, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199923 BINDING SITE, designated SEQ ID:42669, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77738] Another function of VGAM2275 is therefore inhibition of LOC199923 (Accession XM_114057). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199923. LOC222160 (Accession XM_168431) is another VGAM2275 host target gene. LOC222160 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222160 BINDING SITE, designated SEQ ID:45167, to the nucleotide sequence of VGAM2275 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4986.

[77739] Another function of VGAM2275 is therefore inhibition of LOC222160 (Accession XM_168431). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222160. LOC255645 (Accession XM_172967) is another VGAM2275 host target gene. LOC255645 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255645, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255645 BINDING SITE, designated SEQ ID:46221, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77740] Another function of VGAM2275 is therefore inhibition of LOC255645 (Accession XM_172967). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255645. LOC90092 (Accession XM_028862) is another VGAM2275 host target gene. LOC90092 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90092, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90092 BINDING SITE, designated SEQ ID:30787, to the nucleotide sequence of VGAM2275 RNA, herein designated VGAM RNA, also designated SEQ ID:4986.

[77741] Another function of VGAM2275 is therefore inhibition of LOC90092 (Accession XM_028862). Accordingly, utilities of VGAM2275 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90092. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2276 (VGAM2276) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77742] VGAM2276 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2276 was detected is described hereinabove with reference to Figs. 1-8.

[77743] VGAM2276 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus

1. VGAM2276 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77744] VGAM2276 gene encodes a VGAM2276 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2276 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2276 precursor RNA is designated SEQ ID:2262, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2262 is located at position 30027 relative to the genome of Alcelaphine Herpesvirus 1.

[77745] VGAM2276 precursor RNA folds onto itself, forming VGAM2276 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77746] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2276 folded precursor RNA into VGAM2276 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM2276 RNA is designated SEQ ID:4987, and is provided hereinbelow with reference to the sequence listing part.

[77747] VGAM2276 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2276 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2276 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77748] VGAM2276 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2276 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2276 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2276 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2276 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77749] The complementary binding of VGAM2276 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2276 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2276 host target RNA into VGAM2276 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77750] It is appreciated that VGAM2276 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2276 host target genes. The mRNA of each one of this plurality of VGAM2276 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2276 RNA, herein designated VGAM RNA, and which when bound by VGAM2276 RNA causes inhibition of translation of respective one or more VGAM2276 host target proteins.

[77751] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2276 gene, herein designated VGAM GENE, on one or more VGAM2276 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77752] It is yet further appreciated that a function of VGAM2276 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2276 correlate with, and may be deduced from, the identity of the host target genes which VGAM2276 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77753] Nucleotide sequences of the VGAM2276 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2276 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2276 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2276 are further described hereinbelow with reference to Table 1.

[77754] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2276 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2276 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77755] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2276 gene, herein designated VGAM is inhibition of expression of VGAM2276 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2276 correlate with, and may be deduced from, the identity of the target genes which VGAM2276 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77756] Ankylosis, Progressive Homolog (mouse) (ANKH, Accession NM_054027) is a VGAM2276 host target gene. ANKH BINDING SITE1 and ANKH BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ANKH, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANKH BINDING SITE1 and ANKH

BINDING SITE2, designated SEQ ID:27635 and SEQ ID:21252 respectively, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77757] A function of VGAM2276 is therefore inhibition of Ankylosis, Progressive Homolog (mouse) (ANKH, Accession NM_054027), a gene which regulates intra- and extracellular levels of inorganic pyrophosphate (ppi), probably functioning as ppi transporter. Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKH. The function of ANKH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1247.Deleted In Lung and Esophageal Cancer 1 (DLEC1, Accession NM_007336) is another VGAM2276 host target gene. DLEC1 BINDING SITE1 and DLEC1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DLEC1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLEC1 BINDING SITE1 and DLEC1 BINDING SITE2, desig-

nated SEQ ID:14264 and SEQ ID:14271 respectively, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77758] Another function of VGAM2276 is therefore inhibition of Deleted In Lung and Esophageal Cancer 1 (DLEC1, Accession NM_007336). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLEC1. LENG4 (Accession NM_024298) is another VGAM2276 host target gene. LENG4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LENG4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LENG4 BINDING SITE, designated SEQ ID:23586, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77759] Another function of VGAM2276 is therefore inhibition of LENG4 (Accession NM_024298), a gene which may be a transmembrane protein. Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LENG4.

The function of LENG4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM259.Lipoprotein Lipase (LPL, Accession NM_000237) is another VGAM2276 host target gene. LPL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LPL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LPL BINDING SITE, designated SEQ ID:5753, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77760] Another function of VGAM2276 is therefore inhibition of Lipoprotein Lipase (LPL, Accession NM_000237), a gene which is the hydrolysis of triglycerides of circulating chylomicrons and very low density lipoproteins (vldl). the enzyme functions in the presence of apolipoprotein c-2 on the luminal surface of vascular. Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LPL. The function of LPL and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to VGAM55.Mannosidase, Alpha, Class 2C, Member 1 (MAN2C1, Accession XM_053585) is another VGAM2276 host target gene. MAN2C1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAN2C1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAN2C1 BINDING SITE, designated SEQ ID:36102, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77761] Another function of VGAM2276 is therefore inhibition of Mannosidase, Alpha, Class 2C, Member 1 (MAN2C1, Accession XM_053585), a gene which is Strongly similar to a region of rat ER alpha-mannosidase. Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAN2C1. The function of MAN2C1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM958.Membrane Protein, Palmitoylated 2 (MAGUK p55 subfamily member 2) (MPP2, Acces-

sion XM_008355) is another VGAM2276 host target gene. MPP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MPP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MPP2 BINDING SITE, designated SEQ ID:30082, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77762] Another function of VGAM2276 is therefore inhibition of Membrane Protein, Palmitoylated 2 (MAGUK p55 subfamily member 2) (MPP2, Accession XM_008355). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPP2. poly(A) Binding Protein, Cytoplasmic 1 (PABPC1, Accession NM_002568) is another VGAM2276 host target gene. PABPC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PABPC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PABPC1 BINDING SITE, designated SEQ ID:8419, to the nucleotide sequence of

VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77763] Another function of VGAM2276 is therefore inhibition of poly(A) Binding Protein, Cytoplasmic 1 (PABPC1, Accession NM_002568), a gene which involves in cytoplasmic regulatory processes of mRNA metabolism. Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PABPC1. The function of PABPC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM280.Solute Carrier Family 13 (sodium-dependent dicarboxylate transporter), Member 3 (SLC13A3, Accession XM_017841) is another VGAM2276 host target gene. SLC13A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC13A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC13A3 BINDING SITE, designated SEQ ID:30329, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77764] Another function of VGAM2276 is therefore inhibition of Solute Carrier Family 13 (sodium-dependent dicarboxylate transporter), Member 3 (SLC13A3, Accession XM_017841). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC13A3. Steroidogenic Acute Regulatory Protein (STAR, Accession NM_000349) is another VGAM2276 host target gene. STAR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STAR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAR BINDING SITE, designated SEQ ID:5904, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77765] Another function of VGAM2276 is therefore inhibition of Steroidogenic Acute Regulatory Protein (STAR, Accession NM_000349). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAR. Suppressor of Fused Homolog (Drosophila) (SUFU, Accession NM_016169) is another VGAM2276 host target gene. SUFU BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SUFU, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SUFU BINDING SITE, designated SEQ ID:18258, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77766] Another function of VGAM2276 is therefore inhibition of Suppressor of Fused Homolog (Drosophila) (SUFU, Accession NM_016169). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUFU. Testis Enhanced Gene Transcript (BAX inhibitor 1) (TEGT, Accession XM_035490) is another VGAM2276 host target gene. TEGT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEGT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEGT BINDING SITE, designated SEQ ID:32275, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77767] Another function of VGAM2276 is therefore inhibition of Testis Enhanced Gene Transcript (BAX inhibitor 1) (TEGT, Accession XM_035490), a gene which is a suppressor of apoptosis. Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEGT. The function of TEGT has been established by previous studies. Walter et al. (1994) identified a single-copy gene in the rat for which 2 transcripts were found in each organ tested. The shorter transcript of about 1 kb was highly abundant in the postpubertal testis. The gene was therefore designated Tegt (for testis enhanced gene transcript). Using a rat Tegt probe, Walter et al. (1995) screened a human testis cDNA library and isolated the human homolog of the rat Tegt gene. The gene in the rat and humans does not belong to any known gene family of vertebrates. The deduced amino acid sequence of the gene and a bacterial protein of unknown function show low but significant homology and very similar hydrophobicity profiles. The 2 different transcripts are due to alternative usage of 2 polyadenylation sites. The presence of a nuclear targeting motif indicates that the gene product must localize to the nucleus. By Southern blot analysis of DNA from rat/human somatic

cell hybrids, Walter et al. (1995) mapped the TEGT gene to human chromosome 12. Fluorescence in situ hybridization refined the assignment to 12q12-q13. This localization agrees with the assignment of the gene to rat chromosome 7 and to mouse chromosome 15. The mammalian proapoptotic protein BAX (OMIM Ref. No. 600040) confers a lethal phenotype when expressed in yeast. By exploiting this phenotype, Xu and Reed (1998) identified a human BAX inhibitor, BI1. BI1 is an evolutionarily conserved integral membrane protein containing 6 predicted membrane-spanning segments and is predominantly localized to intracellular membranes, similar to BCL2 family proteins. The predicted protein contains 237 amino acids and is identical to TEGT. BI1 can interact with BCL2 (OMIM Ref. No. 151430) and BCLX(L) but not BAX or BAK, as demonstrated by in vivo crosslinking and coimmunoprecipitation studies. When overexpressed in mammalian cells, BI1 suppressed apoptosis induced by BAX, etoposide, staurosporine, and growth factor deprivation, but not by FAS (CD95). Conversely, BI1 antisense induced apoptosis. BI1 thus represents a regulator of cell death pathways controlled by BCL2 and BAX.

[77768] Full details of the abovementioned studies are described

in the following publications, the disclosure of which are hereby incorporated by reference:

[77769] Walter, L.; Marynen, P.; Szpirer, J.; Levan, G.; Gunther, E. : Identification of a novel conserved human gene, TEGT. Genomics 28: 301-304, 1995. ; and

[77770] Xu, Q.; Reed, J. C. : Bax inhibitor-1, a mammalian apoptosis suppressor identified by functional screening in yeast. Molec. Cell 1: 337-346, 1998.

[77771] Further studies establishing the function and utilities of TEGT are found in John Hopkins OMIM database record ID 600748, and in sited publications numbered 7568-7570 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.DKFZp434K2435 (Accession NM_032256) is another VGAM2276 host target gene. DKFZp434K2435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434K2435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434K2435 BINDING SITE, designated SEQ ID:26000, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77772] Another function of VGAM2276 is therefore inhibition of DKFZp434K2435 (Accession NM_032256). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434K2435. DKFZp547E052 (Accession NM_032276) is another VGAM2276 host target gene. DKFZp547E052 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp547E052, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547E052 BINDING SITE, designated SEQ ID:26031, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77773] Another function of VGAM2276 is therefore inhibition of DKFZp547E052 (Accession NM_032276). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547E052. FLJ12287 (Accession NM_022367) is another VGAM2276 host target gene. FLJ12287 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12287, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12287 BINDING SITE, designated SEQ ID:22755, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77774] Another function of VGAM2276 is therefore inhibition of FLJ12287 (Accession NM_022367). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12287. FLJ13162 (Accession NM_025002) is another VGAM2276 host target gene. FLJ13162 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13162 BINDING SITE, designated SEQ ID:24573, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77775] Another function of VGAM2276 is therefore inhibition of FLJ13162 (Accession NM_025002). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ13162. FLJ14743 (Accession XM_042708) is another VGAM2276 host target gene. FLJ14743 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14743, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14743 BINDING SITE, designated SEQ ID:33761, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77776] Another function of VGAM2276 is therefore inhibition of FLJ14743 (Accession XM_042708). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14743. FLJ20739 (Accession XM_042197) is another VGAM2276 host target gene. FLJ20739 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20739, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20739 BINDING SITE, designated SEQ ID:33703, to the nucleotide

sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77777] Another function of VGAM2276 is therefore inhibition of FLJ20739 (Accession XM_042197). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20739. KIAA0082 (Accession XM_166400) is another VGAM2276 host target gene. KIAA0082 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0082, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0082 BINDING SITE, designated SEQ ID:44264, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77778] Another function of VGAM2276 is therefore inhibition of KIAA0082 (Accession XM_166400). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0082. KIAA0494 (Accession NM_014774) is another VGAM2276 host target gene. KIAA0494 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA0494, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0494 BINDING SITE, designated SEQ ID:16588, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77779] Another function of VGAM2276 is therefore inhibition of KIAA0494 (Accession NM_014774). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0494. KIAA0872 (Accession NM_014940) is another VGAM2276 host target gene. KIAA0872 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0872, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0872 BINDING SITE, designated SEQ ID:17248, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77780] Another function of VGAM2276 is therefore inhibition of KIAA0872 (Accession NM_014940). Accordingly, utilities

of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0872. KIAA1344 (Accession XM_051699) is another VGAM2276 host target gene. KIAA1344 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1344, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1344 BINDING SITE, designated SEQ ID:35873, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77781] Another function of VGAM2276 is therefore inhibition of KIAA1344 (Accession XM_051699). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1344. KIAA1416 (Accession XM_098762) is another VGAM2276 host target gene. KIAA1416 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1416 BINDING SITE, designated SEQ ID:41804, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77782] Another function of VGAM2276 is therefore inhibition of KIAA1416 (Accession XM_098762). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1416. KIAA1821 (Accession XM_050101) is another VGAM2276 host target gene. KIAA1821 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1821, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1821 BINDING SITE, designated SEQ ID:35554, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77783] Another function of VGAM2276 is therefore inhibition of KIAA1821 (Accession XM_050101). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1821. KIAA1870 (Accession NM_032888) is another VGAM2276 host target gene. KIAA1870 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1870, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1870 BINDING SITE, designated SEQ ID:26712, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77784] Another function of VGAM2276 is therefore inhibition of KIAA1870 (Accession NM_032888). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1870. MGC10334 (Accession NM_030575) is another VGAM2276 host target gene. MGC10334 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC10334, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10334 BINDING SITE, designated SEQ ID:24949, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77785] Another function of VGAM2276 is therefore inhibition of

MGC10334 (Accession NM_030575). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10334. Paralemmin (PALM, Accession NM_002579) is another VGAM2276 host target gene. PALM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PALM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PALM BINDING SITE, designated SEQ ID:8438, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77786] Another function of VGAM2276 is therefore inhibition of Paralemmin (PALM, Accession NM_002579). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PALM. Placenta-specific 3 (PLAC3, Accession XM_045115) is another VGAM2276 host target gene. PLAC3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PLAC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of PLAC3 BINDING SITE, designated SEQ ID:34365, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77787] Another function of VGAM2276 is therefore inhibition of Placenta-specific 3 (PLAC3, Accession XM_045115). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAC3. PRO2015 (Accession NM_018512) is another VGAM2276 host target gene. PRO2015 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2015, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2015 BINDING SITE, designated SEQ ID:20586, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77788] Another function of VGAM2276 is therefore inhibition of PRO2015 (Accession NM_018512). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

PRO2015. Signal-regulatory Protein Beta 1 (SIRPB1, Accession NM_006065) is another VGAM2276 host target gene. SIRPB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIRPB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIRPB1 BINDING SITE, designated SEQ ID:12711, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77789] Another function of VGAM2276 is therefore inhibition of Signal-regulatory Protein Beta 1 (SIRPB1, Accession NM_006065). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIRPB1. TU3A (Accession NM_007177) is another VGAM2276 host target gene. TU3A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TU3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TU3A BINDING SITE, designated SEQ ID:14036,

to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77790] Another function of VGAM2276 is therefore inhibition of TU3A (Accession NM_007177). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TU3A. ZFP100 (Accession XM_046390) is another VGAM2276 host target gene. ZFP100 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZFP100, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZFP100 BINDING SITE, designated SEQ ID:34707, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77791] Another function of VGAM2276 is therefore inhibition of ZFP100 (Accession XM_046390). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP100. LOC129642 (Accession NM_138799) is another VGAM2276 host target gene. LOC129642 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by LOC129642, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC129642 BINDING SITE, designated SEQ ID:29021, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77792] Another function of VGAM2276 is therefore inhibition of LOC129642 (Accession NM_138799). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129642. LOC143666 (Accession XM_096465) is another VGAM2276 host target gene. LOC143666 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143666, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143666 BINDING SITE, designated SEQ ID:40371, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77793] Another function of VGAM2276 is therefore inhibition of LOC143666 (Accession XM_096465). Accordingly, utilities

of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143666. LOC147229 (Accession XM_085742) is another VGAM2276 host target gene. LOC147229 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147229 BINDING SITE, designated SEQ ID:38322, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77794] Another function of VGAM2276 is therefore inhibition of LOC147229 (Accession XM_085742). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147229. LOC150319 (Accession XM_086816) is another VGAM2276 host target gene. LOC150319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150319, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC150319 BINDING SITE, designated SEQ ID:38892, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77795] Another function of VGAM2276 is therefore inhibition of LOC150319 (Accession XM_086816). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150319. LOC157918 (Accession XM_098842) is another VGAM2276 host target gene. LOC157918 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157918, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157918 BINDING SITE, designated SEQ ID:41895, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77796] Another function of VGAM2276 is therefore inhibition of LOC157918 (Accession XM_098842). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157918. LOC157919 (Accession XM_088420) is another VGAM2276 host target gene. LOC157919 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157919, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157919 BINDING SITE, designated SEQ ID:39682, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77797] Another function of VGAM2276 is therefore inhibition of LOC157919 (Accession XM_088420). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157919. LOC200197 (Accession XM_114148) is another VGAM2276 host target gene. LOC200197 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200197, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200197 BINDING SITE, designated SEQ ID:42731, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77798] Another function of VGAM2276 is therefore inhibition of

LOC200197 (Accession XM_114148). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200197. LOC200583 (Accession XM_114265) is another VGAM2276 host target gene. LOC200583 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200583, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200583 BINDING SITE, designated SEQ ID:42822, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77799] Another function of VGAM2276 is therefore inhibition of LOC200583 (Accession XM_114265). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200583. LOC202052 (Accession XM_117355) is another VGAM2276 host target gene. LOC202052 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202052, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC202052 BINDING SITE, designated SEQ ID:43409, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77800] Another function of VGAM2276 is therefore inhibition of LOC202052 (Accession XM_117355). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202052. LOC220827 (Accession XM_166052) is another VGAM2276 host target gene. LOC220827 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220827, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220827 BINDING SITE, designated SEQ ID:43844, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77801] Another function of VGAM2276 is therefore inhibition of LOC220827 (Accession XM_166052). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220827. LOC222008 (Accession XM_168361) is an-

other VGAM2276 host target gene. LOC222008 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222008, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222008 BINDING SITE, designated SEQ ID:45126, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77802] Another function of VGAM2276 is therefore inhibition of LOC222008 (Accession XM_168361). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222008. LOC92017 (Accession XM_042234) is another VGAM2276 host target gene. LOC92017 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92017, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92017 BINDING SITE, designated SEQ ID:33710, to the nucleotide sequence of VGAM2276 RNA, herein designated VGAM RNA, also designated SEQ ID:4987.

[77803] Another function of VGAM2276 is therefore inhibition of LOC92017 (Accession XM_042234). Accordingly, utilities of VGAM2276 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92017. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2277 (VGAM2277) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77804] VGAM2277 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2277 was detected is described hereinabove with reference to Figs. 1-8.

[77805] VGAM2277 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2277 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77806] VGAM2277 gene encodes a VGAM2277 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2277 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2277 precursor RNA is designated SEQ ID:2263, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2263 is located at position 27286 relative to the genome of Alcelaphine Herpesvirus 1.

[77807] VGAM2277 precursor RNA folds onto itself, forming VGAM2277 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77808] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2277 folded precursor RNA into VGAM2277 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2277 RNA is designated SEQ ID:4988, and is provided hereinbelow with reference to the sequence listing part.

[77809] VGAM2277 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2277 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2277 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77810] VGAM2277 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2277 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2277 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2277 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2277 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77811] The complementary binding of VGAM2277 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2277 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2277 host target RNA into VGAM2277 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77812] It is appreciated that VGAM2277 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2277 host target genes. The mRNA of each one of this plurality of VGAM2277 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2277 RNA, herein designated VGAM RNA, and which when bound by VGAM2277 RNA causes inhibition of translation of respective one or more VGAM2277 host target proteins.

[77813] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2277 gene, herein designated VGAM GENE, on one or more VGAM2277 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77814] It is yet further appreciated that a function of VGAM2277 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2277 correlate with, and may be deduced from, the identity of the host target genes which VGAM2277 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77815] Nucleotide sequences of the VGAM2277 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2277 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2277 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2277 are further described hereinbelow with reference to Table 1.

[77816] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2277 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2277 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[77817] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2277 gene, herein designated VGAM is inhibition of expression of VGAM2277 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2277 correlate with, and may be deduced from, the identity of the target genes which VGAM2277 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77818] ATPase, Aminophospholipid Transporter-like, Class I, Type 8A, Member 2 (ATP8A2, Accession XM_167916) is a VGAM2277 host target gene. ATP8A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP8A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP8A2 BINDING SITE, designated SEQ ID:44920, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77819] A function of VGAM2277 is therefore inhibition of ATPase, Aminophospholipid Transporter-like, Class I, Type 8A, Member 2 (ATP8A2, Accession XM_167916). Accordingly,

utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8A2. Filamin B, Beta (actin binding protein 278) (FLNB, Accession XM_030806) is another VGAM2277 host target gene. FLNB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLNB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLNB BINDING SITE, designated SEQ ID:31138, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77820] Another function of VGAM2277 is therefore inhibition of Filamin B, Beta (actin binding protein 278) (FLNB, Accession XM_030806), a gene which Filamin B, beta; binds actin, interacts with cytoplasmic domain of Ibalpha. Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLNB. The function of FLNB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM416.Myxovirus (influenza

virus) Resistance 2 (mouse) (MX2, Accession NM_002463) is another VGAM2277 host target gene. MX2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MX2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MX2 BINDING SITE, designated SEQ ID:8294, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77821] Another function of VGAM2277 is therefore inhibition of Myxovirus (influenza virus) Resistance 2 (mouse) (MX2, Accession NM_002463). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MX2. PAG (Accession NM_018440) is another VGAM2277 host target gene. PAG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAG BINDING SITE, designated SEQ ID:20511, to the nucleotide sequence of VGAM2277 RNA,

herein designated VGAM RNA, also designated SEQ ID:4988.

[77822] Another function of VGAM2277 is therefore inhibition of PAG (Accession NM_018440). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAG. Protocadherin 9 (PCDH9, Accession XM_096054) is another VGAM2277 host target gene. PCDH9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PCDH9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH9 BINDING SITE, designated SEQ ID:40293, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77823] Another function of VGAM2277 is therefore inhibition of Protocadherin 9 (PCDH9, Accession XM_096054). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH9. Ribonuclease/angiogenin Inhibitor (RNH, Accession NM_002939) is another VGAM2277 host target gene. RNH BINDING SITE is HOST TARGET binding

site found in the 5` untranslated region of mRNA encoded by RNH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNH BINDING SITE, designated SEQ ID:8843, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77824] Another function of VGAM2277 is therefore inhibition of Ribonuclease/angiogenin Inhibitor (RNH, Accession NM_002939), a gene which is an inhibitor of pancreatic rnase and angiogenin. may also function in the modulation of cellular activities. Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNH. The function of RNH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM484.Tumor Necrosis Factor (ligand) Superfamily, Member 8 (TNFSF8, Accession NM_001244) is another VGAM2277 host target gene. TNFSF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFSF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFSF8 BINDING SITE, designated SEQ ID:6915, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77825] Another function of VGAM2277 is therefore inhibition of Tumor Necrosis Factor (ligand) Superfamily, Member 8 (TNFSF8, Accession NM_001244), a gene which cytokine that binds to tnfrsf8/cd30. induces proliferation of t cells. Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFSF8. The function of TNFSF8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM655.ARP3 Actin-related Protein 3 Homolog (yeast) (ACTR3, Accession NM_005721) is another VGAM2277 host target gene. ACTR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ACTR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACTR3 BINDING SITE, designated SEQ

ID:12273, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77826] Another function of VGAM2277 is therefore inhibition of ARP3 Actin-related Protein 3 Homolog (yeast) (ACTR3, Accession NM_005721). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACTR3. ERp44 (Accession XM_088476) is another VGAM2277 host target gene. ERp44 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERp44, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERp44 BINDING SITE, designated SEQ ID:39721, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77827] Another function of VGAM2277 is therefore inhibition of ERp44 (Accession XM_088476). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERp44. FLJ10330 (Accession NM_018061) is another VGAM2277

host target gene. FLJ10330 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10330, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10330 BINDING SITE, designated SEQ ID:19832, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77828] Another function of VGAM2277 is therefore inhibition of FLJ10330 (Accession NM_018061). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10330. FLJ10849 (Accession NM_018243) is another VGAM2277 host target gene. FLJ10849 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10849, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10849 BINDING SITE, designated SEQ ID:20203, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77829] Another function of VGAM2277 is therefore inhibition of FLJ10849 (Accession NM_018243). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10849. FLJ23121 (Accession NM_024694) is another VGAM2277 host target gene. FLJ23121 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23121 BINDING SITE, designated SEQ ID:24003, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77830] Another function of VGAM2277 is therefore inhibition of FLJ23121 (Accession NM_024694). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23121. FLJ23519 (Accession NM_032240) is another VGAM2277 host target gene. FLJ23519 BINDING SITE1 and FLJ23519 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ23519, corresponding to HOST TARGET binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23519 BINDING SITE1 and FLJ23519 BINDING SITE2, designated SEQ ID:25973 and SEQ ID:34306 respectively, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77831] Another function of VGAM2277 is therefore inhibition of FLJ23519 (Accession NM_032240). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23519. KIAA1130 (Accession XM_031104) is another VGAM2277 host target gene. KIAA1130 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1130, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1130 BINDING SITE, designated SEQ ID:31279, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77832] Another function of VGAM2277 is therefore inhibition of KIAA1130 (Accession XM_031104). Accordingly, utilities

of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1130. KIAA1238 (Accession XM_048675) is another VGAM2277 host target gene. KIAA1238 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1238, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1238 BINDING SITE, designated SEQ ID:35216, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77833] Another function of VGAM2277 is therefore inhibition of KIAA1238 (Accession XM_048675). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1238. LAP1B (Accession XM_035429) is another VGAM2277 host target gene. LAP1B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LAP1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAP1B BINDING SITE,

designated SEQ ID:32262, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77834] Another function of VGAM2277 is therefore inhibition of LAP1B (Accession XM_035429). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAP1B. MGC14289 (Accession NM_080660) is another VGAM2277 host target gene. MGC14289 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC14289, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC14289 BINDING SITE, designated SEQ ID:27947, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77835] Another function of VGAM2277 is therefore inhibition of MGC14289 (Accession NM_080660). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14289. Purinergic Receptor P2X, Ligand-gated Ion Channel, 1 (P2RX1, Accession XM_040635) is another

VGAM2277 host target gene. P2RX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P2RX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P2RX1 BINDING SITE, designated SEQ ID:33351, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77836] Another function of VGAM2277 is therefore inhibition of Purinergic Receptor P2X, Ligand-gated Ion Channel, 1 (P2RX1, Accession XM_040635). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RX1. SYNCOILIN (Accession NM_030786) is another VGAM2277 host target gene. SYNCOILIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYNCOILIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYNCOILIN BINDING SITE, designated SEQ ID:25080, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA,

also designated SEQ ID:4988.

[77837] Another function of VGAM2277 is therefore inhibition of SYNCOILIN (Accession NM_030786). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYNCOILIN. LOC132880 (Accession XM_059609) is another VGAM2277 host target gene. LOC132880 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC132880, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132880 BINDING SITE, designated SEQ ID:37030, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77838] Another function of VGAM2277 is therefore inhibition of LOC132880 (Accession XM_059609). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132880. LOC158014 (Accession XM_088442) is another VGAM2277 host target gene. LOC158014 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158014, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158014 BINDING SITE, designated SEQ ID:39691, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77839] Another function of VGAM2277 is therefore inhibition of LOC158014 (Accession XM_088442). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158014. LOC158357 (Accession XM_088553) is another VGAM2277 host target gene. LOC158357 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158357, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158357 BINDING SITE, designated SEQ ID:39819, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77840] Another function of VGAM2277 is therefore inhibition of LOC158357 (Accession XM_088553). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC158357. LOC162137 (Accession XM_102426) is another VGAM2277 host target gene. LOC162137 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC162137, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162137 BINDING SITE, designated SEQ ID:42113, to the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77841] Another function of VGAM2277 is therefore inhibition of LOC162137 (Accession XM_102426). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162137. LOC253596 (Accession XM_170934) is another VGAM2277 host target gene. LOC253596 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253596, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253596 BINDING SITE, designated SEQ ID:45722, to

the nucleotide sequence of VGAM2277 RNA, herein designated VGAM RNA, also designated SEQ ID:4988.

[77842] Another function of VGAM2277 is therefore inhibition of LOC253596 (Accession XM_170934). Accordingly, utilities of VGAM2277 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253596. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2278 (VGAM2278) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77843] VGAM2278 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2278 was detected is described hereinabove with reference to Figs. 1-8.

[77844] VGAM2278 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2278 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77845] VGAM2278 gene encodes a VGAM2278 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2278 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2278 precursor RNA is designated SEQ ID:2264, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2264 is located at position 29724 relative to the genome of Alcelaphine Herpesvirus 1.

[77846] VGAM2278 precursor RNA folds onto itself, forming VGAM2278 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77847] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2278 folded precursor RNA into VGAM2278 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2278 RNA is designated SEQ ID:4989, and is provided hereinbelow with reference to the sequence listing part.

[77848] VGAM2278 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2278 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2278 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77849] VGAM2278 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2278 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2278 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2278 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2278 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77850] The complementary binding of VGAM2278 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2278 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2278 host target RNA into VGAM2278 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77851] It is appreciated that VGAM2278 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2278 host target genes. The mRNA of each one of this plurality of VGAM2278 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2278 RNA, herein designated VGAM RNA, and which when bound by VGAM2278 RNA causes inhibition of translation of respective one or more VGAM2278 host target proteins.

[77852] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2278 gene, herein designated VGAM GENE, on one or more VGAM2278 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77853] It is yet further appreciated that a function of VGAM2278 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2278 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2278 correlate with, and may be deduced from, the identity of the host target genes which VGAM2278 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77854] Nucleotide sequences of the VGAM2278 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2278 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2278 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2278 are further described hereinbelow with reference to Table 1.

[77855] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2278 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2278 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77856] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2278 gene, herein designated VGAM is inhibition of expression of VGAM2278 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2278 correlate with, and may be deduced from, the identity of the target genes which VGAM2278 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77857] LOC200339 (Accession XM_117226) is a VGAM2278 host target gene. LOC200339 BINDING SITE1 and LOC200339 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC200339, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200339 BINDING SITE1 and LOC200339 BINDING SITE2, designated SEQ ID:43301 and SEQ ID:43302 respectively, to the nucleotide sequence of VGAM2278 RNA, herein designated VGAM RNA, also designated SEQ ID:4989.

[77858] A function of VGAM2278 is therefore inhibition of LOC200339 (Accession XM_117226). Accordingly, utilities of VGAM2278 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200339. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2279 (VGAM2279) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77859] VGAM2279 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2279 was detected is described hereinabove with reference to Figs. 1-8.

[77860] VGAM2279 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2279 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77861] VGAM2279 gene encodes a VGAM2279 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2279 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2279 precursor RNA is designated SEQ ID:2265, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2265 is located at position 26039 relative to the genome of Alcelaphine Herpesvirus 1.

[77862] VGAM2279 precursor RNA folds onto itself, forming VGAM2279 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77863] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2279 folded precursor RNA into VGAM2279 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2279 RNA is designated SEQ ID:4990, and is provided hereinbelow with reference to the sequence listing part.

[77864] VGAM2279 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2279 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2279 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77865] VGAM2279 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2279 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2279 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2279 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2279 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77866] The complementary binding of VGAM2279 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2279 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2279 host target RNA into VGAM2279 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77867] It is appreciated that VGAM2279 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2279 host target genes. The mRNA of each one of this plurality of VGAM2279 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2279 RNA, herein designated VGAM RNA, and which when bound by VGAM2279 RNA causes inhibition of translation of respective one or more VGAM2279 host target proteins.

[77868] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2279 gene, herein designated VGAM GENE, on one or more VGAM2279 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77869] It is yet further appreciated that a function of VGAM2279 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2279 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2279 correlate with, and may be deduced from, the identity of the host target genes which VGAM2279 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77870] Nucleotide sequences of the VGAM2279 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2279 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2279 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2279 are further described hereinbelow with reference to Table 1.

[77871] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2279 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2279 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[77872] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2279 gene, herein designated VGAM is inhibition of expression of VGAM2279 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2279 correlate with, and may be deduced from, the identity of the target genes which VGAM2279 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77873] Guanine Nucleotide Binding Protein (G protein), Alpha Z Polypeptide (GNAZ, Accession NM_002073) is a VGAM2279 host target gene. GNAZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNAZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNAZ BINDING SITE, designated SEQ ID:7844, to the nucleotide sequence of VGAM2279 RNA, herein designated VGAM RNA, also designated SEQ ID:4990.

[77874] A function of VGAM2279 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Alpha Z Polypeptide (GNAZ, Accession NM_002073), a gene which func-

tions as modulator or transducer in various transmembrane signaling systems. Accordingly, utilities of VGAM2279 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNAZ. The function of GNAZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1508.Zinc Finger Protein 265 (ZNF265, Accession NM_005455) is another VGAM2279 host target gene. ZNF265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF265 BINDING SITE, designated SEQ ID:11939, to the nucleotide sequence of VGAM2279 RNA, herein designated VGAM RNA, also designated SEQ ID:4990.

[77875] Another function of VGAM2279 is therefore inhibition of Zinc Finger Protein 265 (ZNF265, Accession NM_005455). Accordingly, utilities of VGAM2279 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF265. BCL2-associated Athano-

gene 2 (BAG2, Accession XM_165779) is another VGAM2279 host target gene. BAG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAG2 BINDING SITE, designated SEQ ID:43751, to the nucleotide sequence of VGAM2279 RNA, herein designated VGAM RNA, also designated SEQ ID:4990.

[77876] Another function of VGAM2279 is therefore inhibition of BCL2-associated Athanogene 2 (BAG2, Accession XM_165779). Accordingly, utilities of VGAM2279 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAG2. DEFCAP (Accession NM_033004) is another VGAM2279 host target gene. DEFCAP BINDING SITE1 through DEFCAP BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DEFCAP, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DEFCAP BINDING SITE1 through DEFCAP BINDING SITE3, designated SEQ

ID:26891, SEQ ID:26892 and SEQ ID:17200 respectively, to the nucleotide sequence of VGAM2279 RNA, herein designated VGAM RNA, also designated SEQ ID:4990.

[77877] Another function of VGAM2279 is therefore inhibition of DEFCAP (Accession NM_033004). Accordingly, utilities of VGAM2279 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DEFCAP. FLJ21140 (Accession NM_024776) is another VGAM2279 host target gene. FLJ21140 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ21140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21140 BINDING SITE, designated SEQ ID:24138, to the nucleotide sequence of VGAM2279 RNA, herein designated VGAM RNA, also designated SEQ ID:4990.

[77878] Another function of VGAM2279 is therefore inhibition of FLJ21140 (Accession NM_024776). Accordingly, utilities of VGAM2279 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21140. RALGPS1A (Accession NM_014636) is another VGAM2279 host target gene. RALGPS1A BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RALGPS1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RALGPS1A BINDING SITE, designated SEQ ID:16015, to the nucleotide sequence of VGAM2279 RNA, herein designated VGAM RNA, also designated SEQ ID:4990.

[77879] Another function of VGAM2279 is therefore inhibition of RALGPS1A (Accession NM_014636). Accordingly, utilities of VGAM2279 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RALGPS1A. Thioesterase, Adipose Associated (THEA, Accession XM_038922) is another VGAM2279 host target gene. THEA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by THEA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of THEA BINDING SITE, designated SEQ ID:32945, to the nucleotide sequence of VGAM2279 RNA, herein designated VGAM RNA, also designated SEQ ID:4990.

[77880] Another function of VGAM2279 is therefore inhibition of

Thioesterase, Adipose Associated (THEA, Accession XM_038922). Accordingly, utilities of VGAM2279 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THEA. LOC146515 (Accession XM_085493) is another VGAM2279 host target gene. LOC146515 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146515, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146515 BINDING SITE, designated SEQ ID:38191, to the nucleotide sequence of VGAM2279 RNA, herein designated VGAM RNA, also designated SEQ ID:4990.

[77881] Another function of VGAM2279 is therefore inhibition of LOC146515 (Accession XM_085493). Accordingly, utilities of VGAM2279 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146515. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2280 (VGAM2280) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[77882] VGAM2280 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2280 was detected is described hereinabove with reference to Figs. 1-8.

[77883] VGAM2280 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Alcelaphine Herpesvirus 1. VGAM2280 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77884] VGAM2280 gene encodes a VGAM2280 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2280 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2280 precursor RNA is designated SEQ ID:2266, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2266 is located at position 27049 relative to the genome of Alcelaphine Herpesvirus 1.

[77885] VGAM2280 precursor RNA folds onto itself, forming VGAM2280 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77886] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2280 folded precursor RNA into VGAM2280 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2280 RNA is designated SEQ ID:4991, and is provided hereinbelow with reference to the sequence listing part.

[77887] VGAM2280 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2280 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2280 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77888] VGAM2280 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2280 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2280 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2280 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2280 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77889] The complementary binding of VGAM2280 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2280 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2280 host target RNA into VGAM2280 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77890] It is appreciated that VGAM2280 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2280 host target genes. The mRNA of each one of this plurality of VGAM2280 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2280 RNA, herein designated VGAM RNA, and which when bound by VGAM2280 RNA causes inhibition of translation of respective one or more VGAM2280 host target proteins.

[77891] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2280 gene, herein designated VGAM GENE, on one or more VGAM2280 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77892] It is yet further appreciated that a function of VGAM2280 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of viral infection by Alcelaphine Herpesvirus 1. Specific functions, and accordingly utilities, of VGAM2280 correlate with, and may be deduced from, the identity of the host target genes which VGAM2280 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[77893] Nucleotide sequences of the VGAM2280 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2280 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2280 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2280 are further described hereinbelow with reference to Table 1.

[77894] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2280 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2280 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77895] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2280 gene, herein designated VGAM is inhibition of expression of VGAM2280 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2280 correlate with, and may be deduced from, the identity of the target genes which VGAM2280 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77896] ATPase, Cu++ Transporting, Alpha Polypeptide (Menkes syndrome) (ATP7A, Accession NM_000052) is a VGAM2280 host target gene. ATP7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:5491, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77897] A function of VGAM2280 is therefore inhibition of ATPase, Cu++ Transporting, Alpha Polypeptide (Menkes syndrome) (ATP7A, Accession NM_000052). Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7A. Dachshund Homolog (Drosophila) (DACH, Accession NM_080759) is another VGAM2280 host target gene. DACH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DACH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of DACH BINDING SITE, designated SEQ ID:28043, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77898] Another function of VGAM2280 is therefore inhibition of Dachshund Homolog (Drosophila) (DACH, Accession NM_080759), a gene which regulates early progenitor cell proliferation during retinogenesis and pituitary development . Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DACH. The function of DACH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM260.Faciogenital Dysplasia (Aarskog-Scott syndrome) (FGD1, Accession NM_004463) is another VGAM2280 host target gene. FGD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGD1 BINDING SITE, designated SEQ ID:10767, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4991.

[77899] Another function of VGAM2280 is therefore inhibition of Faciogenital Dysplasia (Aarskog-Scott syndrome) (FGD1, Accession NM_004463), a gene which activates the ras-like family of rho- and rac proteins by exchanging bound gdp for free gtp. Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGD1. The function of FGD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1593.Glycogenin (GYG, Accession NM_004130) is another VGAM2280 host target gene. GYG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GYG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GYG BINDING SITE, designated SEQ ID:10337, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77900] Another function of VGAM2280 is therefore inhibition of Glycogenin (GYG, Accession NM_004130), a gene which

primes de novo glycogen synthesis. Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GYG. The function of GYG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM777.PCTAIRE Protein Kinase 1 (PCTK1, Accession NM_006201) is another VGAM2280 host target gene. PCTK1 BINDING SITE1 through PCTK1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCTK1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCTK1 BINDING SITE1 through PCTK1 BINDING SITE3, designated SEQ ID:12871, SEQ ID:26906 and SEQ ID:26912 respectively, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77901] Another function of VGAM2280 is therefore inhibition of PCTAIRE Protein Kinase 1 (PCTK1, Accession NM_006201), a gene which may play a role in signal transduction cascades in terminally differentiated cells. Accordingly, utilities of VGAM2280 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with PCTK1. The function of PCTK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM75.RalA Binding Protein 1 (RALBP1, Accession NM_006788) is another VGAM2280 host target gene. RALBP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RALBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RALBP1 BINDING SITE, designated SEQ ID:13658, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77902] Another function of VGAM2280 is therefore inhibition of RalA Binding Protein 1 (RALBP1, Accession NM_006788), a gene which plays a role in signal transduction and catalyzes the transport of glutathione conjugates and xenobiotics. Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RALBP1. The function of RALBP1 and its association with various diseases and clin-

ical conditions, has been established by previous studies, as described hereinabove with reference to VGAM345.Solute Carrier Family 35 (CMP-sialic acid transporter), Member 1 (SLC35A1, Accession NM_006416) is another VGAM2280 host target gene. SLC35A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC35A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC35A1 BINDING SITE, designated SEQ ID:13125, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77903] Another function of VGAM2280 is therefore inhibition of Solute Carrier Family 35 (CMP-sialic acid transporter), Member 1 (SLC35A1, Accession NM_006416), a gene which transports cmp-sialic acid from the cytosol into golgi vesicles. Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35A1. The function of SLC35A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM152.Transient Receptor Potential Cation Channel, Subfamily V, Member 1 (TRPV1, Accession NM_080704) is another VGAM2280 host target gene. TRPV1 BINDING SITE1 through TRPV1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TRPV1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 through TRPV1 BINDING SITE4, designated SEQ ID:27993, SEQ ID:28001, SEQ ID:28009 and SEQ ID:20813 respectively, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77904] Another function of VGAM2280 is therefore inhibition of Transient Receptor Potential Cation Channel, Subfamily V, Member 1 (TRPV1, Accession NM_080704), a gene which functions as a receptor for capsaicin. Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPV1. The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM146.Oxysterol Binding Protein-like 10

(OSBPL10, Accession NM_017784) is another VGAM2280 host target gene. OSBPL10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL10 BINDING SITE, designated SEQ ID:19415, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77905] Another function of VGAM2280 is therefore inhibition of Oxysterol Binding Protein-like 10 (OSBPL10, Accession NM_017784). Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL10. Transducin-like Enhancer of Split 4 (E(sp1) Homolog, Drosophila) (TLE4, Accession XM_042357) is another VGAM2280 host target gene. TLE4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TLE4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TLE4 BINDING SITE, designated SEQ ID:33719,

to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77906] Another function of VGAM2280 is therefore inhibition of Transducin-like Enhancer of Split 4 (E(sp1) Homolog, Drosophila) (TLE4, Accession XM_042357). Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLE4. Ubiquitin-like, Containing PHD and RING Finger Domains, 1 (UHRF1, Accession NM_013282) is another VGAM2280 host target gene. UHRF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UHRF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UHRF1 BINDING SITE, designated SEQ ID:14950, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77907] Another function of VGAM2280 is therefore inhibition of Ubiquitin-like, Containing PHD and RING Finger Domains, 1 (UHRF1, Accession NM_013282). Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UHRF1.

LOC126133 (Accession XM_058991) is another VGAM2280 host target gene. LOC126133 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC126133, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126133 BINDING SITE, designated SEQ ID:36804, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77908] Another function of VGAM2280 is therefore inhibition of LOC126133 (Accession XM_058991). Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126133. LOC142948 (Accession XM_096364) is another VGAM2280 host target gene. LOC142948 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC142948, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC142948 BINDING SITE, designated SEQ ID:40325, to the nucleotide sequence of VGAM2280 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:4991.

[77909] Another function of VGAM2280 is therefore inhibition of LOC142948 (Accession XM_096364). Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142948. LOC159160 (Accession XM_018413) is another VGAM2280 host target gene. LOC159160 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC159160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159160 BINDING SITE, designated SEQ ID:30358, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77910] Another function of VGAM2280 is therefore inhibition of LOC159160 (Accession XM_018413). Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159160. LOC91947 (Accession XM_041721) is another VGAM2280 host target gene. LOC91947 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91947, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91947 BINDING SITE, designated SEQ ID:33570, to the nucleotide sequence of VGAM2280 RNA, herein designated VGAM RNA, also designated SEQ ID:4991.

[77911] Another function of VGAM2280 is therefore inhibition of LOC91947 (Accession XM_041721). Accordingly, utilities of VGAM2280 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91947. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2281 (VGAM2281) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77912] VGAM2281 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2281 was detected is described hereinabove with reference to Figs. 1-8.

[77913] VGAM2281 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus.

VGAM2281 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77914] VGAM2281 gene encodes a VGAM2281 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2281 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2281 precursor RNA is designated SEQ ID:2267, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2267 is located at position 22070 relative to the genome of Murine Hepatitis Virus.

[77915] VGAM2281 precursor RNA folds onto itself, forming VGAM2281 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77916] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2281 folded precursor RNA into VGAM2281 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2281 RNA is designated SEQ ID:4992, and is provided hereinbelow with reference to the sequence listing part.

[77917] VGAM2281 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2281 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2281 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77918] VGAM2281 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2281 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2281 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2281 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2281 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77919] The complementary binding of VGAM2281 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2281 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2281 host target RNA into VGAM2281 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77920] It is appreciated that VGAM2281 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2281 host target genes. The mRNA of each one of this plurality of VGAM2281 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2281 RNA, herein designated VGAM RNA, and which when bound by VGAM2281 RNA causes inhibition of translation of respective one or more VGAM2281 host target proteins.

[77921] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2281 gene, herein designated VGAM GENE, on one or more VGAM2281 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77922] It is yet further appreciated that a function of VGAM2281 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2281 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2281 correlate with, and may be deduced from, the identity of the host target genes which VGAM2281 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77923] Nucleotide sequences of the VGAM2281 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2281 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2281 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2281 are further described hereinbelow with reference to Table 1.

[77924] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2281 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2281 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77925] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2281 gene, herein designated VGAM is inhibition of expression of VGAM2281 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2281 correlate with, and may be deduced from, the identity of the target genes which VGAM2281 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77926] Forkhead Box D2 (FOXD2, Accession NM_004474) is a VGAM2281 host target gene. FOXD2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FOXD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOXD2 BINDING SITE, designated SEQ ID:10791, to the nucleotide se-

quence of VGAM2281 RNA, herein designated VGAM RNA, also designated SEQ ID:4992.

[77927] A function of VGAM2281 is therefore inhibition of Forkhead Box D2 (FOXD2, Accession NM_004474). Accordingly, utilities of VGAM2281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXD2. Glioblastoma Amplified Sequence (GBAS, Accession NM_001483) is another VGAM2281 host target gene. GBAS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GBAS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GBAS BINDING SITE, designated SEQ ID:7226, to the nucleotide sequence of VGAM2281 RNA, herein designated VGAM RNA, also designated SEQ ID:4992.

[77928] Another function of VGAM2281 is therefore inhibition of Glioblastoma Amplified Sequence (GBAS, Accession NM_001483), a gene which might be involved in vesicular transport. Accordingly, utilities of VGAM2281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GBAS. The function of GBAS and its association with various diseases and clinical con-

ditions, has been established by previous studies, as described hereinabove with reference to VGAM859.Hyaluronan Synthase 3 (HAS3, Accession NM_005329) is another VGAM2281 host target gene. HAS3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HAS3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HAS3 BINDING SITE, designated SEQ ID:11804, to the nucleotide sequence of VGAM2281 RNA, herein designated VGAM RNA, also designated SEQ ID:4992.

[77929] Another function of VGAM2281 is therefore inhibition of Hyaluronan Synthase 3 (HAS3, Accession NM_005329), a gene which plays a role in hyaluronan/hyaluronic acid (ha) synthesis. Accordingly, utilities of VGAM2281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAS3. The function of HAS3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM498.Phosphoribosylaminoimidazole Carboxylase, Phosphoribosylaminoimidazole Succinocarboxamide Syn-

thetase (PAICS, Accession NM_006452) is another VGAM2281 host target gene. PAICS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAICS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAICS BINDING SITE, designated SEQ ID:13164, to the nucleotide sequence of VGAM2281 RNA, herein designated VGAM RNA, also designated SEQ ID:4992.

[77930] Another function of VGAM2281 is therefore inhibition of Phosphoribosylaminoimidazole Carboxylase, Phosphoribosylaminoimidazole Succinocarboxamide Synthetase (PAICS, Accession NM_006452), a gene which is required for purine biosynthesis. Accordingly, utilities of VGAM2281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAICS. The function of PAICS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM894.CLONE24945 (Accession NM_015683) is another VGAM2281 host target gene. CLONE24945 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by CLONE24945, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLONE24945 BINDING SITE, designated SEQ ID:17906, to the nucleotide sequence of VGAM2281 RNA, herein designated VGAM RNA, also designated SEQ ID:4992.

[77931] Another function of VGAM2281 is therefore inhibition of CLONE24945 (Accession NM_015683). Accordingly, utilities of VGAM2281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLONE24945. CRMP5 (Accession NM_020134) is another VGAM2281 host target gene. CRMP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRMP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRMP5 BINDING SITE, designated SEQ ID:21333, to the nucleotide sequence of VGAM2281 RNA, herein designated VGAM RNA, also designated SEQ ID:4992.

[77932] Another function of VGAM2281 is therefore inhibition of CRMP5 (Accession NM_020134). Accordingly, utilities of

VGAM2281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRMP5. KIAA0420 (Accession XM_032693) is another VGAM2281 host target gene. KIAA0420 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0420, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0420 BINDING SITE, designated SEQ ID:31725, to the nucleotide sequence of VGAM2281 RNA, herein designated VGAM RNA, also designated SEQ ID:4992.

[77933] Another function of VGAM2281 is therefore inhibition of KIAA0420 (Accession XM_032693). Accordingly, utilities of VGAM2281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0420. KIAA1198 (Accession XM_032674) is another VGAM2281 host target gene. KIAA1198 BINDING SITE1 and KIAA1198 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1198, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of KIAA1198 BINDING SITE1 and KIAA1198 BINDING SITE2, designated SEQ ID:31705 and SEQ ID:31717 respectively, to the nucleotide sequence of VGAM2281 RNA, herein designated VGAM RNA, also designated SEQ ID:4992.

[77934] Another function of VGAM2281 is therefore inhibition of KIAA1198 (Accession XM_032674). Accordingly, utilities of VGAM2281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1198. LOC148114 (Accession XM_086050) is another VGAM2281 host target gene. LOC148114 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148114, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148114 BINDING SITE, designated SEQ ID:38464, to the nucleotide sequence of VGAM2281 RNA, herein designated VGAM RNA, also designated SEQ ID:4992.

[77935] Another function of VGAM2281 is therefore inhibition of LOC148114 (Accession XM_086050). Accordingly, utilities of VGAM2281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC148114. LOC257354 (Accession XM_170810) is another VGAM2281 host target gene. LOC257354 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257354, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257354 BINDING SITE, designated SEQ ID:45578, to the nucleotide sequence of VGAM2281 RNA, herein designated VGAM RNA, also designated SEQ ID:4992.

[77936] Another function of VGAM2281 is therefore inhibition of LOC257354 (Accession XM_170810). Accordingly, utilities of VGAM2281 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257354. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2282 (VGAM2282) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77937] VGAM2282 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2282 was detected is described hereinabove with reference to Figs. 1-8.

[77938] VGAM2282 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus. VGAM2282 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77939] VGAM2282 gene encodes a VGAM2282 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2282 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2282 precursor RNA is designated SEQ ID:2268, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2268 is located at position 26667 relative to the genome of Murine Hepatitis Virus.

[77940] VGAM2282 precursor RNA folds onto itself, forming VGAM2282 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77941] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2282 folded precursor RNA into VGAM2282 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2282 RNA is designated SEQ ID:4993, and is provided hereinbelow with reference to the sequence listing part.

[77942] VGAM2282 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2282 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2282 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77943] VGAM2282 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2282 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2282 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2282 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2282 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77944] The complementary binding of VGAM2282 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2282 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2282 host target RNA into VGAM2282 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77945] It is appreciated that VGAM2282 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2282 host target genes. The mRNA of each one of this plurality of VGAM2282 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2282 RNA, herein designated VGAM RNA, and which when bound by VGAM2282 RNA causes inhibition of translation of respective one or more VGAM2282 host target proteins.

[77946] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2282 gene, herein designated VGAM GENE, on one or more VGAM2282 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[77947] It is yet further appreciated that a function of VGAM2282 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2282 correlate with, and may be deduced from, the identity of the host target genes which VGAM2282 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[77948] Nucleotide sequences of the VGAM2282 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2282 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2282 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2282 are further described hereinbelow with reference to Table 1.

[77949] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2282 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2282 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[77950] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2282 gene, herein designated VGAM is inhibition of expression of VGAM2282 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2282 correlate with, and may be deduced from, the identity of the target genes which VGAM2282 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[77951] Rac/Cdc42 Guanine Nucleotide Exchange Factor (GEF) 6 (ARHGEF6, Accession XM_042963) is a VGAM2282 host target gene. ARHGEF6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by ARHGEF6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGEF6 BINDING SITE, designated SEQ ID:33844, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77952] A function of VGAM2282 is therefore inhibition of Rac/Cdc42 Guanine Nucleotide Exchange Factor (GEF) 6 (ARHGEF6, Accession XM_042963). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF6. Bromodomain Adjacent to Zinc Finger Domain, 1B (BAZ1B, Accession NM_032408) is another VGAM2282 host target gene. BAZ1B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAZ1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAZ1B BINDING SITE, designated SEQ ID:26191, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77953] Another function of VGAM2282 is therefore inhibition of Bromodomain Adjacent to Zinc Finger Domain, 1B (BAZ1B, Accession NM_032408). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAZ1B. Casein Kinase 1, Gamma 3 (CSNK1G3, Accession NM_004384) is another VGAM2282 host target gene. CSNK1G3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSNK1G3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSNK1G3 BINDING SITE, designated SEQ ID:10610, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77954] Another function of VGAM2282 is therefore inhibition of Casein Kinase 1, Gamma 3 (CSNK1G3, Accession NM_004384). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK1G3. Glutaminase (GLS, Accession NM_014905) is another VGAM2282 host target gene. GLS BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by GLS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GLS BINDING SITE, designated SEQ ID:17108, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77955] Another function of VGAM2282 is therefore inhibition of Glutaminase (GLS, Accession NM_014905). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLS. LENG4 (Accession NM_024298) is another VGAM2282 host target gene. LENG4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LENG4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LENG4 BINDING SITE, designated SEQ ID:23580, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77956] Another function of VGAM2282 is therefore inhibition of LENG4 (Accession NM_024298), a gene which may be a

transmembrane protein. Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LENG4. The function of LENG4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM259.Polycystic Kidney Disease 2 (autosomal dominant) (PKD2, Accession XM_011124) is another VGAM2282 host target gene. PKD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PKD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PKD2 BINDING SITE, designated SEQ ID:30177, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77957] Another function of VGAM2282 is therefore inhibition of Polycystic Kidney Disease 2 (autosomal dominant) (PKD2, Accession XM_011124). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKD2. Synaptosomal-associated Protein, 25kDa (SNAP25, Acces-

sion NM_130811) is another VGAM2282 host target gene. SNAP25 BINDING SITE1 and SNAP25 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SNAP25, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNAP25 BINDING SITE1 and SNAP25 BINDING SITE2, designated SEQ ID:28318 and SEQ ID:9055 respectively, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77958] Another function of VGAM2282 is therefore inhibition of Synaptosomal-associated Protein, 25kDa (SNAP25, Accession NM_130811). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNAP25. WAS Protein Family, Member 3 (WASF3, Accession NM_006646) is another VGAM2282 host target gene. WASF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WASF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WASF3 BIND-

ING SITE, designated SEQ ID:13440, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77959] Another function of VGAM2282 is therefore inhibition of WAS Protein Family, Member 3 (WASF3, Accession NM_006646), a gene which stimulates actin polymerization. Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WASF3. The function of WASF3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1692.Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_014919) is another VGAM2282 host target gene. WHSC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WHSC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WHSC1 BINDING SITE, designated SEQ ID:17176, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77960] Another function of VGAM2282 is therefore inhibition of Wolf-Hirschhorn Syndrome Candidate 1 (WHSC1, Accession NM_014919), a gene which binds covalently to and repairs g/t mismatches. Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WHSC1. The function of WHSC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Rho Guanine Nucleotide Exchange Factor (GEF) 3 (ARHGEF3, Accession NM_019555) is another VGAM2282 host target gene. ARHGEF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHGEF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGEF3 BINDING SITE, designated SEQ ID:21211, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77961] Another function of VGAM2282 is therefore inhibition of Rho Guanine Nucleotide Exchange Factor (GEF) 3 (ARHGEF3, Accession NM_019555). Accordingly, utilities

of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF3. BCE-1 (Accession NM_007005) is another VGAM2282 host target gene. BCE-1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BCE-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCE-1 BINDING SITE, designated SEQ ID:13868, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77962] Another function of VGAM2282 is therefore inhibition of BCE-1 (Accession NM_007005). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCE-1. Chromosome 19 Open Reading Frame 7 (C19orf7, Accession XM_028253) is another VGAM2282 host target gene. C19orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C19orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of C19orf7 BINDING SITE, designated SEQ ID:30635, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77963] Another function of VGAM2282 is therefore inhibition of Chromosome 19 Open Reading Frame 7 (C19orf7, Accession XM_028253). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C19orf7. Chromosome 20 Open Reading Frame 36 (C20orf36, Accession NM_018257) is another VGAM2282 host target gene. C20orf36 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf36, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf36 BINDING SITE, designated SEQ ID:20222, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77964] Another function of VGAM2282 is therefore inhibition of Chromosome 20 Open Reading Frame 36 (C20orf36, Accession NM_018257). Accordingly, utilities of VGAM2282

include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf36. CHCR (Accession NM_018388) is another VGAM2282 host target gene. CHCR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHCR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHCR BINDING SITE, designated SEQ ID:20421, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77965] Another function of VGAM2282 is therefore inhibition of CHCR (Accession NM_018388). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHCR. Elongation of Very Long Chain Fatty Acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (ELOVL2, Accession NM_017770) is another VGAM2282 host target gene. ELOVL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELOVL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

ELOVL2 BINDING SITE, designated SEQ ID:19388, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77966] Another function of VGAM2282 is therefore inhibition of Elongation of Very Long Chain Fatty Acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 2 (ELOVL2, Accession NM_017770). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELOVL2. ERAP140 (Accession XM_059748) is another VGAM2282 host target gene. ERAP140 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ERAP140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERAP140 BINDING SITE, designated SEQ ID:37083, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77967] Another function of VGAM2282 is therefore inhibition of ERAP140 (Accession XM_059748). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

ERAP140. FLJ10781 (Accession NM_018215) is another VGAM2282 host target gene. FLJ10781 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10781, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10781 BINDING SITE, designated SEQ ID:20139, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77968] Another function of VGAM2282 is therefore inhibition of FLJ10781 (Accession NM_018215). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10781. FLJ13162 (Accession NM_025002) is another VGAM2282 host target gene. FLJ13162 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13162 BINDING SITE, designated SEQ ID:24572, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM

RNA, also designated SEQ ID:4993.

[77969] Another function of VGAM2282 is therefore inhibition of FLJ13162 (Accession NM_025002). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13162. FLJ20130 (Accession NM_017681) is another VGAM2282 host target gene. FLJ20130 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20130, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20130 BINDING SITE, designated SEQ ID:19226, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77970] Another function of VGAM2282 is therefore inhibition of FLJ20130 (Accession NM_017681). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20130. FLJ20344 (Accession NM_017776) is another VGAM2282 host target gene. FLJ20344 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20344, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20344 BINDING SITE, designated SEQ ID:19402, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77971] Another function of VGAM2282 is therefore inhibition of FLJ20344 (Accession NM_017776). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20344. FLJ20972 (Accession NM_025030) is another VGAM2282 host target gene. FLJ20972 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20972, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20972 BINDING SITE, designated SEQ ID:24623, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77972] Another function of VGAM2282 is therefore inhibition of FLJ20972 (Accession NM_025030). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20972. FLJ23462 (Accession NM_024843) is another VGAM2282 host target gene. FLJ23462 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23462, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23462 BINDING SITE, designated SEQ ID:24262, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77973] Another function of VGAM2282 is therefore inhibition of FLJ23462 (Accession NM_024843). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23462. Golgi Autoantigen, Golgin Subfamily A, 1 (GOLGA1, Accession NM_002077) is another VGAM2282 host target gene. GOLGA1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GOLGA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GOLGA1 BINDING SITE,

designated SEQ ID:7861, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77974] Another function of VGAM2282 is therefore inhibition of Golgi Autoantigen, Golgin Subfamily A, 1 (GOLGA1, Accession NM_002077). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLGA1. KIAA0820 (Accession XM_044463) is another VGAM2282 host target gene. KIAA0820 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0820, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0820 BINDING SITE, designated SEQ ID:34217, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77975] Another function of VGAM2282 is therefore inhibition of KIAA0820 (Accession XM_044463). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0820. KIAA1281 (Accession XM_114432) is another

VGAM2282 host target gene. KIAA1281 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1281, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1281 BINDING SITE, designated SEQ ID:42960, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77976] Another function of VGAM2282 is therefore inhibition of KIAA1281 (Accession XM_114432). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1281. KIAA1775 (Accession NM_033100) is another VGAM2282 host target gene. KIAA1775 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1775, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1775 BINDING SITE, designated SEQ ID:26938, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77977] Another function of VGAM2282 is therefore inhibition of KIAA1775 (Accession NM_033100). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1775. KIAA1925 (Accession XM_166375) is another VGAM2282 host target gene. KIAA1925 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1925, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1925 BINDING SITE, designated SEQ ID:44207, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77978] Another function of VGAM2282 is therefore inhibition of KIAA1925 (Accession XM_166375). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1925. KIAA1987 (Accession XM_113870) is another VGAM2282 host target gene. KIAA1987 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1987, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1987 BINDING SITE, designated SEQ ID:42492, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77979] Another function of VGAM2282 is therefore inhibition of KIAA1987 (Accession XM_113870). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1987. N-ethylmaleimide-sensitive Factor Attachment Protein, Gamma (NAPG, Accession XM_172983) is another VGAM2282 host target gene. NAPG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NAPG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAPG BINDING SITE, designated SEQ ID:46253, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77980] Another function of VGAM2282 is therefore inhibition of N-ethylmaleimide-sensitive Factor Attachment Protein, Gamma (NAPG, Accession XM_172983). Accordingly, utili-

ties of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAPG. Peroxisomal Biogenesis Factor 12 (PEX12, Accession NM_000286) is another VGAM2282 host target gene. PEX12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PEX12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEX12 BINDING SITE, designated SEQ ID:5831, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77981] Another function of VGAM2282 is therefore inhibition of Peroxisomal Biogenesis Factor 12 (PEX12, Accession NM_000286). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEX12. PSR (Accession XM_036784) is another VGAM2282 host target gene. PSR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of PSR BINDING SITE, designated SEQ ID:32497, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77982] Another function of VGAM2282 is therefore inhibition of PSR (Accession XM_036784). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSR. SES2 (Accession NM_031459) is another VGAM2282 host target gene. SES2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SES2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SES2 BINDING SITE, designated SEQ ID:25480, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77983] Another function of VGAM2282 is therefore inhibition of SES2 (Accession NM_031459). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SES2. Thioesterase, Adipose Associated (THEA, Accession

XM_038922) is another VGAM2282 host target gene. THEA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by THEA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of THEA BINDING SITE, designated SEQ ID:32947, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77984] Another function of VGAM2282 is therefore inhibition of Thioesterase, Adipose Associated (THEA, Accession XM_038922). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THEA. Ubiquitin Specific Protease 24 (USP24, Accession XM_165973) is another VGAM2282 host target gene. USP24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP24 BINDING SITE, designated SEQ ID:43814, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:4993.

[77985] Another function of VGAM2282 is therefore inhibition of Ubiquitin Specific Protease 24 (USP24, Accession XM_165973). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP24. LOC145815 (Accession XM_096874) is another VGAM2282 host target gene. LOC145815 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145815, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145815 BINDING SITE, designated SEQ ID:40607, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77986] Another function of VGAM2282 is therefore inhibition of LOC145815 (Accession XM_096874). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145815. LOC146449 (Accession XM_028046) is another VGAM2282 host target gene. LOC146449 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC146449, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146449 BINDING SITE, designated SEQ ID:30611, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77987] Another function of VGAM2282 is therefore inhibition of LOC146449 (Accession XM_028046). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146449. LOC197414 (Accession XM_113880) is another VGAM2282 host target gene. LOC197414 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197414, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197414 BINDING SITE, designated SEQ ID:42515, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77988] Another function of VGAM2282 is therefore inhibition of LOC197414 (Accession XM_113880). Accordingly, utilities

of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197414. LOC221002 (Accession XM_166156) is another VGAM2282 host target gene. LOC221002 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221002, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221002 BINDING SITE, designated SEQ ID:43976, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77989] Another function of VGAM2282 is therefore inhibition of LOC221002 (Accession XM_166156). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221002. LOC83693 (Accession NM_031463) is another VGAM2282 host target gene. LOC83693 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC83693, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC83693 BINDING SITE, designated SEQ ID:25498, to the nucleotide sequence of VGAM2282 RNA, herein designated VGAM RNA, also designated SEQ ID:4993.

[77990] Another function of VGAM2282 is therefore inhibition of LOC83693 (Accession NM_031463). Accordingly, utilities of VGAM2282 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC83693. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2283 (VGAM2283) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[77991] VGAM2283 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2283 was detected is described hereinabove with reference to Figs. 1-8.

[77992] VGAM2283 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus. VGAM2283 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[77993] VGAM2283 gene encodes a VGAM2283 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2283 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2283 precursor RNA is designated SEQ ID:2269, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2269 is located at position 23988 relative to the genome of Murine Hepatitis Virus.

[77994] VGAM2283 precursor RNA folds onto itself, forming VGAM2283 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[77995] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2283 folded precursor RNA into VGAM2283 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2283 RNA is designated SEQ ID:4994, and is provided hereinbelow with reference to the sequence listing part.

[77996] VGAM2283 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2283 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2283 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[77997] VGAM2283 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2283 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2283 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2283 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2283 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[77998] The complementary binding of VGAM2283 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2283 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2283 host target RNA into VGAM2283 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[77999] It is appreciated that VGAM2283 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2283 host target genes. The mRNA of each one of this plurality of VGAM2283 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2283 RNA, herein designated VGAM RNA, and which when bound by VGAM2283 RNA causes inhibition of translation of respective one or more VGAM2283 host target proteins.

[78000] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2283 gene, herein designated VGAM GENE, on one or more VGAM2283 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78001] It is yet further appreciated that a function of VGAM2283 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2283 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2283 correlate with, and may be deduced from, the identity of the host target genes which VGAM2283 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78002] Nucleotide sequences of the VGAM2283 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2283 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2283 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2283 are further described hereinbelow with reference to Table 1.

[78003] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2283 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2283 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78004] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2283 gene, herein designated VGAM is inhibition of expression of VGAM2283 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2283 correlate with, and may be deduced from, the identity of the target genes which VGAM2283 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78005] Frizzled Homolog 10 (Drosophila) (FZD10, Accession NM_007197) is a VGAM2283 host target gene. FZD10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FZD10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FZD10 BINDING SITE, designated SEQ ID:14052, to the nucleotide sequence of VGAM2283 RNA, herein designated VGAM RNA, also designated SEQ ID:4994.

[78006] A function of VGAM2283 is therefore inhibition of Frizzled

Homolog 10 (Drosophila) (FZD10, Accession NM_007197). Accordingly, utilities of VGAM2283 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FZD10. Chromosome 17 Open Reading Frame 31 (C17orf31, Accession NM_017575) is another VGAM2283 host target gene. C17orf31 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C17orf31, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C17orf31 BINDING SITE, designated SEQ ID:18997, to the nucleotide sequence of VGAM2283 RNA, herein designated VGAM RNA, also designated SEQ ID:4994.

[78007] Another function of VGAM2283 is therefore inhibition of Chromosome 17 Open Reading Frame 31 (C17orf31, Accession NM_017575). Accordingly, utilities of VGAM2283 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C17orf31. CL683 (Accession NM_015696) is another VGAM2283 host target gene. CL683 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CL683, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CL683 BINDING SITE, designated SEQ ID:17925, to the nucleotide sequence of VGAM2283 RNA, herein designated VGAM RNA, also designated SEQ ID:4994.

[78008] Another function of VGAM2283 is therefore inhibition of CL683 (Accession NM_015696). Accordingly, utilities of VGAM2283 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CL683. FLJ13710 (Accession NM_024817) is another VGAM2283 host target gene. FLJ13710 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13710, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13710 BINDING SITE, designated SEQ ID:24203, to the nucleotide sequence of VGAM2283 RNA, herein designated VGAM RNA, also designated SEQ ID:4994.

[78009] Another function of VGAM2283 is therefore inhibition of FLJ13710 (Accession NM_024817). Accordingly, utilities of VGAM2283 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ13710. KIAA1679 (Accession XM_046570) is another VGAM2283 host target gene. KIAA1679 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1679, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1679 BINDING SITE, designated SEQ ID:34749, to the nucleotide sequence of VGAM2283 RNA, herein designated VGAM RNA, also designated SEQ ID:4994.

[78010] Another function of VGAM2283 is therefore inhibition of KIAA1679 (Accession XM_046570). Accordingly, utilities of VGAM2283 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1679. PLU-1 (Accession XM_113375) is another VGAM2283 host target gene. PLU-1 BINDING SITE1 and PLU-1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PLU-1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLU-1 BINDING SITE1 and PLU-1 BINDING

SITE2, designated SEQ ID:42250 and SEQ ID:13401 respectively, to the nucleotide sequence of VGAM2283 RNA, herein designated VGAM RNA, also designated SEQ ID:4994.

[78011] Another function of VGAM2283 is therefore inhibition of PLU-1 (Accession XM_113375). Accordingly, utilities of VGAM2283 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLU-1. Heterogeneous Nuclear Ribonucleoprotein U (scaffold attachment factor A) (HNRPU, Accession NM_004501) is another VGAM2284 host target gene. HNRPU BINDING SITE1 and HNRPU BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HNRPU, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNRPU BINDING SITE1 and HNRPU BINDING SITE2, designated SEQ ID:10836 and SEQ ID:25580 respectively, to the nucleotide sequence of VGAM2284 RNA, herein designated VGAM RNA, also designated SEQ ID:4995.

[78012] Another function of VGAM2284 is therefore inhibition of Heterogeneous Nuclear Ribonucleoprotein U (scaffold at-

tachment factor A) (HNRPU, Accession NM_004501). Accordingly, utilities of VGAM2284 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNRPU. LOC148254 (Accession XM_086121) is another VGAM2284 host target gene. LOC148254 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148254, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148254 BINDING SITE, designated SEQ ID:38501, to the nucleotide sequence of VGAM2284 RNA, herein designated VGAM RNA, also designated SEQ ID:4995.

[78013] Another function of VGAM2284 is therefore inhibition of LOC148254 (Accession XM_086121). Accordingly, utilities of VGAM2284 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148254. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2285 (VGAM2285) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[78014] VGAM2285 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2285 was detected is described hereinabove with reference to Figs. 1-8.

[78015] VGAM2285 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus. VGAM2285 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78016] VGAM2285 gene encodes a VGAM2285 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2285 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2285 precursor RNA is designated SEQ ID:2271, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2271 is located at position 13151 relative to the genome of Murine Hepatitis Virus.

[78017] VGAM2285 precursor RNA folds onto itself, forming VGAM2285 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78018] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2285 folded precursor RNA into VGAM2285 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2285 RNA is designated SEQ ID:4996, and is provided hereinbelow with reference to the sequence listing part.

[78019] VGAM2285 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2285 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2285 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78020] VGAM2285 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2285 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2285 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2285 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2285 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78021] The complementary binding of VGAM2285 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2285 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2285 host target RNA into VGAM2285 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78022] It is appreciated that VGAM2285 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2285 host target genes. The mRNA of each one of this plurality of VGAM2285 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2285 RNA, herein designated VGAM RNA, and which when bound by VGAM2285 RNA causes inhibition of translation of respective one or more VGAM2285 host target proteins.

[78023] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2285 gene, herein designated VGAM GENE, on one or more VGAM2285 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78024] It is yet further appreciated that a function of VGAM2285 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2285 correlate with, and may be deduced from, the identity of the host target genes which VGAM2285 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[78025] Nucleotide sequences of the VGAM2285 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2285 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2285 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2285 are further described hereinbelow with reference to Table 1.

[78026] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2285 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2285 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78027] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2285 gene, herein designated VGAM is inhibition of expression of VGAM2285 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2285 correlate with, and may be deduced from, the identity of the target genes which VGAM2285 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78028] Adrenergic, Alpha-2B-, Receptor (ADRA2B, Accession NM_000682) is a VGAM2285 host target gene. ADRA2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADRA2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADRA2B BINDING SITE, designated SEQ ID:6339, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78029] A function of VGAM2285 is therefore inhibition of Adrenergic, Alpha-2B-, Receptor (ADRA2B, Accession NM_000682), a gene which mediate the catecholamine-induced inhibition of adenylate cyclase through the action of g proteins. Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADRA2B. The function of ADRA2B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM609.B-cell CLL/lymphoma 2 (BCL2, Accession NM_000633) is another VGAM2285 host target gene.

BCL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL2 BINDING SITE, designated SEQ ID:6254, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78030] Another function of VGAM2285 is therefore inhibition of B-cell CLL/lymphoma 2 (BCL2, Accession NM_000633). Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL2. Clock Homolog (mouse) (CLOCK, Accession NM_004898) is another VGAM2285 host target gene. CLOCK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLOCK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLOCK BINDING SITE, designated SEQ ID:11334, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78031] Another function of VGAM2285 is therefore inhibition of Clock Homolog (mouse) (CLOCK, Accession NM_004898). Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLOCK. Contactin Associated Protein-like 2 (CNTNAP2, Accession NM_014141) is another VGAM2285 host target gene. CNTNAP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNTNAP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNTNAP2 BINDING SITE, designated SEQ ID:15415, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78032] Another function of VGAM2285 is therefore inhibition of Contactin Associated Protein-like 2 (CNTNAP2, Accession NM_014141). Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNTNAP2. Hepatocyte Growth Factor (hepapoietin A; scatter factor) (HGF, Accession XM_168542) is another VGAM2285 host target gene. HGF BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by HGF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HGF BINDING SITE, designated SEQ ID:45218, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78033] Another function of VGAM2285 is therefore inhibition of Hepatocyte Growth Factor (hepapoietin A; scatter factor) (HGF, Accession XM_168542), a gene which may be required for normal embryonic development; strongly similar to murine Hgf, has kringle domains. Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HGF. The function of HGF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM174.Potassium Intermediate/small Conductance Calcium-activated Channel, Subfamily N, Member 2 (KCNN2, Accession NM_021614) is another VGAM2285 host target gene. KCNN2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCNN2, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNN2 BINDING SITE, designated SEQ ID:22242, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78034] Another function of VGAM2285 is therefore inhibition of Potassium Intermediate/small Conductance Calcium-activated Channel, Subfamily N, Member 2 (KCNN2, Accession NM_021614), a gene which forms a voltage-independent potassium channel activated by intracellular calcium. Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNN2. The function of KCNN2 has been established by previous studies. Calcium-activated potassium channels respond to changes in intracellular calcium concentration and couple calcium metabolism to potassium flux and membrane excitability. Based on their electrophysiologic properties, calcium-activated potassium channels are classified as large conductance, calcium- and voltage-gated channels (BK, e.g., KCNMB4; 605223), intermediate conductance, voltage-independent channels (IK, e.g., KCNN4; 602754), and

small conductance, voltage-independent channels (SK, e.g., KCNN3; 602983). By screening a Jurkat T-cell cDNA library using RT-PCR with degenerate primers based on rat and human SK channels, followed by searching an EST database, Desai et al. (2000) isolated a cDNA encoding KCNN2, which they termed SK2. Sequence analysis predicted that the 579-amino acid protein, which is 97% identical to the rat sequence, contains multiple phosphorylation sites and no N-glycosylation sites. Northern blot analysis detected a major 2.5-kb transcript that was expressed most strongly in liver and brain, with lower levels in kidney and Jurkat (but not peripheral) T cells. A minor 4.4-kb transcript was expressed in heart and skeletal muscle, and a 1.3-kb transcript was expressed in brain and liver. Functional analysis showed that KCNN2 expresses a potassium current that is sensitive to apamin, scyllatoxin, and tubocurarine and is insensitive to charybdotoxin. Schumacher et al. (2001) determined the crystal structure of calmodulin (OMIM Ref. No. 114180) bound to KCNN2. The calmodulin-binding domain forms an elongated dimer with a calmodulin molecule bound at each end; each calmodulin wraps around 3 alpha helices, 2 from 1 calmodulin-binding domain subunit and 1 from

the other.

[78035] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[78036] Desai, R.; Peretz, A.; Idelson, H.; Lazarovici, P.; Attali, B. : Ca(2+)-activated K(+) channels in human leukemic Jurkat T cells: molecular cloning, biochemical and functional characterization. J. Biol. Chem. 275: 39954-39963, 2000. ; and

[78037] Schumacher, M. A.; Rivard, A. F.; Bachinger, H. P.; Adelman, J. P. : Structure of the gating domain of a Ca(2+)-activated K+ channel complexed with Ca(2+)/calmodulin. Nature 410: 1120-.

[78038] Further studies establishing the function and utilities of KCNN2 are found in John Hopkins OMIM database record ID 605879, and in sited publications numbered 700 and 12582 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Arginyl Aminopeptidase (aminopeptidase B)-like 1 (RNPEPL1, Accession NM_018226) is another VGAM2285 host target gene. RNPEPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNPEPL1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNPEPL1 BINDING SITE, designated SEQ ID:20159, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78039] Another function of VGAM2285 is therefore inhibition of Arginyl Aminopeptidase (aminopeptidase B)-like 1 (RNPEPL1, Accession NM_018226). Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNPEPL1. TM7SF3 (Accession XM_006748) is another VGAM2285 host target gene. TM7SF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TM7SF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TM7SF3 BINDING SITE, designated SEQ ID:30010, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78040] Another function of VGAM2285 is therefore inhibition of TM7SF3 (Accession XM_006748). Accordingly, utilities of

VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TM7SF3. FLJ10388 (Accession NM_018082) is another VGAM2285 host target gene. FLJ10388 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10388, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10388 BINDING SITE, designated SEQ ID:19844, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78041] Another function of VGAM2285 is therefore inhibition of FLJ10388 (Accession NM_018082). Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10388. KIAA1879 (Accession XM_056635) is another VGAM2285 host target gene. KIAA1879 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1879, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1879 BINDING SITE, designated SEQ ID:36409, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78042] Another function of VGAM2285 is therefore inhibition of KIAA1879 (Accession XM_056635). Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1879. LOC157697 (Accession XM_088365) is another VGAM2285 host target gene. LOC157697 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157697, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157697 BINDING SITE, designated SEQ ID:39647, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78043] Another function of VGAM2285 is therefore inhibition of LOC157697 (Accession XM_088365). Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157697. LOC219894 (Accession XM_167782) is another VGAM2285 host target gene. LOC219894 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219894, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219894 BINDING SITE, designated SEQ ID:44794, to the nucleotide sequence of VGAM2285 RNA, herein designated VGAM RNA, also designated SEQ ID:4996.

[78044] Another function of VGAM2285 is therefore inhibition of LOC219894 (Accession XM_167782). Accordingly, utilities of VGAM2285 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219894. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2286 (VGAM2286) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78045] VGAM2286 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2286 was detected is described hereinabove with reference to Figs. 1-8.

[78046] VGAM2286 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus. VGAM2286 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78047] VGAM2286 gene encodes a VGAM2286 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2286 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2286 precursor RNA is designated SEQ ID:2272, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2272 is located at position 4778 relative to the genome of Murine Hepatitis Virus.

[78048] VGAM2286 precursor RNA folds onto itself, forming VGAM2286 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[78049] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2286 folded precursor RNA into VGAM2286 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 54%) nucleotide sequence of VGAM2286 RNA is designated SEQ ID:4997, and is provided hereinbelow with reference to the sequence listing part.

[78050] VGAM2286 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2286 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2286 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78051] VGAM2286 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2286 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2286 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2286 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2286 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78052] The complementary binding of VGAM2286 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2286 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2286 host target RNA into VGAM2286 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78053] It is appreciated that VGAM2286 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2286 host target genes. The mRNA of each one of this plurality of VGAM2286 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2286 RNA, herein designated VGAM RNA, and which when bound by VGAM2286 RNA causes inhibition of translation of respective one or more VGAM2286 host target proteins.

[78054] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2286 gene, herein designated VGAM GENE, on one or more VGAM2286 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78055] It is yet further appreciated that a function of VGAM2286 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2286 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2286 correlate with, and may be deduced from, the identity of the host target genes which VGAM2286 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78056] Nucleotide sequences of the VGAM2286 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2286 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2286 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2286 are further described hereinbelow with reference to Table 1.

[78057] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2286 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2286 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78058] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2286 gene, herein designated VGAM is inhibition of expression of VGAM2286 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2286 correlate with, and may be deduced from, the identity of the target genes which VGAM2286 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78059] FLJ14346 (Accession NM_025029) is a VGAM2286 host target gene. FLJ14346 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14346, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of FLJ14346 BINDING SITE, designated SEQ ID:24620, to the nucleotide sequence of VGAM2286 RNA, herein designated VGAM RNA, also designated SEQ ID:4997.

[78060] A function of VGAM2286 is therefore inhibition of FLJ14346 (Accession NM_025029). Accordingly, utilities of VGAM2286 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14346. FLJ20366 (Accession NM_017786) is another VGAM2286 host target gene. FLJ20366 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20366, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20366 BINDING SITE, designated SEQ ID:19418, to the nucleotide sequence of VGAM2286 RNA, herein designated VGAM RNA, also designated SEQ ID:4997.

[78061] Another function of VGAM2286 is therefore inhibition of FLJ20366 (Accession NM_017786). Accordingly, utilities of VGAM2286 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20366. NIR3 (Accession XM_038799) is another

VGAM2286 host target gene. NIR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NIR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NIR3 BINDING SITE, designated SEQ ID:32928, to the nucleotide sequence of VGAM2286 RNA, herein designated VGAM RNA, also designated SEQ ID:4997.

[78062] Another function of VGAM2286 is therefore inhibition of NIR3 (Accession XM_038799). Accordingly, utilities of VGAM2286 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NIR3. LOC92492 (Accession XM_045396) is another VGAM2286 host target gene. LOC92492 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92492, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92492 BINDING SITE, designated SEQ ID:34452, to the nucleotide sequence of VGAM2286 RNA, herein designated VGAM RNA, also designated SEQ ID:4997.

[78063] Another function of VGAM2286 is therefore inhibition of LOC92492 (Accession XM_045396). Accordingly, utilities of VGAM2286 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92492. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2287 (VGAM2287) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78064] VGAM2287 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2287 was detected is described hereinabove with reference to Figs. 1-8.

[78065] VGAM2287 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus. VGAM2287 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78066] VGAM2287 gene encodes a VGAM2287 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2287 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2287 precursor RNA is designated SEQ ID:2273, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2273 is located at position 3614 relative to the genome of Murine Hepatitis Virus.

[78067] VGAM2287 precursor RNA folds onto itself, forming VGAM2287 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78068] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2287 folded precursor RNA into VGAM2287 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2287 RNA is designated SEQ ID:4998, and is provided hereinbelow with reference to the sequence listing part.

[78069] VGAM2287 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2287 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2287 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78070] VGAM2287 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2287 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2287 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2287 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2287 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78071] The complementary binding of VGAM2287 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2287 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2287 host target RNA into VGAM2287 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78072] It is appreciated that VGAM2287 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2287 host target genes. The mRNA of each one of this plurality of VGAM2287 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2287 RNA, herein designated VGAM RNA, and which when bound by VGAM2287 RNA causes inhibition of translation of respective one or more VGAM2287 host target proteins.

[78073] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2287 gene, herein designated VGAM GENE, on one or more VGAM2287 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78074] It is yet further appreciated that a function of VGAM2287 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2287 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2287 correlate with, and may be deduced from, the identity of the host target genes which VGAM2287 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78075] Nucleotide sequences of the VGAM2287 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2287 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2287 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2287 are further described hereinbelow with reference to Table 1.

[78076] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2287 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2287 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[78077] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2287 gene, herein designated VGAM is inhibition of expression of VGAM2287 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2287 correlate with, and may be deduced from, the identity of the target genes which VGAM2287 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78078] FLJ13646 (Accession NM_024584) is a VGAM2287 host target gene. FLJ13646 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13646, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13646 BINDING SITE, designated SEQ ID:23811, to the nucleotide sequence of VGAM2287 RNA, herein designated VGAM RNA, also designated SEQ ID:4998.

[78079] A function of VGAM2287 is therefore inhibition of FLJ13646 (Accession NM_024584). Accordingly, utilities of VGAM2287 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ13646. KIAA1937 (Accession XM_057107) is another VGAM2287 host target gene. KIAA1937 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1937, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1937 BINDING SITE, designated SEQ ID:36482, to the nucleotide sequence of VGAM2287 RNA, herein designated VGAM RNA, also designated SEQ ID:4998.

[78080] Another function of VGAM2287 is therefore inhibition of KIAA1937 (Accession XM_057107). Accordingly, utilities of VGAM2287 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1937. Neuronal Guanine Nucleotide Exchange Factor (NGEF, Accession XM_044799) is another VGAM2287 host target gene. NGEF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NGEF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NGEF BINDING SITE, designated SEQ ID:34275, to the nucleotide sequence of VGAM2287 RNA,

herein designated VGAM RNA, also designated SEQ ID:4998.

[78081] Another function of VGAM2287 is therefore inhibition of Neuronal Guanine Nucleotide Exchange Factor (NGEF, Accession XM_044799). Accordingly, utilities of VGAM2287 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NGEF. LOC152765 (Accession XM_087519) is another VGAM2287 host target gene. LOC152765 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152765, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152765 BINDING SITE, designated SEQ ID:39318, to the nucleotide sequence of VGAM2287 RNA, herein designated VGAM RNA, also designated SEQ ID:4998.

[78082] Another function of VGAM2287 is therefore inhibition of LOC152765 (Accession XM_087519). Accordingly, utilities of VGAM2287 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152765. LOC255045 (Accession XM_171243) is another VGAM2287 host target gene. LOC255045 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255045, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255045 BINDING SITE, designated SEQ ID:46030, to the nucleotide sequence of VGAM2287 RNA, herein designated VGAM RNA, also designated SEQ ID:4998.

[78083] Another function of VGAM2287 is therefore inhibition of LOC255045 (Accession XM_171243). Accordingly, utilities of VGAM2287 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255045. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2288 (VGAM2288) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78084] VGAM2288 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2288 was detected is described hereinabove with reference to Figs. 1-8.

[78085] VGAM2288 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus. VGAM2288 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78086] VGAM2288 gene encodes a VGAM2288 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2288 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2288 precursor RNA is designated SEQ ID:2274, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2274 is located at position 23052 relative to the genome of Murine Hepatitis Virus.

[78087] VGAM2288 precursor RNA folds onto itself, forming VGAM2288 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[78088] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2288 folded precursor RNA into VGAM2288 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2288 RNA is designated SEQ ID:4999, and is provided hereinbelow with reference to the sequence listing part.

[78089] VGAM2288 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2288 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2288 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78090] VGAM2288 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2288 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2288 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2288 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2288 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78091] The complementary binding of VGAM2288 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2288 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2288 host target RNA into VGAM2288 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78092] It is appreciated that VGAM2288 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2288 host target genes. The mRNA of each one of this plurality of VGAM2288 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2288 RNA, herein designated VGAM RNA, and which when bound by VGAM2288 RNA causes inhibition of translation of respective one or more VGAM2288 host target proteins.

[78093] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2288 gene, herein designated VGAM GENE, on one or more VGAM2288 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78094] It is yet further appreciated that a function of VGAM2288 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2288 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2288 correlate with, and may be deduced from, the identity of the host target genes which VGAM2288 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78095] Nucleotide sequences of the VGAM2288 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2288 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2288 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2288 are further described hereinbelow with reference to Table 1.

[78096] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2288 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2288 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78097] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2288 gene, herein designated VGAM is inhibition of expression of VGAM2288 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2288 correlate with, and may be deduced from, the identity of the target genes which VGAM2288 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78098] ATPase, Na+/K+ Transporting, Alpha 2 (+) Polypeptide (ATP1A2, Accession NM_000702) is a VGAM2288 host target gene. ATP1A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP1A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP1A2 BINDING SITE, designated SEQ ID:6370, to the nucleotide sequence of VGAM2288 RNA, herein designated VGAM RNA, also designated SEQ ID:4999.

[78099] A function of VGAM2288 is therefore inhibition of ATPase, Na+/K+ Transporting, Alpha 2 (+) Polypeptide (ATP1A2, Accession NM_000702). Accordingly, utilities of VGAM2288 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP1A2. HCA4 (Accession XM_085287) is another VGAM2288 host target gene. HCA4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCA4 BINDING SITE, designated SEQ ID:38027, to the nucleotide sequence of VGAM2288 RNA, herein designated VGAM RNA, also designated SEQ ID:4999.

[78100] Another function of VGAM2288 is therefore inhibition of HCA4 (Accession XM_085287). Accordingly, utilities of VGAM2288 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with HCA4. KIAA0247 (Accession NM_014734) is another VGAM2288 host target gene. KIAA0247 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0247, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0247 BINDING SITE, designated SEQ ID:16379, to the nucleotide sequence of VGAM2288 RNA, herein designated VGAM RNA, also designated SEQ ID:4999.

[78101] Another function of VGAM2288 is therefore inhibition of KIAA0247 (Accession NM_014734). Accordingly, utilities of VGAM2288 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0247. KIAA0319 (Accession NM_014809) is another VGAM2288 host target gene. KIAA0319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0319, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0319 BINDING SITE, designated SEQ ID:16760, to the

nucleotide sequence of VGAM2288 RNA, herein designated VGAM RNA, also designated SEQ ID:4999.

[78102] Another function of VGAM2288 is therefore inhibition of KIAA0319 (Accession NM_014809). Accordingly, utilities of VGAM2288 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0319. KIAA0794 (Accession XM_087353) is another VGAM2288 host target gene. KIAA0794 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0794 BINDING SITE, designated SEQ ID:39185, to the nucleotide sequence of VGAM2288 RNA, herein designated VGAM RNA, also designated SEQ ID:4999.

[78103] Another function of VGAM2288 is therefore inhibition of KIAA0794 (Accession XM_087353). Accordingly, utilities of VGAM2288 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0794. LOC153810 (Accession XM_087778) is another VGAM2288 host target gene. LOC153810 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC153810, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153810 BINDING SITE, designated SEQ ID:39411, to the nucleotide sequence of VGAM2288 RNA, herein designated VGAM RNA, also designated SEQ ID:4999.

[78104] Another function of VGAM2288 is therefore inhibition of LOC153810 (Accession XM_087778). Accordingly, utilities of VGAM2288 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153810. LOC253272 (Accession XM_170906) is another VGAM2288 host target gene. LOC253272 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253272, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253272 BINDING SITE, designated SEQ ID:45664, to the nucleotide sequence of VGAM2288 RNA, herein designated VGAM RNA, also designated SEQ ID:4999.

[78105] Another function of VGAM2288 is therefore inhibition of LOC253272 (Accession XM_170906). Accordingly, utilities

of VGAM2288 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253272. LOC90643 (Accession XM_033145) is another VGAM2288 host target gene. LOC90643 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90643, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90643 BINDING SITE, designated SEQ ID:31855, to the nucleotide sequence of VGAM2288 RNA, herein designated VGAM RNA, also designated SEQ ID:4999.

[78106] Another function of VGAM2288 is therefore inhibition of LOC90643 (Accession XM_033145). Accordingly, utilities of VGAM2288 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90643. LOC93206 (Accession XM_049838) is another VGAM2288 host target gene. LOC93206 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93206, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC93206 BINDING SITE, designated SEQ ID:35518, to the nucleotide sequence of VGAM2288 RNA, herein designated VGAM RNA, also designated SEQ ID:4999.

[78107] Another function of VGAM2288 is therefore inhibition of LOC93206 (Accession XM_049838). Accordingly, utilities of VGAM2288 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93206. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2289 (VGAM2289) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78108] VGAM2289 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2289 was detected is described hereinabove with reference to Figs. 1-8.

[78109] VGAM2289 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus. VGAM2289 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78110] VGAM2289 gene encodes a VGAM2289 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2289 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2289 precursor RNA is designated SEQ ID:2275, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2275 is located at position 12369 relative to the genome of Murine Hepatitis Virus.

[78111] VGAM2289 precursor RNA folds onto itself, forming VGAM2289 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78112] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2289 folded precursor RNA into VGAM2289 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2289 RNA is designated SEQ ID:5000, and is provided hereinbelow with reference to the sequence listing part.

[78113] VGAM2289 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2289 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2289 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78114] VGAM2289 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2289 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2289 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2289 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2289 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78115] The complementary binding of VGAM2289 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2289 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2289 host target RNA into VGAM2289 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78116] It is appreciated that VGAM2289 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2289 host target genes. The mRNA of each one of this plurality of VGAM2289 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2289 RNA, herein designated VGAM RNA, and which when bound by VGAM2289 RNA causes inhibition of translation of respective one or more VGAM2289 host target proteins.

[78117] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2289 gene, herein designated VGAM GENE, on one or more VGAM2289 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78118] It is yet further appreciated that a function of VGAM2289 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2289 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2289 correlate with, and may be deduced from, the identity of the host target genes which VGAM2289 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78119] Nucleotide sequences of the VGAM2289 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2289 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2289 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2289 are further described hereinbelow with reference to Table 1.

[78120] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2289 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2289 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78121] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2289 gene, herein designated VGAM is inhibition of expression of VGAM2289 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2289 correlate with, and may be deduced from, the identity of the target genes which VGAM2289 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78122] NORE1 (Accession NM_031437) is a VGAM2289 host target gene. NORE1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NORE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NORE1 BINDING SITE, designated SEQ ID:25445, to the nucleotide sequence of VGAM2289 RNA, herein designated VGAM RNA, also designated SEQ ID:5000.

[78123] A function of VGAM2289 is therefore inhibition of NORE1

(Accession NM_031437), a gene which may modulate intracellular signal transduction pathways. Accordingly, utilities of VGAM2289 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NORE1. The function of NORE1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM276.FLJ13117 (Accession NM_023071) is another VGAM2289 host target gene. FLJ13117 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13117, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13117 BINDING SITE, designated SEQ ID:23327, to the nucleotide sequence of VGAM2289 RNA, herein designated VGAM RNA, also designated SEQ ID:5000.

[78124] Another function of VGAM2289 is therefore inhibition of FLJ13117 (Accession NM_023071). Accordingly, utilities of VGAM2289 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13117. KIAA0212 (Accession NM_014674) is another

VGAM2289 host target gene. KIAA0212 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0212, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0212 BINDING SITE, designated SEQ ID:16143, to the nucleotide sequence of VGAM2289 RNA, herein designated VGAM RNA, also designated SEQ ID:5000.

[78125] Another function of VGAM2289 is therefore inhibition of KIAA0212 (Accession NM_014674). Accordingly, utilities of VGAM2289 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0212. KIAA0982 (Accession NM_014023) is another VGAM2289 host target gene. KIAA0982 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0982, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0982 BINDING SITE, designated SEQ ID:15248, to the nucleotide sequence of VGAM2289 RNA, herein designated VGAM RNA, also designated SEQ ID:5000.

[78126] Another function of VGAM2289 is therefore inhibition of KIAA0982 (Accession NM_014023). Accordingly, utilities of VGAM2289 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0982. KIAA1164 (Accession XM_045358) is another VGAM2289 host target gene. KIAA1164 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1164, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1164 BINDING SITE, designated SEQ ID:34442, to the nucleotide sequence of VGAM2289 RNA, herein designated VGAM RNA, also designated SEQ ID:5000.

[78127] Another function of VGAM2289 is therefore inhibition of KIAA1164 (Accession XM_045358). Accordingly, utilities of VGAM2289 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1164. MGC13090 (Accession NM_032711) is another VGAM2289 host target gene. MGC13090 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC13090, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13090 BINDING SITE, designated SEQ ID:26428, to the nucleotide sequence of VGAM2289 RNA, herein designated VGAM RNA, also designated SEQ ID:5000.

[78128] Another function of VGAM2289 is therefore inhibition of MGC13090 (Accession NM_032711). Accordingly, utilities of VGAM2289 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13090. Oxysterol Binding Protein-like 8 (OSBPL8, Accession NM_020841) is another VGAM2289 host target gene. OSBPL8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL8 BINDING SITE, designated SEQ ID:21906, to the nucleotide sequence of VGAM2289 RNA, herein designated VGAM RNA, also designated SEQ ID:5000.

[78129] Another function of VGAM2289 is therefore inhibition of Oxysterol Binding Protein-like 8 (OSBPL8, Accession NM_020841). Accordingly, utilities of VGAM2289 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL8. PTK6 Protein Tyrosine Kinase 6 (PTK6, Accession NM_005975) is another VGAM2289 host target gene. PTK6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTK6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTK6 BINDING SITE, designated SEQ ID:12601, to the nucleotide sequence of VGAM2289 RNA, herein designated VGAM RNA, also designated SEQ ID:5000.

[78130] Another function of VGAM2289 is therefore inhibition of PTK6 Protein Tyrosine Kinase 6 (PTK6, Accession NM_005975). Accordingly, utilities of VGAM2289 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTK6. SB52 (Accession NM_138335) is another VGAM2289 host target gene. SB52 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SB52, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

SB52 BINDING SITE, designated SEQ ID:28734, to the nucleotide sequence of VGAM2289 RNA, herein designated VGAM RNA, also designated SEQ ID:5000.

[78131] Another function of VGAM2289 is therefore inhibition of SB52 (Accession NM_138335). Accordingly, utilities of VGAM2289 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SB52. Solute Carrier Family 5 (choline transporter), Member 7 (SLC5A7, Accession NM_021815) is another VGAM2289 host target gene. SLC5A7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC5A7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC5A7 BINDING SITE, designated SEQ ID:22393, to the nucleotide sequence of VGAM2289 RNA, herein designated VGAM RNA, also designated SEQ ID:5000.

[78132] Another function of VGAM2289 is therefore inhibition of Solute Carrier Family 5 (choline transporter), Member 7 (SLC5A7, Accession NM_021815). Accordingly, utilities of VGAM2289 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

SLC5A7. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2290 (VGAM2290) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78133] VGAM2290 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2290 was detected is described hereinabove with reference to Figs. 1-8.

[78134] VGAM2290 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus. VGAM2290 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78135] VGAM2290 gene encodes a VGAM2290 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2290 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2290 precursor RNA is designated SEQ ID:2276, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2276 is located at position 16166 relative to the genome of Murine Hepatitis Virus.

[78136] VGAM2290 precursor RNA folds onto itself, forming VGAM2290 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78137] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2290 folded precursor RNA into VGAM2290 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2290 RNA is designated SEQ ID:5001, and is provided hereinbelow with reference to the sequence listing part.

[78138] VGAM2290 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2290 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2290 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78139] VGAM2290 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2290 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2290 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2290 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2290 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78140] The complementary binding of VGAM2290 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2290 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2290 host target RNA into VGAM2290 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78141] It is appreciated that VGAM2290 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2290 host target genes. The mRNA of each one of this plurality of VGAM2290 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2290 RNA, herein designated VGAM RNA, and which when bound by VGAM2290 RNA causes

inhibition of translation of respective one or more VGAM2290 host target proteins.

[78142] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2290 gene, herein designated VGAM GENE, on one or more VGAM2290 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78143] It is yet further appreciated that a function of VGAM2290 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2290 include diagnosis, prevention and

treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2290 correlate with, and may be deduced from, the identity of the host target genes which VGAM2290 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78144] Nucleotide sequences of the VGAM2290 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2290 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2290 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2290 are further described hereinbelow with reference to Table 1.

[78145] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2290 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2290 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78146] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2290 gene, herein designated VGAM is inhibition of expression of VGAM2290 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2290 correlate with, and may be deduced from, the identity of the target genes which VGAM2290 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78147] FLJ13912 (Accession NM_022770) is a VGAM2290 host target gene. FLJ13912 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13912, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13912 BINDING SITE, designated SEQ ID:23030, to the nucleotide sequence of VGAM2290 RNA, herein designated VGAM RNA, also designated SEQ ID:5001.

[78148] A function of VGAM2290 is therefore inhibition of FLJ13912 (Accession NM_022770). Accordingly, utilities of VGAM2290 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13912. Junctional Adhesion Molecule 1 (JAM1, Accession NM_144503) is another VGAM2290 host target gene. JAM1 BINDING SITE1 and JAM1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of

mRNA encoded by JAM1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JAM1 BINDING SITE1 and JAM1 BINDING SITE2, designated SEQ ID:29338 and SEQ ID:29349 respectively, to the nucleotide sequence of VGAM2290 RNA, herein designated VGAM RNA, also designated SEQ ID:5001.

[78149] Another function of VGAM2290 is therefore inhibition of Junctional Adhesion Molecule 1 (JAM1, Accession NM_144503). Accordingly, utilities of VGAM2290 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAM1. Mitogen-activated Protein Kinase 8 Interacting Protein 3 (MAPK8IP3, Accession NM_033392) is another VGAM2290 host target gene. MAPK8IP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAPK8IP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPK8IP3 BINDING SITE, designated SEQ ID:27219, to the nucleotide sequence of VGAM2290 RNA, herein designated VGAM RNA, also designated SEQ

ID:5001.

[78150] Another function of VGAM2290 is therefore inhibition of Mitogen-activated Protein Kinase 8 Interacting Protein 3 (MAPK8IP3, Accession NM_033392). Accordingly, utilities of VGAM2290 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK8IP3. Olfactory Receptor, Family 2, Subfamily C, Member 3 (OR2C3, Accession XM_060575) is another VGAM2290 host target gene. OR2C3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by OR2C3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OR2C3 BINDING SITE, designated SEQ ID:37178, to the nucleotide sequence of VGAM2290 RNA, herein designated VGAM RNA, also designated SEQ ID:5001.

[78151] Another function of VGAM2290 is therefore inhibition of Olfactory Receptor, Family 2, Subfamily C, Member 3 (OR2C3, Accession XM_060575). Accordingly, utilities of VGAM2290 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OR2C3. Protein Phosphatase 1, Regulatory Subunit 10 (PPP1R10,

Accession NM_002714) is another VGAM2290 host target gene. PPP1R10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R10 BINDING SITE, designated SEQ ID:8576, to the nucleotide sequence of VGAM2290 RNA, herein designated VGAM RNA, also designated SEQ ID:5001.

[78152] Another function of VGAM2290 is therefore inhibition of Protein Phosphatase 1, Regulatory Subunit 10 (PPP1R10, Accession NM_002714). Accordingly, utilities of VGAM2290 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R10. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2291 (VGAM2291) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78153] VGAM2291 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2291 was detected is described hereinabove with reference to Figs. 1-8.

[78154] VGAM2291 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus. VGAM2291 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78155] VGAM2291 gene encodes a VGAM2291 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2291 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2291 precursor RNA is designated SEQ ID:2277, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2277 is located at position 15049 relative to the genome of Murine Hepatitis Virus.

[78156] VGAM2291 precursor RNA folds onto itself, forming VGAM2291 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78157] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2291 folded precursor RNA into VGAM2291 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2291 RNA is designated SEQ ID:5002, and is provided hereinbelow with reference to the sequence listing part.

[78158] VGAM2291 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2291 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2291 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78159] VGAM2291 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2291 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2291 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2291 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2291 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78160] The complementary binding of VGAM2291 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2291 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2291 host target RNA into VGAM2291 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78161] It is appreciated that VGAM2291 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2291 host target genes. The mRNA of each one of this plurality of VGAM2291 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2291 RNA, herein designated VGAM RNA, and which when bound by VGAM2291 RNA causes inhibition of translation of respective one or more VGAM2291 host target proteins.

[78162] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2291 gene, herein designated VGAM GENE, on one or more VGAM2291 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78163] It is yet further appreciated that a function of VGAM2291 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2291 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2291 correlate with, and may be deduced from, the identity of the host target genes which VGAM2291 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78164] Nucleotide sequences of the VGAM2291 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2291 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2291 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2291 are further described hereinbelow with reference to Table 1.

[78165] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2291 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2291 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78166] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2291 gene, herein designated VGAM is inhibition of expression of VGAM2291 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2291 correlate with, and may be deduced from, the identity of the target genes which VGAM2291 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78167] Transient Receptor Potential Cation Channel, Subfamily M, Member 8 (TRPM8, Accession NM_024080) is a VGAM2291 host target gene. TRPM8 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRPM8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPM8 BINDING SITE, designated SEQ ID:23515, to the nucleotide sequence of VGAM2291 RNA, herein designated VGAM RNA, also designated SEQ ID:5002.

[78168] A function of VGAM2291 is therefore inhibition of Transient Receptor Potential Cation Channel, Subfamily M, Member 8 (TRPM8, Accession NM_024080), a gene which is thought to form a receptor-activated calcium permeant cation channel. Accordingly, utilities of VGAM2291 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPM8. The function of TRPM8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM201.Paired Mesoderm Homeobox 2b (PMX2B, Accession NM_003924) is another VGAM2291 host target gene. PMX2B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PMX2B, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMX2B BINDING SITE, designated SEQ ID:10015, to the nucleotide sequence of VGAM2291 RNA, herein designated VGAM RNA, also designated SEQ ID:5002.

[78169] Another function of VGAM2291 is therefore inhibition of Paired Mesoderm Homeobox 2b (PMX2B, Accession NM_003924). Accordingly, utilities of VGAM2291 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMX2B. LOC130813 (Accession XM_065904) is another VGAM2291 host target gene. LOC130813 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130813, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130813 BINDING SITE, designated SEQ ID:37309, to the nucleotide sequence of VGAM2291 RNA, herein designated VGAM RNA, also designated SEQ ID:5002.

[78170] Another function of VGAM2291 is therefore inhibition of LOC130813 (Accession XM_065904). Accordingly, utilities

of VGAM2291 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130813. LOC135818 (Accession XM_059804) is another VGAM2291 host target gene. LOC135818 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC135818, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC135818 BINDING SITE, designated SEQ ID:37092, to the nucleotide sequence of VGAM2291 RNA, herein designated VGAM RNA, also designated SEQ ID:5002.

[78171] Another function of VGAM2291 is therefore inhibition of LOC135818 (Accession XM_059804). Accordingly, utilities of VGAM2291 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135818. LOC196528 (Accession XM_113745) is another VGAM2291 host target gene. LOC196528 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196528, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC196528 BINDING SITE, designated SEQ ID:42405, to the nucleotide sequence of VGAM2291 RNA, herein designated VGAM RNA, also designated SEQ ID:5002.

[78172] Another function of VGAM2291 is therefore inhibition of LOC196528 (Accession XM_113745). Accordingly, utilities of VGAM2291 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196528. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2292 (VGAM2292) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78173] VGAM2292 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2292 was detected is described hereinabove with reference to Figs. 1-8.

[78174] VGAM2292 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus. VGAM2292 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78175] VGAM2292 gene encodes a VGAM2292 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2292 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2292 precursor RNA is designated SEQ ID:2278, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2278 is located at position 5645 relative to the genome of Murine Hepatitis Virus.

[78176] VGAM2292 precursor RNA folds onto itself, forming VGAM2292 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78177] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2292 folded precursor RNA into VGAM2292 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2292 RNA is designated SEQ ID:5003, and is provided hereinbelow with reference to the sequence listing part.

[78178] VGAM2292 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2292 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2292 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78179] VGAM2292 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2292 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2292 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2292 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2292 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78180] The complementary binding of VGAM2292 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2292 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2292 host target RNA into VGAM2292 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78181] It is appreciated that VGAM2292 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2292 host target genes. The mRNA of each one of this plurality of VGAM2292 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2292 RNA, herein designated VGAM RNA, and which when bound by VGAM2292 RNA causes inhibition of translation of respective one or more VGAM2292 host target proteins.

[78182] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2292 gene, herein designated VGAM GENE, on one or more VGAM2292 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78183] It is yet further appreciated that a function of VGAM2292 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2292 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2292 correlate with, and may be deduced from, the identity of the host target genes which VGAM2292 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78184] Nucleotide sequences of the VGAM2292 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2292 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2292 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2292 are further described hereinbelow with reference to Table 1.

[78185] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2292 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2292 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78186] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2292 gene, herein designated VGAM is inhibition of expression of VGAM2292 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2292 correlate with, and may be deduced from, the identity of the target genes which VGAM2292 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78187] DKFZP564D0478 (Accession NM_032125) is a VGAM2292 host target gene. DKFZP564D0478 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564D0478, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564D0478 BINDING SITE, designated SEQ ID:25811, to the nucleotide sequence of VGAM2292 RNA, herein designated VGAM RNA, also designated SEQ ID:5003.

[78188] A function of VGAM2292 is therefore inhibition of DK-

FZP564D0478 (Accession NM_032125). Accordingly, utilities of VGAM2292 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564D0478. DKFZP566G1424 (Accession XM_097771) is another VGAM2292 host target gene. DKFZP566G1424 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP566G1424, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566G1424 BINDING SITE, designated SEQ ID:41118, to the nucleotide sequence of VGAM2292 RNA, herein designated VGAM RNA, also designated SEQ ID:5003.

[78189] Another function of VGAM2292 is therefore inhibition of DKFZP566G1424 (Accession XM_097771). Accordingly, utilities of VGAM2292 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566G1424. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2293 (VGAM2293) viral gene, which modulates expression of respective host tar-

get genes thereof, the function and utility of which host target genes is known in the art.

[78190] VGAM2293 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2293 was detected is described hereinabove with reference to Figs. 1-8.

[78191] VGAM2293 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus. VGAM2293 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78192] VGAM2293 gene encodes a VGAM2293 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2293 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2293 precursor RNA is designated SEQ ID:2279, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2279 is located at position 25465 relative to the genome of Murine Hepatitis Virus.

[78193] VGAM2293 precursor RNA folds onto itself, forming VGAM2293 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78194] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2293 folded precursor RNA into VGAM2293 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 76%) nucleotide sequence of VGAM2293 RNA is designated SEQ ID:5004, and is provided hereinbelow with reference to the sequence listing part.

[78195] VGAM2293 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2293 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2293 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78196] VGAM2293 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2293 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2293 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2293 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2293 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78197] The complementary binding of VGAM2293 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2293 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2293 host target RNA into VGAM2293 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78198] It is appreciated that VGAM2293 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2293 host target genes. The mRNA of each one of this plurality of VGAM2293 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2293 RNA, herein designated VGAM RNA, and which when bound by VGAM2293 RNA causes inhibition of translation of respective one or more VGAM2293 host target proteins.

[78199] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2293 gene, herein designated VGAM GENE, on one or more VGAM2293 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78200] It is yet further appreciated that a function of VGAM2293 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2293 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2293 correlate with, and may be deduced from, the identity of the host target genes which VGAM2293 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[78201] Nucleotide sequences of the VGAM2293 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2293 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2293 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2293 are further described hereinbelow with reference to Table 1.

[78202] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2293 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2293 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78203] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2293 gene, herein designated VGAM is inhibition of expression of VGAM2293 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2293 correlate with, and may be deduced from, the identity of the target genes which VGAM2293 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78204] Microtubule-associated Protein 1A (MAP1A, Accession NM_002373) is a VGAM2293 host target gene. MAP1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP1A BINDING SITE, designated SEQ ID:8185, to the nucleotide sequence of VGAM2293 RNA, herein designated VGAM RNA, also designated SEQ ID:5004.

[78205] A function of VGAM2293 is therefore inhibition of Microtubule-associated Protein 1A (MAP1A, Accession NM_002373), a gene which is a structural protein involved in the filamentous cross- bridging between microtubules and other skeletal elements. Accordingly, utilities of VGAM2293 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP1A. The function of MAP1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM315.Villin 2 (ezrin) (VIL2, Accession NM_003379) is another VGAM2293 host target gene. VIL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by VIL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VIL2 BINDING SITE, designated SEQ ID:9410, to the nucleotide sequence of VGAM2293 RNA, herein designated VGAM RNA, also designated SEQ ID:5004.

[78206] Another function of VGAM2293 is therefore inhibition of Villin 2 (ezrin) (VIL2, Accession NM_003379), a gene which is involved in the formation of the immunological synapse and in T cell activation. Accordingly, utilities of VGAM2293 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIL2. The function of VIL2 has been established by previous studies. The immunologic synapse is the T cell-APC (antigen-presenting cell) contact site where T-cell receptors, coreceptors, signaling molecules, and adhesion receptors polarize upon antigen recognition. The formation of the immunologic synapse is thought to be important for receptor signal transduction and full T-lymphocyte activation. Using superantigen-stimulated Jurkat cells and confocal microscopy, Roumier et al. (2001) demonstrated that ezrin, F-actin (see OMIM Ref. No. ACTA1; 102610),

and CD43 (OMIM Ref. No. 182160) relocalize to the sides, not the center, of the T cell-APC contact area after T-cell activation, suggesting that ezrin may contribute to setting the scaffold between the actin cytoskeleton and transmembrane proteins facilitating cell-cell interactions and receptor retention. Using mouse helper T cell lines and confocal microscopy, Allenspach et al. (2001) determined that the cytoplasmic tail of CD43 is necessary and sufficient for CD43 removal from the immunologic synapse. In at least some cells, CD43 is located at the distal pole of the T cell together with ezrin and moesin. No differences in the behavior of ezrin and moesin were noted throughout the study. Using cells from Cd43 -/- mice, Allenspach et al. (2001) observed that ERM proteins move independently of the large CD43 mucin. Overexpression of a dominant-negative ERM mutant containing the N-terminal 320 amino acids of ezrin inhibited the activation-induced movement of CD43 without affecting conjugate formation. The dominant-negative mutant reduced cytokine production but not the expression of T-cell activation markers

[78207] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[78208] Roumier, A.; Olivo-Marin, J. C.; Arpin, M.; Michel, F.; Martin, M.; Mangeat, P.; Acuto, O.; Dautry-Varsat, A.; Alcover, A. : The membrane-microfilament linker ezrin is involved in the formation of the immunological synapse and in T cell activation. Immunity 15: 715-728, 2001. ; and

[78209] Allenspach, E. J.; Cullinan, P.; Tong, J.; Tang, Q.; Tesciuba, A. G.; Cannon, J. L.; Takahashi, S. M.; Morgan, R.; Burkhardt, J. K.; Sperling, A. I. : ERM-dependent movement of CD43 defin.

[78210] Further studies establishing the function and utilities of VIL2 are found in John Hopkins OMIM database record ID 123900, and in sited publications numbered 4347-4355 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.ATP-binding Cassette, Sub-family A (ABC1), Member 10 (ABCA10, Accession NM_080282) is another VGAM2293 host target gene. ABCA10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ABCA10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCA10 BINDING SITE, designated SEQ ID:27825, to the nucleotide sequence of VGAM2293 RNA,

herein designated VGAM RNA, also designated SEQ ID:5004.

[78211] Another function of VGAM2293 is therefore inhibition of ATP-binding Cassette, Sub-family A (ABC1), Member 10 (ABCA10, Accession NM_080282). Accordingly, utilities of VGAM2293 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCA10. Chromosome 11 Open Reading Frame 23 (C11orf23, Accession NM_018312) is another VGAM2293 host target gene. C11orf23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf23 BINDING SITE, designated SEQ ID:20301, to the nucleotide sequence of VGAM2293 RNA, herein designated VGAM RNA, also designated SEQ ID:5004.

[78212] Another function of VGAM2293 is therefore inhibition of Chromosome 11 Open Reading Frame 23 (C11orf23, Accession NM_018312). Accordingly, utilities of VGAM2293 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf23.

KIAA0472 (Accession XM_050147) is another VGAM2293 host target gene. KIAA0472 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0472, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0472 BINDING SITE, designated SEQ ID:35575, to the nucleotide sequence of VGAM2293 RNA, herein designated VGAM RNA, also designated SEQ ID:5004.

[78213] Another function of VGAM2293 is therefore inhibition of KIAA0472 (Accession XM_050147). Accordingly, utilities of VGAM2293 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0472. KIAA0847 (Accession XM_085298) is another VGAM2293 host target gene. KIAA0847 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0847, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0847 BINDING SITE, designated SEQ ID:38047, to the nucleotide sequence of VGAM2293 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5004.

[78214] Another function of VGAM2293 is therefore inhibition of KIAA0847 (Accession XM_085298). Accordingly, utilities of VGAM2293 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0847. LBP-9 (Accession NM_014553) is another VGAM2293 host target gene. LBP-9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LBP-9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LBP-9 BINDING SITE, designated SEQ ID:15876, to the nucleotide sequence of VGAM2293 RNA, herein designated VGAM RNA, also designated SEQ ID:5004.

[78215] Another function of VGAM2293 is therefore inhibition of LBP-9 (Accession NM_014553). Accordingly, utilities of VGAM2293 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LBP-9. LOC143914 (Accession XM_084654) is another VGAM2293 host target gene. LOC143914 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143914, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143914 BINDING SITE, designated SEQ ID:37634, to the nucleotide sequence of VGAM2293 RNA, herein designated VGAM RNA, also designated SEQ ID:5004.

[78216] Another function of VGAM2293 is therefore inhibition of LOC143914 (Accession XM_084654). Accordingly, utilities of VGAM2293 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143914. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2294 (VGAM2294) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78217] VGAM2294 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2294 was detected is described hereinabove with reference to Figs. 1-8.

[78218] VGAM2294 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Murine Hepatitis Virus.

VGAM2294 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78219] VGAM2294 gene encodes a VGAM2294 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2294 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2294 precursor RNA is designated SEQ ID:2280, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2280 is located at position 22784 relative to the genome of Murine Hepatitis Virus.

[78220] VGAM2294 precursor RNA folds onto itself, forming VGAM2294 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78221] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2294 folded precursor RNA into VGAM2294 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2294 RNA is designated SEQ ID:5005, and is provided hereinbelow with reference to the sequence listing part.

[78222] VGAM2294 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2294 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2294 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78223] VGAM2294 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2294 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2294 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2294 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2294 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78224] The complementary binding of VGAM2294 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2294 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2294 host target RNA into VGAM2294 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78225] It is appreciated that VGAM2294 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2294 host target genes. The mRNA of each one of this plurality of VGAM2294 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2294 RNA, herein designated VGAM RNA, and which when bound by VGAM2294 RNA causes inhibition of translation of respective one or more VGAM2294 host target proteins.

[78226] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2294 gene, herein designated VGAM GENE, on one or more VGAM2294 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78227] It is yet further appreciated that a function of VGAM2294 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2294 include diagnosis, prevention and treatment of viral infection by Murine Hepatitis Virus. Specific functions, and accordingly utilities, of VGAM2294 correlate with, and may be deduced from, the identity of the host target genes which VGAM2294 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78228] Nucleotide sequences of the VGAM2294 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2294 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2294 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2294 are further described hereinbelow with reference to Table 1.

[78229] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2294 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2294 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78230] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2294 gene, herein designated VGAM is inhibition of expression of VGAM2294 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2294 correlate with, and may be deduced from, the identity of the target genes which VGAM2294 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78231] A Disintegrin and Metalloproteinase Domain 19 (meltrin beta) (ADAM19, Accession NM_033274) is a VGAM2294 host target gene. ADAM19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADAM19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAM19 BINDING SITE,

designated SEQ ID:27093, to the nucleotide sequence of VGAM2294 RNA, herein designated VGAM RNA, also designated SEQ ID:5005.

[78232] A function of VGAM2294 is therefore inhibition of A Disintegrin and Metalloproteinase Domain 19 (meltrin beta) (ADAM19, Accession NM_033274), a gene which participates in the proteolytic processing of beta-type neuregulin isoforms . Accordingly, utilities of VGAM2294 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAM19. The function of ADAM19 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM179.LOC92228 (Accession XM_043731) is another VGAM2294 host target gene. LOC92228 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92228, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92228 BINDING SITE, designated SEQ ID:34002, to the nucleotide sequence of VGAM2294 RNA, herein designated VGAM RNA, also designated SEQ ID:5005.

[78233] Another function of VGAM2294 is therefore inhibition of LOC92228 (Accession XM_043731). Accordingly, utilities of VGAM2294 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92228. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2295 (VGAM2295) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78234] VGAM2295 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2295 was detected is described hereinabove with reference to Figs. 1-8.

[78235] VGAM2295 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2295 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78236] VGAM2295 gene encodes a VGAM2295 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2295 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2295 precursor RNA is designated SEQ ID:2281, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2281 is located at position 43938 relative to the genome of Ectromelia Virus.

[78237] VGAM2295 precursor RNA folds onto itself, forming VGAM2295 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78238] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2295 folded precursor RNA into VGAM2295 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2295 RNA is designated SEQ ID:5006, and is provided hereinbelow with reference to the sequence listing part.

[78239] VGAM2295 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2295 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2295 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78240] VGAM2295 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2295 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2295 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2295 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2295 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78241] The complementary binding of VGAM2295 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2295 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2295 host target RNA into VGAM2295 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78242] It is appreciated that VGAM2295 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2295 host target genes. The mRNA of each one of this plurality of VGAM2295 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2295 RNA, herein designated VGAM RNA, and which when bound by VGAM2295 RNA causes inhibition of translation of respective one or more VGAM2295 host target proteins.

[78243] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2295 gene, herein designated VGAM GENE, on one or more VGAM2295 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78244] It is yet further appreciated that a function of VGAM2295 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2295 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2295 correlate with, and may be deduced from, the identity of the host target genes which VGAM2295 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78245] Nucleotide sequences of the VGAM2295 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2295 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2295 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2295 are further described hereinbelow with reference to Table 1.

[78246] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2295 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2295 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[78247] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2295 gene, herein designated VGAM is inhibition of expression of VGAM2295 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2295 correlate with, and may be deduced from, the identity of the target genes which VGAM2295 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78248] TAF9 RNA Polymerase II, TATA Box Binding Protein (TBP)-associated Factor, 32kDa (TAF9, Accession NM_003187) is a VGAM2295 host target gene. TAF9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TAF9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAF9 BINDING SITE, designated SEQ ID:9163, to the nucleotide sequence of VGAM2295 RNA, herein designated VGAM RNA, also designated SEQ ID:5006.

[78249] A function of VGAM2295 is therefore inhibition of TAF9 RNA Polymerase II, TATA Box Binding Protein (TBP)-associated Factor, 32kDa (TAF9, Accession

NM_003187), a gene which may function as a coactivator of transcription. Accordingly, utilities of VGAM2295 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAF9. The function of TAF9 has been established by previous studies. Klemm et al. (1995) cloned a human TFIID subunit, which they termed hTAFII32. The 32-kD protein was isolated from HeLa cell nuclear extracts and partially sequenced. A degenerate oligomer was designed and used to probe a human HeLa cell cDNA library. The identified cDNA has a deduced amino acid sequence of 264 residues and is related to the Drosophila TAFII40. Klemm et al. (1995) showed that TAFII32 interacts with GTF2B (OMIM Ref. No. 189963) and with the viral transcriptional transactivator VP16. The authors showed that recombinantly expressed TAFII32 was functional in a partial recombinant TFIID complex and that the recombinant complex mediated activation by a GAL4-VP16 fusion protein. Lu and Levine (1995) cloned TAF9, which they called TAFII31. TAF9 encodes a 264-amino acid protein. Immunoprecipitation and binding analyses showed interaction of TAF9 with the N-terminal domain of p53 (OMIM Ref. No. 191170) at sites identical to those bound by MDM2 (OMIM Ref. No. 164785), the

major cellular negative regulator of p53 activity. Antibodies to TAF9 inhibited p53-activated transcription. Lu and Levine (1995) concluded that p53 activity is regulated by 2 proteins competing for the same region of the p53 protein.

[78250] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[78251] Klemm, R. D.; Goodrich, J. A.; Zhou, S.; Tjian, R. : Molecular cloning and expression of the 32-kDa subunit of human TFIID reveals interactions with VP16 and TFIIB that mediate transcriptional activation. Proc. Nat. Acad. Sci. 92: 5788-5792, 1995. ; and

[78252] Lu, H.; Levine, A. J. : Human TAFII31 protein is a transcriptional coactivator of the p53 protein. Proc. Nat. Acad. Sci. 92: 5154-5158, 1995.

[78253] Further studies establishing the function and utilities of TAF9 are found in John Hopkins OMIM database record ID 600822, and in sited publications numbered 7536-7538 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.KIAA1866 (Accession XM_027658) is another VGAM2295 host target gene. KIAA1866 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by KIAA1866, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1866 BINDING SITE, designated SEQ ID:30554, to the nucleotide sequence of VGAM2295 RNA, herein designated VGAM RNA, also designated SEQ ID:5006.

[78254] Another function of VGAM2295 is therefore inhibition of KIAA1866 (Accession XM_027658). Accordingly, utilities of VGAM2295 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1866. LOC200269 (Accession XM_114175) is another VGAM2295 host target gene. LOC200269 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200269, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200269 BINDING SITE, designated SEQ ID:42757, to the nucleotide sequence of VGAM2295 RNA, herein designated VGAM RNA, also designated SEQ ID:5006.

[78255] Another function of VGAM2295 is therefore inhibition of

LOC200269 (Accession XM_114175). Accordingly, utilities of VGAM2295 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200269. LOC255461 (Accession XM_173207) is another VGAM2295 host target gene. LOC255461 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255461, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255461 BINDING SITE, designated SEQ ID:46461, to the nucleotide sequence of VGAM2295 RNA, herein designated VGAM RNA, also designated SEQ ID:5006.

[78256] Another function of VGAM2295 is therefore inhibition of LOC255461 (Accession XM_173207). Accordingly, utilities of VGAM2295 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255461. LOC255516 (Accession XM_173212) is another VGAM2295 host target gene. LOC255516 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC255516 BINDING SITE, designated SEQ ID:46467, to the nucleotide sequence of VGAM2295 RNA, herein designated VGAM RNA, also designated SEQ ID:5006.

[78257] Another function of VGAM2295 is therefore inhibition of LOC255516 (Accession XM_173212). Accordingly, utilities of VGAM2295 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255516. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2296 (VGAM2296) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78258] VGAM2296 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2296 was detected is described hereinabove with reference to Figs. 1-8.

[78259] VGAM2296 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2296 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[78260] VGAM2296 gene encodes a VGAM2296 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2296 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2296 precursor RNA is designated SEQ ID:2282, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2282 is located at position 27612 relative to the genome of Ectromelia Virus.

[78261] VGAM2296 precursor RNA folds onto itself, forming VGAM2296 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78262] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2296 folded precursor RNA into VGAM2296 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2296 RNA is designated SEQ ID:5007, and is provided hereinbelow with reference to the sequence listing part.

[78263] VGAM2296 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2296 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2296 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78264] VGAM2296 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2296 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2296 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2296 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2296 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78265] The complementary binding of VGAM2296 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2296 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2296 host target RNA into VGAM2296 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78266] It is appreciated that VGAM2296 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2296 host target genes. The mRNA of each one of this plurality of VGAM2296 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2296 RNA, herein designated VGAM RNA, and which when bound by VGAM2296 RNA causes inhibition of translation of respective one or more VGAM2296 host target proteins.

[78267] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2296 gene, herein designated VGAM GENE, on one or more VGAM2296 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78268] It is yet further appreciated that a function of VGAM2296 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2296 correlate with, and may be deduced from, the identity of the host target genes which VGAM2296 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78269] Nucleotide sequences of the VGAM2296 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2296 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2296 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2296 are further described hereinbelow with reference to Table 1.

[78270] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2296 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2296 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78271] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2296 gene, herein designated VGAM is inhibition of expression of VGAM2296 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2296 correlate with, and may be deduced from, the identity of the target genes which VGAM2296 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78272] Cadherin 11, Type 2, OB-cadherin (osteoblast) (CDH11, Accession NM_033664) is a VGAM2296 host target gene. CDH11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDH11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDH11 BINDING SITE, designated SEQ ID:27392, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ

ID:5007.

[78273] A function of VGAM2296 is therefore inhibition of Cadherin 11, Type 2, OB-cadherin (osteoblast) (CDH11, Accession NM_033664), a gene which plays an role in development and maintenance of tissues. Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH11. The function of CDH11 has been established by previous studies. Cadherins are a group of cell surface glycoproteins that mediate Ca(2+)-dependent cell-cell adhesion (Tanihara et al., 1994). These proteins have a molecular mass of about 120 kD and are composed of an extracellular domain at the N-terminal end and a relatively small cytoplasmic domain at the C-terminal end; the 2 domains are connected by a single membrane-spanning sequence. The extracellular domain consists of 5 subdomains, each of which contains a cadherin-specific motif. Cadherin expression is regulated spatially as well as temporally. Cadherins are thought to play an important role in development and maintenance of tissues through selective cell-cell adhesion activity and may be involved also in the invasion and metastasis of malignant tumors. Okazaki et al. (1994) identified a new member of the cadherin

family, which they called OB (osteoblast)-cadherin, in a mouse osteoblastic cell line and human osteosarcoma. OB-cadherin was also weakly expressed in stroma cell lines that are the progenitor cells of osteoblasts. Expression of the CDHOB gene in the osteoblastic cell line was up-regulated during differentiation, suggesting a specific function in bone cell differentiation and bone formation. Two different forms of human OB-cadherin cDNA were cloned; one was a counterpart of the mouse gene and the other encoded a protein with a truncated cytoplasmic domain. The protein was designated cadherin-11 (symbol: CDH11) by the Human Genome Nomenclature Committee.

[78274] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[78275] Kools, P.; Vanhalst, K.; Wan den Eynde, E.; van Roy, F. : The human cadherin-10 gene: complete coding sequence, predominant expression in the brain and mapping on chromosome 5p13-13. FEBS Lett. 452: 328-334, 1999. ; and

[78276] Suzuki, S.; Sano, K.; Tanihara, H. : Diversity of the cadherin family: evidence for eight new cadherins in nervous tissue. Cell Regul. 2: 261-270, 1991.

[78277] Further studies establishing the function and utilities of CDH11 are found in John Hopkins OMIM database record ID 600023, and in sited publications numbered 833 and 11646-8336 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Enolase 2, (gamma, neuronal) (ENO2, Accession NM_001975) is another VGAM2296 host target gene. ENO2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ENO2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ENO2 BINDING SITE, designated SEQ ID:7704, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ ID:5007.

[78278] Another function of VGAM2296 is therefore inhibition of Enolase 2, (gamma, neuronal) (ENO2, Accession NM_001975), a gene which converts 2-phospho-D-glycerate to phosphoenolpyruvate in glycolysis. Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENO2. The function of ENO2 and its association with various diseases and clinical con-

ditions, has been established by previous studies, as described hereinabove with reference to VGAM1151.Klotho (KL, Accession NM_004795) is another VGAM2296 host target gene. KL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KL BINDING SITE, designated SEQ ID:11203, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ ID:5007.

[78279] Another function of VGAM2296 is therefore inhibition of Klotho (KL, Accession NM_004795), a gene which has similarity to beta-glucosidases. Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KL. The function of KL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1730.Claudin 1 (CLDN1, Accession NM_021101) is another VGAM2296 host target gene. CLDN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLDN1, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLDN1 BINDING SITE, designated SEQ ID:22079, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ ID:5007.

[78280] Another function of VGAM2296 is therefore inhibition of Claudin 1 (CLDN1, Accession NM_021101). Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLDN1. Golgi Associated, Gamma Adaptin Ear Containing, ARF Binding Protein 2 (GGA2, Accession NM_138640) is another VGAM2296 host target gene. GGA2 BINDING SITE1 and GGA2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GGA2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE1 and GGA2 BINDING SITE2, designated SEQ ID:28918 and SEQ ID:17398 respectively, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ ID:5007.

[78281] Another function of VGAM2296 is therefore inhibition of Golgi Associated, Gamma Adaptin Ear Containing, ARF Binding Protein 2 (GGA2, Accession NM_138640). Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2. KIAA0323 (Accession XM_032634) is another VGAM2296 host target gene. KIAA0323 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0323 BINDING SITE, designated SEQ ID:31694, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ ID:5007.

[78282] Another function of VGAM2296 is therefore inhibition of KIAA0323 (Accession XM_032634). Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0323. KIAA1582 (Accession XM_037262) is another VGAM2296 host target gene. KIAA1582 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1582, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1582 BINDING SITE, designated SEQ ID:32585, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ ID:5007.

[78283] Another function of VGAM2296 is therefore inhibition of KIAA1582 (Accession XM_037262). Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1582. phorbolin-1 (Accession XM_114206) is another VGAM2296 host target gene. phorbolin-1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by phorbolin-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of phorbolin-1 BINDING SITE, designated SEQ ID:42797, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ ID:5007.

[78284] Another function of VGAM2296 is therefore inhibition of phorbolin-1 (Accession XM_114206). Accordingly, utilities of VGAM2296 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with phorbolin-1. Proline-rich Gla (G-carboxyglutamic acid) Polypeptide 1 (PRRG1, Accession NM_000950) is another VGAM2296 host target gene. PRRG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRRG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRRG1 BINDING SITE, designated SEQ ID:6654, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ ID:5007.

[78285] Another function of VGAM2296 is therefore inhibition of Proline-rich Gla (G-carboxyglutamic acid) Polypeptide 1 (PRRG1, Accession NM_000950). Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRRG1. Three Prime Repair Exonuclease 1 (TREX1, Accession NM_033627) is another VGAM2296 host target gene. TREX1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TREX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of TREX1 BINDING SITE, designated SEQ ID:27339, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ ID:5007.

[78286] Another function of VGAM2296 is therefore inhibition of Three Prime Repair Exonuclease 1 (TREX1, Accession NM_033627). Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TREX1. LOC219653 (Accession XM_166093) is another VGAM2296 host target gene. LOC219653 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219653, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219653 BINDING SITE, designated SEQ ID:43866, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ ID:5007.

[78287] Another function of VGAM2296 is therefore inhibition of LOC219653 (Accession XM_166093). Accordingly, utilities of VGAM2296 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC219653. LOC51285 (Accession NM_016563) is another VGAM2296 host target gene. LOC51285 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51285, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51285 BINDING SITE, designated SEQ ID:18635, to the nucleotide sequence of VGAM2296 RNA, herein designated VGAM RNA, also designated SEQ ID:5007.

[78288] Another function of VGAM2296 is therefore inhibition of LOC51285 (Accession NM_016563). Accordingly, utilities of VGAM2296 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51285. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2297 (VGAM2297) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78289] VGAM2297 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2297 was detected is described hereinabove with reference to Figs. 1-8.

[78290] VGAM2297 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2297 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78291] VGAM2297 gene encodes a VGAM2297 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2297 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2297 precursor RNA is designated SEQ ID:2283, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2283 is located at position 28555 relative to the genome of Ectromelia Virus.

[78292] VGAM2297 precursor RNA folds onto itself, forming VGAM2297 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78293] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2297 folded precursor RNA into VGAM2297 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2297 RNA is designated SEQ ID:5008, and is provided hereinbelow with reference to the sequence listing part.

[78294] VGAM2297 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2297 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2297 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78295] VGAM2297 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2297 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2297 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2297 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2297 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78296] The complementary binding of VGAM2297 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2297 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2297 host target RNA into VGAM2297 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78297] It is appreciated that VGAM2297 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2297 host target genes. The mRNA of each one of this plurality of VGAM2297 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2297 RNA, herein designated VGAM RNA, and which when bound by VGAM2297 RNA causes inhibition of translation of respective one or more VGAM2297 host target proteins.

[78298] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2297 gene, herein designated VGAM GENE, on one or more VGAM2297 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78299] It is yet further appreciated that a function of VGAM2297 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2297 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2297 correlate with, and may be deduced from, the identity of the host target genes which VGAM2297 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78300] Nucleotide sequences of the VGAM2297 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2297 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2297 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2297 are further described hereinbelow with reference to Table 1.

[78301] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2297 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2297 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78302] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2297 gene, herein designated VGAM is inhibition of expression of VGAM2297 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2297 correlate with, and may be deduced from, the identity of the target genes which VGAM2297 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78303] Mitogen-activated Protein Kinase 14 (MAPK14, Accession NM_001315) is a VGAM2297 host target gene. MAPK14 BINDING SITE1 through MAPK14 BINDING SITE3 are HOST

TARGET binding sites found in untranslated regions of mRNA encoded by MAPK14, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPK14 BINDING SITE1 through MAPK14 BINDING SITE3, designated SEQ ID:7005, SEQ ID:29109 and SEQ ID:29116 respectively, to the nucleotide sequence of VGAM2297 RNA, herein designated VGAM RNA, also designated SEQ ID:5008.

[78304] A function of VGAM2297 is therefore inhibition of Mitogen-activated Protein Kinase 14 (MAPK14, Accession NM_001315), a gene which is important for cytokine production; responds to changes in extracellular osmolarity. Accordingly, utilities of VGAM2297 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK14. The function of MAPK14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM107.FLJ25415 (Accession NM_144708) is another VGAM2297 host target gene. FLJ25415 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ25415, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ25415 BINDING SITE, designated SEQ ID:29532, to the nucleotide sequence of VGAM2297 RNA, herein designated VGAM RNA, also designated SEQ ID:5008.

[78305] Another function of VGAM2297 is therefore inhibition of FLJ25415 (Accession NM_144708). Accordingly, utilities of VGAM2297 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25415. PRO2032 (Accession NM_018615) is another VGAM2297 host target gene. PRO2032 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO2032, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2032 BINDING SITE, designated SEQ ID:20686, to the nucleotide sequence of VGAM2297 RNA, herein designated VGAM RNA, also designated SEQ ID:5008.

[78306] Another function of VGAM2297 is therefore inhibition of PRO2032 (Accession NM_018615). Accordingly, utilities of VGAM2297 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with PRO2032. PRO2730 (Accession NM_025222) is another VGAM2297 host target gene. PRO2730 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2730, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2730 BINDING SITE, designated SEQ ID:24899, to the nucleotide sequence of VGAM2297 RNA, herein designated VGAM RNA, also designated SEQ ID:5008.

[78307] Another function of VGAM2297 is therefore inhibition of PRO2730 (Accession NM_025222). Accordingly, utilities of VGAM2297 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2730. LOC149830 (Accession XM_097746) is another VGAM2297 host target gene. LOC149830 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149830, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149830 BINDING SITE, designated SEQ ID:41094, to

the nucleotide sequence of VGAM2297 RNA, herein designated VGAM RNA, also designated SEQ ID:5008.

[78308] Another function of VGAM2297 is therefore inhibition of LOC149830 (Accession XM_097746). Accordingly, utilities of VGAM2297 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149830. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2298 (VGAM2298) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78309] VGAM2298 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2298 was detected is described hereinabove with reference to Figs. 1-8.

[78310] VGAM2298 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2298 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78311] VGAM2298 gene encodes a VGAM2298 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2298 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2298 precursor RNA is designated SEQ ID:2284, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2284 is located at position 32155 relative to the genome of Ectromelia Virus.

[78312] VGAM2298 precursor RNA folds onto itself, forming VGAM2298 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78313] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2298 folded precursor RNA into VGAM2298 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2298 RNA is designated SEQ ID:5009, and is provided hereinbelow with reference to the sequence listing part.

[78314] VGAM2298 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2298 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2298 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78315] VGAM2298 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2298 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2298 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2298 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2298 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78316] The complementary binding of VGAM2298 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2298 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2298 host target RNA into VGAM2298 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78317] It is appreciated that VGAM2298 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2298 host target genes. The mRNA of each one of this plurality of VGAM2298 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2298 RNA, herein designated VGAM RNA, and which when bound by VGAM2298 RNA causes inhibition of translation of respective one or more VGAM2298 host target proteins.

[78318] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2298 gene, herein designated VGAM GENE, on one or more VGAM2298 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78319] It is yet further appreciated that a function of VGAM2298 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2298 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2298 correlate with, and may be deduced from, the identity of the host target genes which VGAM2298 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78320] Nucleotide sequences of the VGAM2298 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2298 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2298 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2298 are further described hereinbelow with reference to Table 1.

[78321] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2298 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2298 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78322] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2298 gene, herein designated VGAM is inhibition of expression of VGAM2298 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2298 correlate with, and may be deduced from, the identity of the target genes which VGAM2298 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78323] FK506 Binding Protein 14, 22 KDa (FKBP14, Accession NM_017946) is a VGAM2298 host target gene. FKBP14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FKBP14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FKBP14 BINDING SITE, designated SEQ ID:19643, to the nucleotide sequence of VGAM2298 RNA, herein designated VGAM RNA, also designated SEQ ID:5009.

[78324] A function of VGAM2298 is therefore inhibition of FK506 Binding Protein 14, 22 KDa (FKBP14, Accession

NM_017946). Accordingly, utilities of VGAM2298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKBP14. MDS028 (Accession NM_018463) is another VGAM2298 host target gene. MDS028 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MDS028, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MDS028 BINDING SITE, designated SEQ ID:20533, to the nucleotide sequence of VGAM2298 RNA, herein designated VGAM RNA, also designated SEQ ID:5009.

[78325] Another function of VGAM2298 is therefore inhibition of MDS028 (Accession NM_018463). Accordingly, utilities of VGAM2298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDS028. LOC203429 (Accession XM_114701) is another VGAM2298 host target gene. LOC203429 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203429, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC203429 BINDING SITE, designated SEQ ID:43047, to the nucleotide sequence of VGAM2298 RNA, herein designated VGAM RNA, also designated SEQ ID:5009.

[78326] Another function of VGAM2298 is therefore inhibition of LOC203429 (Accession XM_114701). Accordingly, utilities of VGAM2298 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203429. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2299 (VGAM2299) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78327] VGAM2299 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2299 was detected is described hereinabove with reference to Figs. 1-8.

[78328] VGAM2299 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2299 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[78329] VGAM2299 gene encodes a VGAM2299 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2299 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2299 precursor RNA is designated SEQ ID:2285, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2285 is located at position 23346 relative to the genome of Ectromelia Virus.

[78330] VGAM2299 precursor RNA folds onto itself, forming VGAM2299 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78331] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2299 folded precursor RNA into VGAM2299 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2299 RNA is designated SEQ ID:5010, and is provided hereinbelow with reference to the sequence listing part.

[78332] VGAM2299 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2299 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2299 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78333] VGAM2299 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2299 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2299 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2299 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2299 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78334] The complementary binding of VGAM2299 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2299 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2299 host target RNA into VGAM2299 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78335] It is appreciated that VGAM2299 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2299 host target genes. The mRNA of each one of this plurality of VGAM2299 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2299 RNA, herein designated VGAM RNA, and which when bound by VGAM2299 RNA causes inhibition of translation of respective one or more VGAM2299 host target proteins.

[78336] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2299 gene, herein designated VGAM GENE, on one or more VGAM2299 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78337] It is yet further appreciated that a function of VGAM2299 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2299 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2299 correlate with, and may be deduced from, the identity of the host target genes which VGAM2299 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78338] Nucleotide sequences of the VGAM2299 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2299 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2299 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2299 are further described hereinbelow with reference to Table 1.

[78339] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2299 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2299 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78340] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2299 gene, herein designated VGAM is inhibition of expression of VGAM2299 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2299 correlate with, and may be deduced from, the identity of the target genes which VGAM2299 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78341] TYRO3 Protein Tyrosine Kinase (TYRO3, Accession NM_006293) is a VGAM2299 host target gene. TYRO3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TYRO3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TYRO3 BINDING SITE, designated SEQ ID:12983, to the nucleotide sequence of VGAM2299 RNA, herein designated VGAM RNA, also designated SEQ ID:5010.

[78342] A function of VGAM2299 is therefore inhibition of TYRO3 Protein Tyrosine Kinase (TYRO3, Accession NM_006293), a gene which may be involved in cell adhesion processes, particularly in the central nervous system. Accordingly, utilities of VGAM2299 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TYRO3. The function of TYRO3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM711.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2300 (VGAM2300) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78343] VGAM2300 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2300 was detected is described hereinabove with reference to Figs. 1-8.

[78344] VGAM2300 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2300 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[78345] VGAM2300 gene encodes a VGAM2300 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2300 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2300 precursor RNA is designated SEQ ID:2286, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2286 is located at position 38978 relative to the genome of Ectromelia Virus.

[78346] VGAM2300 precursor RNA folds onto itself, forming VGAM2300 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78347] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2300 folded precursor RNA into VGAM2300

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2300 RNA is designated SEQ ID:5011, and is provided hereinbelow with reference to the sequence listing part.

[78348] VGAM2300 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2300 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2300 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78349] VGAM2300 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2300 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2300 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2300 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2300 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78350] The complementary binding of VGAM2300 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2300 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2300 host target RNA into VGAM2300 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[78351] It is appreciated that VGAM2300 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2300 host target genes. The mRNA of each one of this plurality of VGAM2300 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2300 RNA, herein designated VGAM RNA, and which when bound by VGAM2300 RNA causes inhibition of translation of respective one or more VGAM2300 host target proteins.

[78352] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2300 gene, herein designated VGAM GENE, on one or more VGAM2300 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78353] It is yet further appreciated that a function of VGAM2300 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2300 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2300 correlate with, and may be deduced from, the identity of the host target genes which VGAM2300 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78354] Nucleotide sequences of the VGAM2300 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2300 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2300 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2300 are further described hereinbelow with reference to Table 1.

[78355] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2300 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2300 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78356] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2300 gene, herein designated VGAM is inhibition of expression of VGAM2300 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2300 correlate with, and may be deduced from, the identity of the target genes which VGAM2300 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78357] RAD17 Homolog (S. pombe) (RAD17, Accession NM_002873) is a VGAM2300 host target gene. RAD17 BINDING SITE1 through RAD17 BINDING SITE6 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RAD17, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD17 BINDING SITE1 through RAD17 BINDING SITE6, designated SEQ ID:8783,

SEQ ID:28480, SEQ ID:28484, SEQ ID:28486, SEQ ID:28488 and SEQ ID:28490 respectively, to the nucleotide sequence of VGAM2300 RNA, herein designated VGAM RNA, also designated SEQ ID:5011.

[78358] A function of VGAM2300 is therefore inhibition of RAD17 Homolog (S. pombe) (RAD17, Accession NM_002873), a gene which may have a role in DNA damage-dependent and DNA replication-dependent cell cycle checkpoints. Accordingly, utilities of VGAM2300 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD17. The function of RAD17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM209.Testis-specific Transcript, Y-linked 2 (TTTY2, Accession XM_099029) is another VGAM2300 host target gene. TTTY2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TTTY2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTTY2 BINDING SITE, designated SEQ ID:42071, to the nucleotide sequence of VGAM2300 RNA,

herein designated VGAM RNA, also designated SEQ ID:5011.

[78359] Another function of VGAM2300 is therefore inhibition of Testis-specific Transcript, Y-linked 2 (TTTY2, Accession XM_099029). Accordingly, utilities of VGAM2300 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTTY2. LOC149606 (Accession XM_086600) is another VGAM2300 host target gene. LOC149606 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149606, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149606 BINDING SITE, designated SEQ ID:38783, to the nucleotide sequence of VGAM2300 RNA, herein designated VGAM RNA, also designated SEQ ID:5011.

[78360] Another function of VGAM2300 is therefore inhibition of LOC149606 (Accession XM_086600). Accordingly, utilities of VGAM2300 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149606. LOC159148 (Accession XM_099030) is another VGAM2300 host target gene. LOC159148 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC159148, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159148 BINDING SITE, designated SEQ ID:42078, to the nucleotide sequence of VGAM2300 RNA, herein designated VGAM RNA, also designated SEQ ID:5011.

[78361] Another function of VGAM2300 is therefore inhibition of LOC159148 (Accession XM_099030). Accordingly, utilities of VGAM2300 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159148. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2301 (VGAM2301) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78362] VGAM2301 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2301 was detected is described hereinabove with reference to Figs. 1-8.

[78363] VGAM2301 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2301 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78364] VGAM2301 gene encodes a VGAM2301 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2301 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2301 precursor RNA is designated SEQ ID:2287, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2287 is located at position 30387 relative to the genome of Ectromelia Virus.

[78365] VGAM2301 precursor RNA folds onto itself, forming VGAM2301 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[78366] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2301 folded precursor RNA into VGAM2301 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2301 RNA is designated SEQ ID:5012, and is provided hereinbelow with reference to the sequence listing part.

[78367] VGAM2301 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2301 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2301 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78368] VGAM2301 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2301 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2301 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2301 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2301 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78369] The complementary binding of VGAM2301 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2301 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2301 host target RNA into VGAM2301 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78370] It is appreciated that VGAM2301 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2301 host target genes. The mRNA of each one of this plurality of VGAM2301 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2301 RNA, herein designated VGAM RNA, and which when bound by VGAM2301 RNA causes inhibition of translation of respective one or more VGAM2301 host target proteins.

[78371] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2301 gene, herein designated VGAM GENE, on one or more VGAM2301 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78372] It is yet further appreciated that a function of VGAM2301 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2301 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2301 correlate with, and may be deduced from, the identity of the host target genes which VGAM2301 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78373] Nucleotide sequences of the VGAM2301 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2301 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2301 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2301 are further described hereinbelow with reference to Table 1.

[78374] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2301 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2301 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78375] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2301 gene, herein designated VGAM is inhibition of expression of VGAM2301 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2301 correlate with, and may be deduced from, the identity of the target genes which VGAM2301 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78376] Ankyrin Repeat Domain 6 (ANKRD6, Accession NM_014942) is a VGAM2301 host target gene. ANKRD6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANKRD6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of ANKRD6 BINDING SITE, designated SEQ ID:17252, to the nucleotide sequence of VGAM2301 RNA, herein designated VGAM RNA, also designated SEQ ID:5012.

[78377] A function of VGAM2301 is therefore inhibition of Ankyrin Repeat Domain 6 (ANKRD6, Accession NM_014942). Accordingly, utilities of VGAM2301 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANKRD6. DKFZP564O1863 (Accession XM_043922) is another VGAM2301 host target gene. DKFZP564O1863 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O1863, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564O1863 BINDING SITE, designated SEQ ID:34044, to the nucleotide sequence of VGAM2301 RNA, herein designated VGAM RNA, also designated SEQ ID:5012.

[78378] Another function of VGAM2301 is therefore inhibition of DKFZP564O1863 (Accession XM_043922). Accordingly, utilities of VGAM2301 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZP564O1863. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2302 (VGAM2302) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78379] VGAM2302 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2302 was detected is described hereinabove with reference to Figs. 1-8.

[78380] VGAM2302 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2302 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78381] VGAM2302 gene encodes a VGAM2302 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2302 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2302 precursor RNA is desig-

nated SEQ ID:2288, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2288 is located at position 44731 relative to the genome of Ectromelia Virus.

[78382] VGAM2302 precursor RNA folds onto itself, forming VGAM2302 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78383] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2302 folded precursor RNA into VGAM2302 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2302 RNA is designated SEQ ID:5013, and is provided hereinbelow with reference to the sequence

listing part.

[78384] VGAM2302 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2302 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2302 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78385] VGAM2302 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2302 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2302 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2302 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2302 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78386] The complementary binding of VGAM2302 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2302 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2302 host target RNA into VGAM2302 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78387] It is appreciated that VGAM2302 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2302 host target genes. The mRNA of each one of this plurality of VGAM2302 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2302 RNA, herein designated VGAM

RNA, and which when bound by VGAM2302 RNA causes inhibition of translation of respective one or more VGAM2302 host target proteins.

[78388] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2302 gene, herein designated VGAM GENE, on one or more VGAM2302 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78389] It is yet further appreciated that a function of VGAM2302 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2302 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2302 correlate with, and may be deduced from, the identity of the host target genes which VGAM2302 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78390] Nucleotide sequences of the VGAM2302 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2302 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2302 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2302 are further described hereinbelow with reference to Table 1.

[78391] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2302 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2302 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78392] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2302 gene, herein designated VGAM is

inhibition of expression of VGAM2302 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2302 correlate with, and may be deduced from, the identity of the target genes which VGAM2302 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78393] Carbonic Anhydrase XII (CA12, Accession NM_001218) is a VGAM2302 host target gene. CA12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CA12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CA12 BINDING SITE, designated SEQ ID:6881, to the nucleotide sequence of VGAM2302 RNA, herein designated VGAM RNA, also designated SEQ ID:5013.

[78394] A function of VGAM2302 is therefore inhibition of Carbonic Anhydrase XII (CA12, Accession NM_001218), a gene which functions in cellular transport and metabolic processes. Accordingly, utilities of VGAM2302 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CA12. The function of CA12 and its association with various diseases and clinical con-

ditions, has been established by previous studies, as described hereinabove with reference to VGAM508.Cytoplasmic Linker Associated Protein 2 (CLASP2, Accession XM_035453) is another VGAM2302 host target gene. CLASP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLASP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLASP2 BINDING SITE, designated SEQ ID:32270, to the nucleotide sequence of VGAM2302 RNA, herein designated VGAM RNA, also designated SEQ ID:5013.

[78395] Another function of VGAM2302 is therefore inhibition of Cytoplasmic Linker Associated Protein 2 (CLASP2, Accession XM_035453), a gene which is involved in the regional regulation of microtubule dynamics in motile fibroblasts. Accordingly, utilities of VGAM2302 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLASP2. The function of CLASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM897.Cytochrome P450, Subfamily XXIV (vitamin D 24-hydroxylase) (CYP24, Accession NM_000782) is another VGAM2302 host target gene. CYP24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP24 BINDING SITE, designated SEQ ID:6427, to the nucleotide sequence of VGAM2302 RNA, herein designated VGAM RNA, also designated SEQ ID:5013.

[78396] Another function of VGAM2302 is therefore inhibition of Cytochrome P450, Subfamily XXIV (vitamin D 24-hydroxylase) (CYP24, Accession NM_000782), a gene which induces the differentiation of promyelocytes into monocytes/macrophages. Accordingly, utilities of VGAM2302 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP24. The function of CYP24 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1204.G Protein-coupled Receptor 48 (GPR48, Accession NM_018490) is another VGAM2302 host target

gene. GPR48 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPR48, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR48 BINDING SITE, designated SEQ ID:20549, to the nucleotide sequence of VGAM2302 RNA, herein designated VGAM RNA, also designated SEQ ID:5013.

[78397] Another function of VGAM2302 is therefore inhibition of G Protein-coupled Receptor 48 (GPR48, Accession NM_018490), a gene which binds to follicle-stimulating hormone and thyroid-stimulating hormone. Accordingly, utilities of VGAM2302 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR48. The function of GPR48 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM376.Phosphatidylinositol Glycan, Class A (paroxysmal nocturnal hemoglobinuria) (PIGA, Accession NM_020472) is another VGAM2302 host target gene. PIGA BINDING SITE1 and PIGA BINDING SITE2 are HOST TARGET binding sites found in untranslated regions

of mRNA encoded by PIGA, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIGA BINDING SITE1 and PIGA BINDING SITE2, designated SEQ ID:21710 and SEQ ID:21717 respectively, to the nucleotide sequence of VGAM2302 RNA, herein designated VGAM RNA, also designated SEQ ID:5013.

[78398] Another function of VGAM2302 is therefore inhibition of Phosphatidylinositol Glycan, Class A (paroxysmal nocturnal hemoglobinuria) (PIGA, Accession NM_020472). Accordingly, utilities of VGAM2302 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGA. Translocase of Outer Mitochondrial Membrane 70 Homolog A (yeast) (TOMM70A, Accession NM_014820) is another VGAM2302 host target gene. TOMM70A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOMM70A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOMM70A BINDING SITE, designated SEQ ID:16787, to the nucleotide sequence of VGAM2302 RNA,

herein designated VGAM RNA, also designated SEQ ID:5013.

[78399] Another function of VGAM2302 is therefore inhibition of Translocase of Outer Mitochondrial Membrane 70 Homolog A (yeast) (TOMM70A, Accession NM_014820). Accordingly, utilities of VGAM2302 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOMM70A. LOC145815 (Accession XM_096874) is another VGAM2302 host target gene. LOC145815 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145815, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145815 BINDING SITE, designated SEQ ID:40606, to the nucleotide sequence of VGAM2302 RNA, herein designated VGAM RNA, also designated SEQ ID:5013.

[78400] Another function of VGAM2302 is therefore inhibition of LOC145815 (Accession XM_096874). Accordingly, utilities of VGAM2302 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145815. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2303 (VGAM2303) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78401] VGAM2303 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2303 was detected is described hereinabove with reference to Figs. 1-8.

[78402] VGAM2303 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2303 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78403] VGAM2303 gene encodes a VGAM2303 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2303 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2303 precursor RNA is designated SEQ ID:2289, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2289 is located at position 38706 relative to the genome of Ectromelia Virus.

[78404] VGAM2303 precursor RNA folds onto itself, forming VGAM2303 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78405] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2303 folded precursor RNA into VGAM2303 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2303 RNA is designated SEQ ID:5014, and is provided hereinbelow with reference to the sequence listing part.

[78406] VGAM2303 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2303 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2303 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78407] VGAM2303 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2303 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2303 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2303 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2303 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78408] The complementary binding of VGAM2303 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2303 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2303 host target RNA into VGAM2303 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78409] It is appreciated that VGAM2303 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2303 host target genes. The mRNA of each one of this plurality of VGAM2303 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2303 RNA, herein designated VGAM RNA, and which when bound by VGAM2303 RNA causes inhibition of translation of respective one or more

VGAM2303 host target proteins.

[78410] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2303 gene, herein designated VGAM GENE, on one or more VGAM2303 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78411] It is yet further appreciated that a function of VGAM2303 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2303 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific

functions, and accordingly utilities, of VGAM2303 correlate with, and may be deduced from, the identity of the host target genes which VGAM2303 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78412] Nucleotide sequences of the VGAM2303 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2303 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2303 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2303 are further described hereinbelow with reference to Table 1.

[78413] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2303 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2303 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78414] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2303 gene, herein designated VGAM is inhibition of expression of VGAM2303 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2303 correlate with, and may be deduced from, the identity of the target genes which VGAM2303 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78415] Actinin, Alpha 2 (ACTN2, Accession NM_001103) is a VGAM2303 host target gene. ACTN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ACTN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACTN2 BINDING SITE, designated SEQ ID:6757, to the nucleotide sequence of VGAM2303 RNA, herein designated VGAM RNA, also designated SEQ ID:5014.

[78416] A function of VGAM2303 is therefore inhibition of Actinin, Alpha 2 (ACTN2, Accession NM_001103), a gene which an actin-binding protein with multiple roles in different cell types. Accordingly, utilities of VGAM2303 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACTN2. The function of ACTN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM88.Centaurin,

Delta 1 (CENTD1, Accession NM_015230) is another VGAM2303 host target gene. CENTD1 BINDING SITE1 and CENTD1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CENTD1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CENTD1 BINDING SITE1 and CENTD1 BINDING SITE2, designated SEQ ID:17561 and SEQ ID:29199 respectively, to the nucleotide sequence of VGAM2303 RNA, herein designated VGAM RNA, also designated SEQ ID:5014.

[78417] Another function of VGAM2303 is therefore inhibition of Centaurin, Delta 1 (CENTD1, Accession NM_015230), a gene which is nvolved in cell signaling/communication. Accordingly, utilities of VGAM2303 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENTD1. The function of CENTD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM445.Synapsin III (SYN3, Accession NM_133633) is another VGAM2303 host target gene. SYN3 BINDING SITE1 through SYN3

BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SYN3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYN3 BINDING SITE1 through SYN3 BINDING SITE3, designated SEQ ID:28594, SEQ ID:9583 and SEQ ID:19543 respectively, to the nucleotide sequence of VGAM2303 RNA, herein designated VGAM RNA, also designated SEQ ID:5014.

[78418] Another function of VGAM2303 is therefore inhibition of Synapsin III (SYN3, Accession NM_133633), a gene which may be involved in the regulation of neurotransmitter release and synaptogenesis. Accordingly, utilities of VGAM2303 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYN3. The function of SYN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM925.LOC219688 (Accession XM_167568) is another VGAM2303 host target gene. LOC219688 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219688, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219688 BINDING SITE, designated SEQ ID:44697, to the nucleotide sequence of VGAM2303 RNA, herein designated VGAM RNA, also designated SEQ ID:5014.

[78419] Another function of VGAM2303 is therefore inhibition of LOC219688 (Accession XM_167568). Accordingly, utilities of VGAM2303 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219688. LOC255533 (Accession XM_173073) is another VGAM2303 host target gene. LOC255533 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255533, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255533 BINDING SITE, designated SEQ ID:46331, to the nucleotide sequence of VGAM2303 RNA, herein designated VGAM RNA, also designated SEQ ID:5014.

[78420] Another function of VGAM2303 is therefore inhibition of LOC255533 (Accession XM_173073). Accordingly, utilities of VGAM2303 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC255533. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2304 (VGAM2304) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78421] VGAM2304 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2304 was detected is described hereinabove with reference to Figs. 1-8.

[78422] VGAM2304 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2304 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78423] VGAM2304 gene encodes a VGAM2304 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2304 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2304 precursor RNA is desig-

nated SEQ ID:2290, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2290 is located at position 35690 relative to the genome of Ectromelia Virus.

[78424] VGAM2304 precursor RNA folds onto itself, forming VGAM2304 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78425] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2304 folded precursor RNA into VGAM2304 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2304 RNA is designated SEQ ID:5015, and is provided hereinbelow with reference to the sequence

listing part.

[78426] VGAM2304 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2304 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2304 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78427] VGAM2304 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2304 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2304 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2304 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2304 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78428] The complementary binding of VGAM2304 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2304 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2304 host target RNA into VGAM2304 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78429] It is appreciated that VGAM2304 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2304 host target genes. The mRNA of each one of this plurality of VGAM2304 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2304 RNA, herein designated VGAM

RNA, and which when bound by VGAM2304 RNA causes inhibition of translation of respective one or more VGAM2304 host target proteins.

[78430] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2304 gene, herein designated VGAM GENE, on one or more VGAM2304 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78431] It is yet further appreciated that a function of VGAM2304 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2304 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2304 correlate with, and may be deduced from, the identity of the host target genes which VGAM2304 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78432] Nucleotide sequences of the VGAM2304 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2304 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2304 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2304 are further described hereinbelow with reference to Table 1.

[78433] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2304 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2304 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78434] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2304 gene, herein designated VGAM is

inhibition of expression of VGAM2304 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2304 correlate with, and may be deduced from, the identity of the target genes which VGAM2304 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78435] CUB and Sushi Multiple Domains 1 (CSMD1, Accession XM_054838) is a VGAM2304 host target gene. CSMD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSMD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSMD1 BINDING SITE, designated SEQ ID:36188, to the nucleotide sequence of VGAM2304 RNA, herein designated VGAM RNA, also designated SEQ ID:5015.

[78436] A function of VGAM2304 is therefore inhibition of CUB and Sushi Multiple Domains 1 (CSMD1, Accession XM_054838). Accordingly, utilities of VGAM2304 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSMD1. DRIL2 (Accession NM_006465) is another VGAM2304 host target gene. DRIL2 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by DRIL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DRIL2 BINDING SITE, designated SEQ ID:13182, to the nucleotide sequence of VGAM2304 RNA, herein designated VGAM RNA, also designated SEQ ID:5015.

[78437] Another function of VGAM2304 is therefore inhibition of DRIL2 (Accession NM_006465). Accordingly, utilities of VGAM2304 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DRIL2. LOC158187 (Accession XM_098892) is another VGAM2304 host target gene. LOC158187 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158187, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158187 BINDING SITE, designated SEQ ID:41919, to the nucleotide sequence of VGAM2304 RNA, herein designated VGAM RNA, also designated SEQ ID:5015.

[78438] Another function of VGAM2304 is therefore inhibition of LOC158187 (Accession XM_098892). Accordingly, utilities

of VGAM2304 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158187. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2305 (VGAM2305) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78439] VGAM2305 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2305 was detected is described hereinabove with reference to Figs. 1-8.

[78440] VGAM2305 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Camelpox Virus. VGAM2305 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78441] VGAM2305 gene encodes a VGAM2305 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2305 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2305 precursor RNA is designated SEQ ID:2291, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2291 is located at position 38932 relative to the genome of Camelpox Virus.

[78442] VGAM2305 precursor RNA folds onto itself, forming VGAM2305 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78443] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2305 folded precursor RNA into VGAM2305 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2305 RNA is designated SEQ ID:5016, and

is provided hereinbelow with reference to the sequence listing part.

[78444] VGAM2305 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2305 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2305 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78445] VGAM2305 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2305 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2305 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2305 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2305 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78446] The complementary binding of VGAM2305 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2305 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2305 host target RNA into VGAM2305 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78447] It is appreciated that VGAM2305 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2305 host target genes. The mRNA of each one of this plurality of VGAM2305 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2305 RNA, herein designated VGAM RNA, and which when bound by VGAM2305 RNA causes inhibition of translation of respective one or more VGAM2305 host target proteins.

[78448] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2305 gene, herein designated VGAM GENE, on one or more VGAM2305 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78449] It is yet further appreciated that a function of VGAM2305 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2305 include diagnosis, prevention and treatment of viral infection by Camelpox Virus. Specific functions, and accordingly utilities, of VGAM2305 correlate with, and may be deduced from, the identity of the host target genes which VGAM2305 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78450] Nucleotide sequences of the VGAM2305 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2305 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2305 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2305 are further described hereinbelow with reference to Table 1.

[78451] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2305 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2305 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78452] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2305 gene, herein designated VGAM is inhibition of expression of VGAM2305 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2305 correlate with, and may be deduced from, the identity of the target genes which VGAM2305 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78453] GA (Accession NM_013267) is a VGAM2305 host target gene. GA BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GA BINDING SITE, designated SEQ ID:14936, to the nucleotide sequence of VGAM2305 RNA, herein designated VGAM RNA, also designated SEQ ID:5016.

[78454] A function of VGAM2305 is therefore inhibition of GA (Accession NM_013267). Accordingly, utilities of VGAM2305 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GA. KIAA0753 (Accession NM_014804) is another VGAM2305 host target gene. KIAA0753 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by KIAA0753, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0753 BINDING SITE, designated SEQ ID:16737, to the nucleotide sequence of VGAM2305 RNA, herein designated VGAM RNA, also designated SEQ ID:5016.

[78455] Another function of VGAM2305 is therefore inhibition of KIAA0753 (Accession NM_014804). Accordingly, utilities of VGAM2305 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0753. KIAA1130 (Accession XM_031104) is another VGAM2305 host target gene. KIAA1130 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1130, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1130 BINDING SITE, designated SEQ ID:31289, to the nucleotide sequence of VGAM2305 RNA, herein designated VGAM RNA, also designated SEQ ID:5016.

[78456] Another function of VGAM2305 is therefore inhibition of KIAA1130 (Accession XM_031104). Accordingly, utilities

of VGAM2305 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1130. Ribosomal Protein L36 (RPL36, Accession NM_015414) is another VGAM2305 host target gene. RPL36 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RPL36, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPL36 BINDING SITE, designated SEQ ID:17715, to the nucleotide sequence of VGAM2305 RNA, herein designated VGAM RNA, also designated SEQ ID:5016.

[78457] Another function of VGAM2305 is therefore inhibition of Ribosomal Protein L36 (RPL36, Accession NM_015414). Accordingly, utilities of VGAM2305 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPL36. LOC56920 (Accession NM_020163) is another VGAM2305 host target gene. LOC56920 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC56920, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of LOC56920 BINDING SITE, designated SEQ ID:21381, to the nucleotide sequence of VGAM2305 RNA, herein designated VGAM RNA, also designated SEQ ID:5016.

[78458] Another function of VGAM2305 is therefore inhibition of LOC56920 (Accession NM_020163). Accordingly, utilities of VGAM2305 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56920. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2306 (VGAM2306) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78459] VGAM2306 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2306 was detected is described hereinabove with reference to Figs. 1-8.

[78460] VGAM2306 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Ectromelia Virus. VGAM2306 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[78461] VGAM2306 gene encodes a VGAM2306 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2306 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2306 precursor RNA is designated SEQ ID:2292, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2292 is located at position 43278 relative to the genome of Ectromelia Virus.

[78462] VGAM2306 precursor RNA folds onto itself, forming VGAM2306 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78463] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2306 folded precursor RNA into VGAM2306

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2306 RNA is designated SEQ ID:5017, and is provided hereinbelow with reference to the sequence listing part.

[78464] VGAM2306 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2306 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2306 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78465] VGAM2306 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2306 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2306 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2306 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2306 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78466] The complementary binding of VGAM2306 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2306 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2306 host target RNA into VGAM2306 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[78467] It is appreciated that VGAM2306 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2306 host target genes. The mRNA of each one of this plurality of VGAM2306 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2306 RNA, herein designated VGAM RNA, and which when bound by VGAM2306 RNA causes inhibition of translation of respective one or more VGAM2306 host target proteins.

[78468] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2306 gene, herein designated VGAM GENE, on one or more VGAM2306 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78469] It is yet further appreciated that a function of VGAM2306 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2306 include diagnosis, prevention and treatment of viral infection by Ectromelia Virus. Specific functions, and accordingly utilities, of VGAM2306 correlate with, and may be deduced from, the identity of the host target genes which VGAM2306 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78470] Nucleotide sequences of the VGAM2306 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2306 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2306 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2306 are further described hereinbelow with reference to Table 1.

[78471] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2306 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2306 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78472] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2306 gene, herein designated VGAM is inhibition of expression of VGAM2306 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2306 correlate with, and may be deduced from, the identity of the target genes which VGAM2306 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78473] BUB3 Budding Uninhibited By Benzimidazoles 3 Homolog (yeast) (BUB3, Accession NM_004725) is a VGAM2306 host target gene. BUB3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BUB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BUB3 BINDING SITE, designated SEQ ID:11094, to the nucleotide sequence of VGAM2306 RNA,

herein designated VGAM RNA, also designated SEQ ID:5017.

[78474] A function of VGAM2306 is therefore inhibition of BUB3 Budding Uninhibited By Benzimidazoles 3 Homolog (yeast) (BUB3, Accession NM_004725), a gene which has a role in the mitotic spindle checkpoint. Accordingly, utilities of VGAM2306 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BUB3. The function of BUB3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1361.Membrane Metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME, Accession NM_007289) is another VGAM2306 host target gene. MME BINDING SITE1 through MME BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MME, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MME BINDING SITE1 through MME BINDING SITE4, designated SEQ ID:14159, SEQ ID:6602, SEQ ID:14150 and SEQ ID:14154 respectively, to the nucleotide sequence of VGAM2306

RNA, herein designated VGAM RNA, also designated SEQ ID:5017.

[78475] Another function of VGAM2306 is therefore inhibition of Membrane Metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME, Accession NM_007289), a gene which is thermolysin-like specificity. Accordingly, utilities of VGAM2306 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MME. The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1332.LOC126669 (Accession XM_060121) is another VGAM2306 host target gene. LOC126669 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126669, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126669 BINDING SITE, designated SEQ ID:37154, to the nucleotide sequence of VGAM2306 RNA, herein designated VGAM RNA, also designated SEQ ID:5017.

[78476] Another function of VGAM2306 is therefore inhibition of

LOC126669 (Accession XM_060121). Accordingly, utilities of VGAM2306 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126669. LOC154789 (Accession XM_088043) is another VGAM2306 host target gene. LOC154789 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154789, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154789 BINDING SITE, designated SEQ ID:39485, to the nucleotide sequence of VGAM2306 RNA, herein designated VGAM RNA, also designated SEQ ID:5017.

[78477] Another function of VGAM2306 is therefore inhibition of LOC154789 (Accession XM_088043). Accordingly, utilities of VGAM2306 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154789. LOC220963 (Accession XM_166145) is another VGAM2306 host target gene. LOC220963 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220963, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC220963 BINDING SITE, designated SEQ ID:43958, to the nucleotide sequence of VGAM2306 RNA, herein designated VGAM RNA, also designated SEQ ID:5017.

[78478] Another function of VGAM2306 is therefore inhibition of LOC220963 (Accession XM_166145). Accordingly, utilities of VGAM2306 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220963. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2307 (VGAM2307) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78479] VGAM2307 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2307 was detected is described hereinabove with reference to Figs. 1-8.

[78480] VGAM2307 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Lumpy Skin Disease Virus. VGAM2307 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78481] VGAM2307 gene encodes a VGAM2307 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2307 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2307 precursor RNA is designated SEQ ID:2293, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2293 is located at position 122989 relative to the genome of Lumpy Skin Disease Virus.

[78482] VGAM2307 precursor RNA folds onto itself, forming VGAM2307 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78483] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2307 folded precursor RNA into VGAM2307 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 77%) nucleotide sequence of VGAM2307 RNA is designated SEQ ID:5018, and is provided hereinbelow with reference to the sequence listing part.

[78484] VGAM2307 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2307 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2307 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[78485] VGAM2307 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2307 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2307 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2307 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2307 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78486] The complementary binding of VGAM2307 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2307 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2307 host target RNA into VGAM2307 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78487] It is appreciated that VGAM2307 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2307 host target genes. The mRNA of each one of this plurality of VGAM2307 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2307 RNA, herein designated VGAM RNA, and which when bound by VGAM2307 RNA causes inhibition of translation of respective one or more VGAM2307 host target proteins.

[78488] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2307 gene, herein designated VGAM GENE, on one or more VGAM2307 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78489] It is yet further appreciated that a function of VGAM2307 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2307 include diagnosis, prevention and treatment of viral infection by Lumpy Skin Disease Virus. Specific functions, and accordingly utilities, of VGAM2307 correlate with, and may be deduced from, the identity of the host target genes which VGAM2307 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78490] Nucleotide sequences of the VGAM2307 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2307 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2307 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2307 are further described hereinbelow with reference to Table 1.

[78491] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2307 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2307 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78492] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2307 gene, herein designated VGAM is inhibition of expression of VGAM2307 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2307 correlate with, and may be deduced from, the identity of the target genes which VGAM2307 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78493] Cadherin 6, Type 2, K-cadherin (fetal kidney) (CDH6, Accession NM_004932) is a VGAM2307 host target gene.

CDH6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDH6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDH6 BINDING SITE, designated SEQ ID:11375, to the nucleotide sequence of VGAM2307 RNA, herein designated VGAM RNA, also designated SEQ ID:5018.

[78494] A function of VGAM2307 is therefore inhibition of Cadherin 6, Type 2, K-cadherin (fetal kidney) (CDH6, Accession NM_004932), a gene which is a calcium dependent cell adhesion protein. Accordingly, utilities of VGAM2307 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH6. The function of CDH6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM60.Carboxypeptidase D (CPD, Accession NM_001304) is another VGAM2307 host target gene. CPD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CPD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of CPD BINDING SITE, designated SEQ ID:6981, to the nucleotide sequence of VGAM2307 RNA, herein designated VGAM RNA, also designated SEQ ID:5018.

[78495] Another function of VGAM2307 is therefore inhibition of Carboxypeptidase D (CPD, Accession NM_001304), a gene which is a membrane-bound metalloprotease. Accordingly, utilities of VGAM2307 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPD. The function of CPD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM596.Norrie Disease (pseudoglioma) (NDP, Accession NM_000266) is another VGAM2307 host target gene. NDP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NDP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDP BINDING SITE, designated SEQ ID:5808, to the nucleotide sequence of VGAM2307 RNA, herein designated VGAM RNA, also designated SEQ ID:5018.

[78496] Another function of VGAM2307 is therefore inhibition of Norrie Disease (pseudoglioma) (NDP, Accession NM_000266), a gene which may be involved in a pathway that regulates neural cell differentiation and proliferation. Accordingly, utilities of VGAM2307 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDP. The function of NDP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM113.Suppressor of Cytokine Signaling 5 (SOCS5, Accession NM_014011) is another VGAM2307 host target gene. SOCS5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOCS5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOCS5 BINDING SITE, designated SEQ ID:15230, to the nucleotide sequence of VGAM2307 RNA, herein designated VGAM RNA, also designated SEQ ID:5018.

[78497] Another function of VGAM2307 is therefore inhibition of Suppressor of Cytokine Signaling 5 (SOCS5, Accession NM_014011). Accordingly, utilities of VGAM2307 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with SOCS5. HSA250839 (Accession NM_018401) is another VGAM2307 host target gene. HSA250839 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSA250839, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSA250839 BINDING SITE, designated SEQ ID:20436, to the nucleotide sequence of VGAM2307 RNA, herein designated VGAM RNA, also designated SEQ ID:5018.

[78498] Another function of VGAM2307 is therefore inhibition of HSA250839 (Accession NM_018401). Accordingly, utilities of VGAM2307 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSA250839. LOC149372 (Accession XM_086509) is another VGAM2307 host target gene. LOC149372 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149372, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC149372 BINDING SITE, designated SEQ ID:38732, to the nucleotide sequence of VGAM2307 RNA, herein designated VGAM RNA, also designated SEQ ID:5018.

[78499] Another function of VGAM2307 is therefore inhibition of LOC149372 (Accession XM_086509). Accordingly, utilities of VGAM2307 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149372. LOC149844 (Accession XM_086675) is another VGAM2307 host target gene. LOC149844 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149844, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149844 BINDING SITE, designated SEQ ID:38820, to the nucleotide sequence of VGAM2307 RNA, herein designated VGAM RNA, also designated SEQ ID:5018.

[78500] Another function of VGAM2307 is therefore inhibition of LOC149844 (Accession XM_086675). Accordingly, utilities of VGAM2307 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149844. LOC51133 (Accession NM_016121) is another VGAM2307 host target gene. LOC51133 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51133, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51133 BINDING SITE, designated SEQ ID:18205, to the nucleotide sequence of VGAM2307 RNA, herein designated VGAM RNA, also designated SEQ ID:5018.

[78501] Another function of VGAM2307 is therefore inhibition of LOC51133 (Accession NM_016121). Accordingly, utilities of VGAM2307 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51133. LOC89135 (Accession XM_016232) is another VGAM2307 host target gene. LOC89135 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC89135, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC89135 BINDING SITE, designated SEQ ID:30249, to the nucleotide sequence of VGAM2307 RNA, herein designated VGAM RNA, also designated SEQ ID:5018.

[78502] Another function of VGAM2307 is therefore inhibition of

LOC89135 (Accession XM_016232). Accordingly, utilities of VGAM2307 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC89135. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2308 (VGAM2308) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78503] VGAM2308 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2308 was detected is described hereinabove with reference to Figs. 1-8.

[78504] VGAM2308 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2308 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78505] VGAM2308 gene encodes a VGAM2308 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2308 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2308 precursor RNA is designated SEQ ID:2294, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2294 is located at position 123501 relative to the genome of Goatpox Virus.

[78506] VGAM2308 precursor RNA folds onto itself, forming VGAM2308 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78507] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2308 folded precursor RNA into VGAM2308 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide se-

quence of VGAM2308 RNA is designated SEQ ID:5019, and is provided hereinbelow with reference to the sequence listing part.

[78508] VGAM2308 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2308 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2308 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78509] VGAM2308 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2308 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2308 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2308 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2308 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78510] The complementary binding of VGAM2308 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2308 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2308 host target RNA into VGAM2308 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78511] It is appreciated that VGAM2308 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2308 host target genes. The mRNA of each one of this plurality of VGAM2308 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2308 RNA, herein designated VGAM RNA, and which when bound by VGAM2308 RNA causes inhibition of translation of respective one or more VGAM2308 host target proteins.

[78512] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2308 gene, herein designated VGAM GENE, on one or more VGAM2308 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78513] It is yet further appreciated that a function of VGAM2308

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2308 correlate with, and may be deduced from, the identity of the host target genes which VGAM2308 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78514] Nucleotide sequences of the VGAM2308 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2308 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2308 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2308 are further described hereinbelow with reference to Table 1.

[78515] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2308 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2308 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78516] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2308 gene, herein designated VGAM is inhibition of expression of VGAM2308 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2308 correlate with, and may be deduced from, the identity of the target genes which VGAM2308 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78517] Giant Axonal Neuropathy (gigaxonin) (GAN, Accession NM_022041) is a VGAM2308 host target gene. GAN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GAN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAN BINDING SITE, designated SEQ ID:22561, to the nucleotide sequence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78518] A function of VGAM2308 is therefore inhibition of Giant Axonal Neuropathy (gigaxonin) (GAN, Accession NM_022041), a gene which plays an important role in neurofilament architecture. Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with GAN. The function of GAN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM606.DKFZP434F0318 (Accession NM_030817) is another VGAM2308 host target gene. DKFZP434F0318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434F0318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434F0318 BINDING SITE, designated SEQ ID:25139, to the nucleotide sequence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78519] Another function of VGAM2308 is therefore inhibition of DKFZP434F0318 (Accession NM_030817). Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F0318. DKFZP761E2110 (Accession NM_030953) is another VGAM2308 host target gene. DKFZP761E2110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

DKFZP761E2110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP761E2110 BINDING SITE, designated SEQ ID:25223, to the nucleotide sequence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78520] Another function of VGAM2308 is therefore inhibition of DKFZP761E2110 (Accession NM_030953). Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761E2110. KIAA1393 (Accession XM_050793) is another VGAM2308 host target gene. KIAA1393 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1393, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1393 BINDING SITE, designated SEQ ID:35686, to the nucleotide sequence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78521] Another function of VGAM2308 is therefore inhibition of KIAA1393 (Accession XM_050793). Accordingly, utilities

of VGAM2308 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1393. KIAA1495 (Accession XM_055080) is another VGAM2308 host target gene. KIAA1495 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1495, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1495 BINDING SITE, designated SEQ ID:36224, to the nucleotide sequence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78522] Another function of VGAM2308 is therefore inhibition of KIAA1495 (Accession XM_055080). Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1495. KIAA1954 (Accession XM_085375) is another VGAM2308 host target gene. KIAA1954 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1954, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1954 BINDING SITE, designated SEQ ID:38096, to the nucleotide sequence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78523] Another function of VGAM2308 is therefore inhibition of KIAA1954 (Accession XM_085375). Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1954. Karyopherin Alpha 6 (importin alpha 7) (KPNA6, Accession NM_012316) is another VGAM2308 host target gene. KPNA6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KPNA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KPNA6 BINDING SITE, designated SEQ ID:14686, to the nucleotide sequence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78524] Another function of VGAM2308 is therefore inhibition of Karyopherin Alpha 6 (importin alpha 7) (KPNA6, Accession NM_012316). Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KPNA6. RAP140 (Accession

NM_015224) is another VGAM2308 host target gene. RAP140 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAP140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAP140 BINDING SITE, designated SEQ ID:17555, to the nucleotide sequence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78525] Another function of VGAM2308 is therefore inhibition of RAP140 (Accession NM_015224). Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP140. Serine Palmitoyltransferase, Long Chain Base Subunit 2 (SPTLC2, Accession NM_004863) is another VGAM2308 host target gene. SPTLC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPTLC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPTLC2 BINDING SITE, designated SEQ ID:11275, to the nucleotide se-

quence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78526] Another function of VGAM2308 is therefore inhibition of Serine Palmitoyltransferase, Long Chain Base Subunit 2 (SPTLC2, Accession NM_004863). Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPTLC2. LOC115219 (Accession XM_055499) is another VGAM2308 host target gene. LOC115219 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115219 BINDING SITE, designated SEQ ID:36277, to the nucleotide sequence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78527] Another function of VGAM2308 is therefore inhibition of LOC115219 (Accession XM_055499). Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115219. LOC202451 (Accession XM_117401) is another VGAM2308 host target gene. LOC202451 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202451, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202451 BINDING SITE, designated SEQ ID:43438, to the nucleotide sequence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78528] Another function of VGAM2308 is therefore inhibition of LOC202451 (Accession XM_117401). Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202451. LOC51185 (Accession NM_016302) is another VGAM2308 host target gene. LOC51185 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51185, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51185 BINDING SITE, designated SEQ ID:18423, to the nucleotide sequence of VGAM2308 RNA, herein designated VGAM RNA, also designated SEQ ID:5019.

[78529] Another function of VGAM2308 is therefore inhibition of

LOC51185 (Accession NM_016302). Accordingly, utilities of VGAM2308 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51185. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2309 (VGAM2309) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78530] VGAM2309 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2309 was detected is described hereinabove with reference to Figs. 1-8.

[78531] VGAM2309 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Lumpy Skin Disease Virus. VGAM2309 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78532] VGAM2309 gene encodes a VGAM2309 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2309 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2309 precursor RNA is designated SEQ ID:2295, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2295 is located at position 127569 relative to the genome of Lumpy Skin Disease Virus.

[78533] VGAM2309 precursor RNA folds onto itself, forming VGAM2309 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78534] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2309 folded precursor RNA into VGAM2309 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM2309 RNA is designated SEQ ID:5020, and is provided hereinbelow with reference to the sequence listing part.

[78535] VGAM2309 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2309 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2309 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78536] VGAM2309 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2309 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2309 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2309 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2309 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78537] The complementary binding of VGAM2309 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2309 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2309 host target RNA into VGAM2309 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78538] It is appreciated that VGAM2309 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2309 host target genes. The mRNA of each one of this plurality of VGAM2309 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2309 RNA, herein designated VGAM RNA, and which when bound by VGAM2309 RNA causes inhibition of translation of respective one or more VGAM2309 host target proteins.

[78539] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2309 gene, herein designated VGAM GENE, on one or more VGAM2309 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78540] It is yet further appreciated that a function of VGAM2309

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2309 include diagnosis, prevention and treatment of viral infection by Lumpy Skin Disease Virus. Specific functions, and accordingly utilities, of VGAM2309 correlate with, and may be deduced from, the identity of the host target genes which VGAM2309 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78541] Nucleotide sequences of the VGAM2309 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2309 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2309 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2309 are further described hereinbelow with reference to Table 1.

[78542] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2309 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2309 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78543] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2309 gene, herein designated VGAM is inhibition of expression of VGAM2309 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2309 correlate with, and may be deduced from, the identity of the target genes which VGAM2309 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78544] FLJ23189 (Accession NM_025057) is a VGAM2309 host target gene. FLJ23189 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23189, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23189 BINDING SITE, designated SEQ ID:24656, to the nucleotide sequence of VGAM2309 RNA, herein designated VGAM RNA, also designated SEQ ID:5020.

[78545] A function of VGAM2309 is therefore inhibition of FLJ23189 (Accession NM_025057). Accordingly, utilities of VGAM2309 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23189. Fig. 1 further provides a conceptual description

of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2310 (VGAM2310) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78546] VGAM2310 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2310 was detected is described hereinabove with reference to Figs. 1-8.

[78547] VGAM2310 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Lumpy Skin Disease Virus. VGAM2310 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78548] VGAM2310 gene encodes a VGAM2310 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2310 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2310 precursor RNA is designated SEQ ID:2296, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2296 is located at position 135569 relative to the genome of Lumpy Skin Disease Virus.

[78549] VGAM2310 precursor RNA folds onto itself, forming VGAM2310 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78550] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2310 folded precursor RNA into VGAM2310 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2310 RNA is designated SEQ ID:5021, and is provided hereinbelow with reference to the sequence listing part.

[78551] VGAM2310 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2310 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2310 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78552] VGAM2310 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2310 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2310 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2310 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2310 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78553] The complementary binding of VGAM2310 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2310 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2310 host target RNA into VGAM2310 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78554] It is appreciated that VGAM2310 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2310 host target genes. The mRNA of each one of this plurality of VGAM2310 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2310 RNA, herein designated VGAM RNA, and which when bound by VGAM2310 RNA causes inhibition of translation of respective one or more

VGAM2310 host target proteins.

[78555] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2310 gene, herein designated VGAM GENE, on one or more VGAM2310 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78556] It is yet further appreciated that a function of VGAM2310 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2310 include diagnosis, prevention and treatment of viral infection by Lumpy Skin Disease Virus.

Specific functions, and accordingly utilities, of VGAM2310 correlate with, and may be deduced from, the identity of the host target genes which VGAM2310 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78557] Nucleotide sequences of the VGAM2310 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2310 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2310 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2310 are further described hereinbelow with reference to Table 1.

[78558] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2310 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2310 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78559] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2310 gene, herein designated VGAM is inhibition of expression of VGAM2310 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2310 correlate with, and may be deduced from, the identity of the target genes which VGAM2310 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78560] Caldesmon 1 (CALD1, Accession NM_033138) is a VGAM2310 host target gene. CALD1 BINDING SITE1 and CALD1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CALD1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CALD1 BINDING SITE1 and CALD1 BINDING SITE2, designated SEQ ID:26991 and SEQ ID:27009 respectively, to the nucleotide sequence of VGAM2310 RNA, herein designated VGAM RNA, also designated SEQ ID:5021.

[78561] A function of VGAM2310 is therefore inhibition of Caldesmon 1 (CALD1, Accession NM_033138), a gene which is implicated in the regulation of actomyosin interactions in smooth muscle and nonmuscle cells. Accordingly, utilities of VGAM2310 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CALD1. The function of CALD1 and its associa-

tion with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1960.Secreted Frizzled-related Protein 4 (SFRP4, Accession NM_003014) is another VGAM2310 host target gene. SFRP4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFRP4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRP4 BINDING SITE, designated SEQ ID:8937, to the nucleotide sequence of VGAM2310 RNA, herein designated VGAM RNA, also designated SEQ ID:5021.

[78562] Another function of VGAM2310 is therefore inhibition of Secreted Frizzled-related Protein 4 (SFRP4, Accession NM_003014). Accordingly, utilities of VGAM2310 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRP4. CG018 (Accession NM_052818) is another VGAM2310 host target gene. CG018 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CG018, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of CG018 BINDING SITE, designated SEQ ID:27404, to the nucleotide sequence of VGAM2310 RNA, herein designated VGAM RNA, also designated SEQ ID:5021.

[78563] Another function of VGAM2310 is therefore inhibition of CG018 (Accession NM_052818). Accordingly, utilities of VGAM2310 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CG018. Hypermethylated In Cancer 2 (HIC2, Accession XM_036937) is another VGAM2310 host target gene. HIC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HIC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIC2 BINDING SITE, designated SEQ ID:32524, to the nucleotide sequence of VGAM2310 RNA, herein designated VGAM RNA, also designated SEQ ID:5021.

[78564] Another function of VGAM2310 is therefore inhibition of Hypermethylated In Cancer 2 (HIC2, Accession XM_036937). Accordingly, utilities of VGAM2310 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with HIC2. HTGN29 (Accession NM_020199) is another VGAM2310 host target gene. HTGN29 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HTGN29, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HTGN29 BINDING SITE, designated SEQ ID:21431, to the nucleotide sequence of VGAM2310 RNA, herein designated VGAM RNA, also designated SEQ ID:5021.

[78565] Another function of VGAM2310 is therefore inhibition of HTGN29 (Accession NM_020199). Accordingly, utilities of VGAM2310 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTGN29. KIAA1257 (Accession XM_031577) is another VGAM2310 host target gene. KIAA1257 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1257, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1257 BINDING SITE, designated SEQ ID:31438, to the

nucleotide sequence of VGAM2310 RNA, herein designated VGAM RNA, also designated SEQ ID:5021.

[78566] Another function of VGAM2310 is therefore inhibition of KIAA1257 (Accession XM_031577). Accordingly, utilities of VGAM2310 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1257. LOC201725 (Accession XM_114370) is another VGAM2310 host target gene. LOC201725 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201725, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201725 BINDING SITE, designated SEQ ID:42904, to the nucleotide sequence of VGAM2310 RNA, herein designated VGAM RNA, also designated SEQ ID:5021.

[78567] Another function of VGAM2310 is therefore inhibition of LOC201725 (Accession XM_114370). Accordingly, utilities of VGAM2310 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201725. LOC221810 (Accession XM_168222) is another VGAM2310 host target gene. LOC221810 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC221810, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221810 BINDING SITE, designated SEQ ID:45082, to the nucleotide sequence of VGAM2310 RNA, herein designated VGAM RNA, also designated SEQ ID:5021.

[78568] Another function of VGAM2310 is therefore inhibition of LOC221810 (Accession XM_168222). Accordingly, utilities of VGAM2310 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221810. LOC256073 (Accession XM_172972) is another VGAM2310 host target gene. LOC256073 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256073, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256073 BINDING SITE, designated SEQ ID:46228, to the nucleotide sequence of VGAM2310 RNA, herein designated VGAM RNA, also designated SEQ ID:5021.

[78569] Another function of VGAM2310 is therefore inhibition of LOC256073 (Accession XM_172972). Accordingly, utilities

of VGAM2310 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256073. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2311 (VGAM2311) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78570] VGAM2311 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2311 was detected is described hereinabove with reference to Figs. 1-8.

[78571] VGAM2311 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Lumpy Skin Disease Virus. VGAM2311 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78572] VGAM2311 gene encodes a VGAM2311 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2311 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2311 precursor RNA is designated SEQ ID:2297, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2297 is located at position 139025 relative to the genome of Lumpy Skin Disease Virus.

[78573] VGAM2311 precursor RNA folds onto itself, forming VGAM2311 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78574] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2311 folded precursor RNA into VGAM2311 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2311 RNA is designated SEQ ID:5022, and

is provided hereinbelow with reference to the sequence listing part.

[78575] VGAM2311 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2311 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2311 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78576] VGAM2311 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2311 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2311 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2311 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2311 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78577] The complementary binding of VGAM2311 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2311 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2311 host target RNA into VGAM2311 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78578] It is appreciated that VGAM2311 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2311 host target genes. The mRNA of each one of this plurality of VGAM2311 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2311 RNA, herein designated VGAM RNA, and which when bound by VGAM2311 RNA causes inhibition of translation of respective one or more VGAM2311 host target proteins.

[78579] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2311 gene, herein designated VGAM GENE, on one or more VGAM2311 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78580] It is yet further appreciated that a function of VGAM2311 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2311 include diagnosis, prevention and treatment of viral infection by Lumpy Skin Disease Virus. Specific functions, and accordingly utilities, of VGAM2311 correlate with, and may be deduced from, the identity of the host target genes which VGAM2311 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78581] Nucleotide sequences of the VGAM2311 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2311 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2311 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2311 are further described hereinbelow with reference to Table 1.

[78582] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2311 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2311 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78583] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2311 gene, herein designated VGAM is inhibition of expression of VGAM2311 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2311 correlate with, and may be deduced from, the identity of the target genes which VGAM2311 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78584] Myotubularin Related Protein 8 (MTMR8, Accession NM_015458) is a VGAM2311 host target gene. MTMR8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MTMR8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MTMR8 BINDING SITE, designated SEQ ID:17746, to the nucleotide sequence of VGAM2311 RNA, herein designated VGAM RNA, also designated SEQ ID:5022.

[78585] A function of VGAM2311 is therefore inhibition of Myotubularin Related Protein 8 (MTMR8, Accession NM_015458), a gene which could be a tyrosine-phosphatase. Accordingly, utilities of VGAM2311 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MTMR8. The function of

MTMR8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM379.PR Domain Containing 4 (PRDM4, Accession NM_012406) is another VGAM2311 host target gene. PRDM4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRDM4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRDM4 BINDING SITE, designated SEQ ID:14786, to the nucleotide sequence of VGAM2311 RNA, herein designated VGAM RNA, also designated SEQ ID:5022.

[78586] Another function of VGAM2311 is therefore inhibition of PR Domain Containing 4 (PRDM4, Accession NM_012406). Accordingly, utilities of VGAM2311 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDM4. Solute Carrier Family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) Transporter), Member 3 (SLC35A3, Accession NM_012243) is another VGAM2311 host target gene. SLC35A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC35A3, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC35A3 BINDING SITE, designated SEQ ID:14548, to the nucleotide sequence of VGAM2311 RNA, herein designated VGAM RNA, also designated SEQ ID:5022.

[78587] Another function of VGAM2311 is therefore inhibition of Solute Carrier Family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) Transporter), Member 3 (SLC35A3, Accession NM_012243). Accordingly, utilities of VGAM2311 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC35A3. SON DNA Binding Protein (SON, Accession NM_058183) is another VGAM2311 host target gene. SON BINDING SITE1 through SON BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SON, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SON BINDING SITE1 through SON BINDING SITE3, designated SEQ ID:27744, SEQ ID:29040 and SEQ ID:29045 respectively, to the nucleotide sequence of VGAM2311 RNA, herein designated VGAM RNA, also designated SEQ

ID:5022.

[78588] Another function of VGAM2311 is therefore inhibition of SON DNA Binding Protein (SON, Accession NM_058183). Accordingly, utilities of VGAM2311 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SON. KIAA1600 (Accession XM_049351) is another VGAM2311 host target gene. KIAA1600 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1600, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1600 BINDING SITE, designated SEQ ID:35390, to the nucleotide sequence of VGAM2311 RNA, herein designated VGAM RNA, also designated SEQ ID:5022.

[78589] Another function of VGAM2311 is therefore inhibition of KIAA1600 (Accession XM_049351). Accordingly, utilities of VGAM2311 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1600. MGC4737 (Accession NM_031466) is another VGAM2311 host target gene. MGC4737 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by MGC4737, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4737 BINDING SITE, designated SEQ ID:25507, to the nucleotide sequence of VGAM2311 RNA, herein designated VGAM RNA, also designated SEQ ID:5022.

[78590] Another function of VGAM2311 is therefore inhibition of MGC4737 (Accession NM_031466). Accordingly, utilities of VGAM2311 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4737. LOC126964 (Accession XM_059100) is another VGAM2311 host target gene. LOC126964 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126964, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126964 BINDING SITE, designated SEQ ID:36884, to the nucleotide sequence of VGAM2311 RNA, herein designated VGAM RNA, also designated SEQ ID:5022.

[78591] Another function of VGAM2311 is therefore inhibition of LOC126964 (Accession XM_059100). Accordingly, utilities

of VGAM2311 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126964. LOC128344 (Accession XM_059234) is another VGAM2311 host target gene. LOC128344 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC128344, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC128344 BINDING SITE, designated SEQ ID:36923, to the nucleotide sequence of VGAM2311 RNA, herein designated VGAM RNA, also designated SEQ ID:5022.

[78592] Another function of VGAM2311 is therefore inhibition of LOC128344 (Accession XM_059234). Accordingly, utilities of VGAM2311 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128344. LOC152245 (Accession XM_098182) is another VGAM2311 host target gene. LOC152245 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152245, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC152245 BINDING SITE, designated SEQ ID:41451, to the nucleotide sequence of VGAM2311 RNA, herein designated VGAM RNA, also designated SEQ ID:5022.

[78593] Another function of VGAM2311 is therefore inhibition of LOC152245 (Accession XM_098182). Accordingly, utilities of VGAM2311 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152245. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2312 (VGAM2312) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78594] VGAM2312 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2312 was detected is described hereinabove with reference to Figs. 1-8.

[78595] VGAM2312 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Lumpy Skin Disease Virus. VGAM2312 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78596] VGAM2312 gene encodes a VGAM2312 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2312 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2312 precursor RNA is designated SEQ ID:2298, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2298 is located at position 2051 relative to the genome of Lumpy Skin Disease Virus.

[78597] VGAM2312 precursor RNA folds onto itself, forming VGAM2312 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78598] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2312 folded precursor RNA into VGAM2312 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2312 RNA is designated SEQ ID:5023, and is provided hereinbelow with reference to the sequence listing part.

[78599] VGAM2312 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2312 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2312 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78600] VGAM2312 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2312 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2312 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2312 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2312 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78601] The complementary binding of VGAM2312 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2312 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2312 host target RNA into VGAM2312 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78602] It is appreciated that VGAM2312 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2312 host target genes. The mRNA of each one of this plurality of VGAM2312 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2312 RNA, herein designated VGAM RNA, and which when bound by VGAM2312 RNA causes inhibition of translation of respective one or more VGAM2312 host target proteins.

[78603] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2312 gene, herein designated VGAM GENE, on one or more VGAM2312 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78604] It is yet further appreciated that a function of VGAM2312 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of viral infection by Lumpy Skin Disease Virus. Specific functions, and accordingly utilities, of VGAM2312 correlate with, and may be deduced from, the identity of the host target genes which VGAM2312 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78605] Nucleotide sequences of the VGAM2312 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2312 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2312 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2312 are further described hereinbelow with reference to Table 1.

[78606] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2312 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2312 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78607] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2312 gene, herein designated VGAM is inhibition of expression of VGAM2312 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2312 correlate with, and may be deduced from, the identity of the target genes which VGAM2312 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78608] Heterogeneous Nuclear Ribonucleoprotein D-like (HNRPDL, Accession NM_005463) is a VGAM2312 host target gene. HNRPDL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HNRPDL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNRPDL BINDING SITE, designated SEQ ID:11956, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78609] A function of VGAM2312 is therefore inhibition of Heterogeneous Nuclear Ribonucleoprotein D-like (HNRPDL, Accession NM_005463), a gene which binds to rna molecules that contain au-rich elements. Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNRPDL. The function of HNRPDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM144.5-hydroxytryptamine (serotonin) Receptor 4 (HTR4, Accession NM_000870) is another VGAM2312 host target gene. HTR4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HTR4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HTR4 BINDING SITE, designated SEQ ID:6544, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78610] Another function of VGAM2312 is therefore inhibition of 5-hydroxytryptamine (serotonin) Receptor 4 (HTR4, Accession NM_000870), a gene which mediates calcium

channel currents. Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR4. The function of HTR4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM65.V-src Sarcoma (Schmidt-Ruppin A-2) Viral Oncogene Homolog (avian) (SRC, Accession NM_005417) is another VGAM2312 host target gene. SRC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SRC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SRC BINDING SITE, designated SEQ ID:11887, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78611] Another function of VGAM2312 is therefore inhibition of V-src Sarcoma (Schmidt-Ruppin A-2) Viral Oncogene Homolog (avian) (SRC, Accession NM_005417), a gene which is a tyrosine kinase. Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRC. The function

of SRC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM721.Sulfotransferase Family, Cytosolic, 1C, Member 1 (SULT1C1, Accession NM_001056) is another VGAM2312 host target gene. SULT1C1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SULT1C1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SULT1C1 BINDING SITE, designated SEQ ID:6720, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78612] Another function of VGAM2312 is therefore inhibition of Sulfotransferase Family, Cytosolic, 1C, Member 1 (SULT1C1, Accession NM_001056). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SULT1C1. Transcription Factor 2, Hepatic; LF-B3; Variant Hepatic Nuclear Factor (TCF2, Accession NM_006481) is another VGAM2312 host target gene. TCF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by TCF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF2 BINDING SITE, designated SEQ ID:13202, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78613] Another function of VGAM2312 is therefore inhibition of Transcription Factor 2, Hepatic; LF-B3; Variant Hepatic Nuclear Factor (TCF2, Accession NM_006481), a gene which probably binds to the inverted palindrome 5'-gttaatnattaac-3'. Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF2. The function of TCF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM118.Testis Enhanced Gene Transcript (BAX inhibitor 1) (TEGT, Accession XM_035490) is another VGAM2312 host target gene. TEGT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEGT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BIND-

ING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEGT BINDING SITE, designated SEQ ID:32274, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78614] Another function of VGAM2312 is therefore inhibition of Testis Enhanced Gene Transcript (BAX inhibitor 1) (TEGT, Accession XM_035490), a gene which is a suppressor of apoptosis. Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEGT. The function of TEGT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2276.Visinin-like 1 (VSNL1, Accession NM_003385) is another VGAM2312 host target gene. VSNL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VSNL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VSNL1 BINDING SITE, designated SEQ ID:9418, to the nucleotide sequence of VGAM2312 RNA, herein designated

VGAM RNA, also designated SEQ ID:5023.

[78615] Another function of VGAM2312 is therefore inhibition of Visinin-like 1 (VSNL1, Accession NM_003385). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VSNL1. DCOHM (Accession NM_032151) is another VGAM2312 host target gene. DCOHM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCOHM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCOHM BINDING SITE, designated SEQ ID:25844, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78616] Another function of VGAM2312 is therefore inhibition of DCOHM (Accession NM_032151). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCOHM. EFS2 (Accession NM_005864) is another VGAM2312 host target gene. EFS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EFS2, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFS2 BINDING SITE, designated SEQ ID:12480, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78617] Another function of VGAM2312 is therefore inhibition of EFS2 (Accession NM_005864). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFS2. FLJ10511 (Accession NM_018120) is another VGAM2312 host target gene. FLJ10511 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10511, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10511 BINDING SITE, designated SEQ ID:19901, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78618] Another function of VGAM2312 is therefore inhibition of FLJ10511 (Accession NM_018120). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ10511. FLJ20040 (Accession NM_018992) is another VGAM2312 host target gene. FLJ20040 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20040 BINDING SITE, designated SEQ ID:21067, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78619] Another function of VGAM2312 is therefore inhibition of FLJ20040 (Accession NM_018992). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20040. FLJ22569 (Accession NM_023925) is another VGAM2312 host target gene. FLJ22569 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22569, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22569 BINDING SITE, designated SEQ ID:23401, to the nucleotide

sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78620] Another function of VGAM2312 is therefore inhibition of FLJ22569 (Accession NM_023925). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22569. FLJ23053 (Accession NM_022907) is another VGAM2312 host target gene. FLJ23053 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23053, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23053 BINDING SITE, designated SEQ ID:23208, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78621] Another function of VGAM2312 is therefore inhibition of FLJ23053 (Accession NM_022907). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23053. Glutamate Receptor, Ionotropic, Delta 1 (GRID1, Accession XM_043613) is another VGAM2312 host target gene. GRID1 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by GRID1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRID1 BINDING SITE, designated SEQ ID:33978, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78622] Another function of VGAM2312 is therefore inhibition of Glutamate Receptor, Ionotropic, Delta 1 (GRID1, Accession XM_043613). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRID1. KIAA0268 (Accession XM_046126) is another VGAM2312 host target gene. KIAA0268 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0268, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0268 BINDING SITE, designated SEQ ID:34684, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78623] Another function of VGAM2312 is therefore inhibition of KIAA0268 (Accession XM_046126). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0268. MGC12466 (Accession XM_086336) is another VGAM2312 host target gene. MGC12466 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC12466, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC12466 BINDING SITE, designated SEQ ID:38610, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78624] Another function of VGAM2312 is therefore inhibition of MGC12466 (Accession XM_086336). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12466. LOC145135 (Accession XM_096721) is another VGAM2312 host target gene. LOC145135 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145135, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145135 BINDING SITE, designated SEQ ID:40498, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78625] Another function of VGAM2312 is therefore inhibition of LOC145135 (Accession XM_096721). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145135. LOC196528 (Accession XM_113745) is another VGAM2312 host target gene. LOC196528 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196528, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196528 BINDING SITE, designated SEQ ID:42407, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78626] Another function of VGAM2312 is therefore inhibition of LOC196528 (Accession XM_113745). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC196528. LOC92303 (Accession XM_044108) is another VGAM2312 host target gene. LOC92303 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92303, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92303 BINDING SITE, designated SEQ ID:34135, to the nucleotide sequence of VGAM2312 RNA, herein designated VGAM RNA, also designated SEQ ID:5023.

[78627] Another function of VGAM2312 is therefore inhibition of LOC92303 (Accession XM_044108). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92303. LOC93587 (Accession XM_052377) is another VGAM2312 host target gene. LOC93587 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93587, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93587 BINDING SITE, designated SEQ ID:35964, to the nucleotide sequence of VGAM2312 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5023.

[78628] Another function of VGAM2312 is therefore inhibition of LOC93587 (Accession XM_052377). Accordingly, utilities of VGAM2312 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93587. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2313 (VGAM2313) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78629] VGAM2313 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2313 was detected is described hereinabove with reference to Figs. 1-8.

[78630] VGAM2313 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Lumpy Skin Disease Virus. VGAM2313 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78631] VGAM2313 gene encodes a VGAM2313 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2313 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2313 precursor RNA is designated SEQ ID:2299, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2299 is located at position 146111 relative to the genome of Lumpy Skin Disease Virus.

[78632] VGAM2313 precursor RNA folds onto itself, forming VGAM2313 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78633] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2313 folded precursor RNA into VGAM2313 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2313 RNA is designated SEQ ID:5024, and is provided hereinbelow with reference to the sequence listing part.

[78634] VGAM2313 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2313 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2313 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78635] VGAM2313 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2313 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2313 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2313 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2313 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78636] The complementary binding of VGAM2313 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2313 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2313 host target RNA into VGAM2313 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78637] It is appreciated that VGAM2313 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2313 host target genes. The mRNA of

each one of this plurality of VGAM2313 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2313 RNA, herein designated VGAM RNA, and which when bound by VGAM2313 RNA causes inhibition of translation of respective one or more VGAM2313 host target proteins.

[78638] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2313 gene, herein designated VGAM GENE, on one or more VGAM2313 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[78639] It is yet further appreciated that a function of VGAM2313 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2313 include diagnosis, prevention and treatment of viral infection by Lumpy Skin Disease Virus. Specific functions, and accordingly utilities, of VGAM2313 correlate with, and may be deduced from, the identity of the host target genes which VGAM2313 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78640] Nucleotide sequences of the VGAM2313 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2313 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2313 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2313 are further described hereinbelow with reference to Table 1.

[78641] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2313 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2313 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78642] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2313 gene, herein designated VGAM is inhibition of expression of VGAM2313 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2313 correlate with, and may be deduced from, the identity of the target genes which VGAM2313 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78643] Glucosaminyl (N-acetyl) Transferase 1, Core 2 (beta-1,6-N-acetylglucosaminyltransferase) (GCNT1, Accession NM_001490) is a VGAM2313 host target gene. GCNT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GCNT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GCNT1 BINDING SITE, designated SEQ ID:7236, to the nucleotide sequence of VGAM2313 RNA, herein designated VGAM RNA, also designated SEQ ID:5024.

[78644] A function of VGAM2313 is therefore inhibition of Glu-

cosaminyl (N-acetyl) Transferase 1, Core 2 (beta-1,6-N-acetylglucosaminyltransferase) (GCNT1, Accession NM_001490), a gene which forms critical branches in o-glycans. Accordingly, utilities of VGAM2313 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GCNT1. The function of GCNT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM149.Serine/threonine Kinase 6 (STK6, Accession NM_003600) is another VGAM2313 host target gene. STK6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STK6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STK6 BINDING SITE, designated SEQ ID:9653, to the nucleotide sequence of VGAM2313 RNA, herein designated VGAM RNA, also designated SEQ ID:5024.

[78645] Another function of VGAM2313 is therefore inhibition of Serine/threonine Kinase 6 (STK6, Accession NM_003600), a gene which is serine/threonine kinase 6 which is most highly expressed during mitosis. Accordingly, utilities of

VGAM2313 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK6. The function of STK6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1212.FLJ12595 (Accession NM_024994) is another VGAM2313 host target gene. FLJ12595 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12595, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12595 BINDING SITE, designated SEQ ID:24555, to the nucleotide sequence of VGAM2313 RNA, herein designated VGAM RNA, also designated SEQ ID:5024.

[78646] Another function of VGAM2313 is therefore inhibition of FLJ12595 (Accession NM_024994). Accordingly, utilities of VGAM2313 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12595. HSPC031 (Accession NM_016101) is another VGAM2313 host target gene. HSPC031 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSPC031, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPC031 BINDING SITE, designated SEQ ID:18183, to the nucleotide sequence of VGAM2313 RNA, herein designated VGAM RNA, also designated SEQ ID:5024.

[78647] Another function of VGAM2313 is therefore inhibition of HSPC031 (Accession NM_016101). Accordingly, utilities of VGAM2313 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC031. KIAA1719 (Accession XM_042936) is another VGAM2313 host target gene. KIAA1719 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1719, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1719 BINDING SITE, designated SEQ ID:33815, to the nucleotide sequence of VGAM2313 RNA, herein designated VGAM RNA, also designated SEQ ID:5024.

[78648] Another function of VGAM2313 is therefore inhibition of KIAA1719 (Accession XM_042936). Accordingly, utilities of VGAM2313 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1719. pcnp (Accession NM_020357) is another VGAM2313 host target gene. pcnp BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by pcnp, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of pcnp BINDING SITE, designated SEQ ID:21624, to the nucleotide sequence of VGAM2313 RNA, herein designated VGAM RNA, also designated SEQ ID:5024.

[78649] Another function of VGAM2313 is therefore inhibition of pcnp (Accession NM_020357). Accordingly, utilities of VGAM2313 include diagnosis, prevention and treatment of diseases and clinical conditions associated with pcnp. Protein Tyrosine Phosphatase, Receptor Type, U (PTPRU, Accession NM_005704) is another VGAM2313 host target gene. PTPRU BINDING SITE1 through PTPRU BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTPRU, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRU BINDING

SITE1 through PTPRU BINDING SITE3, designated SEQ ID:12253, SEQ ID:28403 and SEQ ID:28398 respectively, to the nucleotide sequence of VGAM2313 RNA, herein designated VGAM RNA, also designated SEQ ID:5024.

[78650] Another function of VGAM2313 is therefore inhibition of Protein Tyrosine Phosphatase, Receptor Type, U (PTPRU, Accession NM_005704). Accordingly, utilities of VGAM2313 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRU. LOC202108 (Accession XM_114442) is another VGAM2313 host target gene. LOC202108 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202108, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202108 BINDING SITE, designated SEQ ID:42964, to the nucleotide sequence of VGAM2313 RNA, herein designated VGAM RNA, also designated SEQ ID:5024.

[78651] Another function of VGAM2313 is therefore inhibition of LOC202108 (Accession XM_114442). Accordingly, utilities of VGAM2313 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC202108. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2314 (VGAM2314) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78652] VGAM2314 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2314 was detected is described hereinabove with reference to Figs. 1-8.

[78653] VGAM2314 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Lumpy Skin Disease Virus. VGAM2314 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78654] VGAM2314 gene encodes a VGAM2314 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2314 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2314 precursor RNA is designated SEQ ID:2300, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2300 is located at position 715 relative to the genome of Lumpy Skin Disease Virus.

[78655] VGAM2314 precursor RNA folds onto itself, forming VGAM2314 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78656] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2314 folded precursor RNA into VGAM2314 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide sequence of VGAM2314 RNA is designated SEQ ID:5025, and is provided hereinbelow with reference to the sequence listing part.

[78657] VGAM2314 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2314 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2314 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78658] VGAM2314 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2314 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2314 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2314 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2314 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78659] The complementary binding of VGAM2314 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2314 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2314 host target RNA into VGAM2314 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78660] It is appreciated that VGAM2314 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2314 host target genes. The mRNA of each one of this plurality of VGAM2314 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2314 RNA, herein designated VGAM RNA, and which when bound by VGAM2314 RNA causes

inhibition of translation of respective one or more VGAM2314 host target proteins.

[78661] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2314 gene, herein designated VGAM GENE, on one or more VGAM2314 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78662] It is yet further appreciated that a function of VGAM2314 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2314 include diagnosis, prevention and

treatment of viral infection by Lumpy Skin Disease Virus. Specific functions, and accordingly utilities, of VGAM2314 correlate with, and may be deduced from, the identity of the host target genes which VGAM2314 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78663] Nucleotide sequences of the VGAM2314 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2314 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2314 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2314 are further described hereinbelow with reference to Table 1.

[78664] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2314 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2314 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78665] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2314 gene, herein designated VGAM is inhibition of expression of VGAM2314 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2314 correlate with, and may be deduced from, the identity of the target genes which VGAM2314 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78666] ATPase, Ca++ Transporting, Cardiac Muscle, Slow Twitch 2 (ATP2A2, Accession NM_001681) is a VGAM2314 host target gene. ATP2A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP2A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP2A2 BINDING SITE, designated SEQ ID:7399, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78667] A function of VGAM2314 is therefore inhibition of ATPase, Ca++ Transporting, Cardiac Muscle, Slow Twitch 2 (ATP2A2, Accession NM_001681). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP2A2. Cartilage Associated Protein (CRTAP, Accession NM_006371) is another VGAM2314 host target gene. CR-

TAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRTAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRTAP BINDING SITE, designated SEQ ID:13059, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78668] Another function of VGAM2314 is therefore inhibition of Cartilage Associated Protein (CRTAP, Accession NM_006371), a gene which is a novel developmentally regulated chick embryo protein. Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRTAP. The function of CRTAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.Casein Kinase 2, Alpha 1 Polypeptide (CSNK2A1, Accession NM_001895) is another VGAM2314 host target gene. CSNK2A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSNK2A1, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSNK2A1 BINDING SITE, designated SEQ ID:7622, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78669] Another function of VGAM2314 is therefore inhibition of Casein Kinase 2, Alpha 1 Polypeptide (CSNK2A1, Accession NM_001895), a gene which cphosphorylates acidic protein such as casein. Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK2A1. The function of CSNK2A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1597.Hippocalcin-like 1 (HPCAL1, Accession NM_002149) is another VGAM2314 host target gene. HPCAL1 BINDING SITE1 and HPCAL1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HPCAL1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HPCAL1 BINDING SITE1

and HPCAL1 BINDING SITE2, designated SEQ ID:7929 and SEQ ID:28636 respectively, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78670] Another function of VGAM2314 is therefore inhibition of Hippocalcin-like 1 (HPCAL1, Accession NM_002149). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HPCAL1. Single-minded Homolog 1 (Drosophila) (SIM1, Accession NM_005068) is another VGAM2314 host target gene. SIM1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SIM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIM1 BINDING SITE, designated SEQ ID:11507, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78671] Another function of VGAM2314 is therefore inhibition of Single-minded Homolog 1 (Drosophila) (SIM1, Accession NM_005068), a gene which may have pleiotropic effects during embryogenesis and in the adult. Accordingly, utili-

ties of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIM1. The function of SIM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM665.Solute Carrier Family 22 (organic anion/cation transporter), Member 12 (SLC22A12, Accession NM_144585) is another VGAM2314 host target gene. SLC22A12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC22A12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC22A12 BINDING SITE, designated SEQ ID:29401, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78672] Another function of VGAM2314 is therefore inhibition of Solute Carrier Family 22 (organic anion/cation transporter), Member 12 (SLC22A12, Accession NM_144585), a gene which is a urate -anion exchanger regulating blood yrate levels. Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with SLC22A12. The function of SLC22A12 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1034.Transforming Growth Factor, Alpha (TGFA, Accession NM_003236) is another VGAM2314 host target gene. TGFA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TGFA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TGFA BINDING SITE, designated SEQ ID:9229, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78673] Another function of VGAM2314 is therefore inhibition of Transforming Growth Factor, Alpha (TGFA, Accession NM_003236), a gene which is able to bind to the egf receptor and to act synergistically with tgf beta to promote anchorage-independent cell proliferation in soft agar. Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGFA. The function of TGFA and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to VGAM328.Ubiquitin-conjugating Enzyme E2B (RAD6 homolog) (UBE2B, Accession NM_003337) is another VGAM2314 host target gene. UBE2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UBE2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE2B BINDING SITE, designated SEQ ID:9344, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78674] Another function of VGAM2314 is therefore inhibition of Ubiquitin-conjugating Enzyme E2B (RAD6 homolog) (UBE2B, Accession NM_003337), a gene which catalyzes the covalent attachment of ubiquitin to other proteins and is required for postreplication repair of uv-damaged dna. Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE2B. The function of UBE2B has been established by previous studies. The RAD6 pathway is central to postreplicative DNA repair in eukaryotic cells.

Two principal elements of this pathway are the ubiquitin-conjugating enzymes RAD6 and the MMS2 (OMIM Ref. No. 603001)-UBC13 (OMIM Ref. No. 603679) heterodimer, which are recruited to chromatin by the RING-finger proteins RAD18 (OMIM Ref. No. 605256) and RAD5 (OMIM Ref. No. 607266), respectively. Hoege et al. (2002) showed that UBC9 (OMIM Ref. No. 601661), a small ubiquitin-related modifier (SUMO)-conjugating enzyme, is also affiliated with this pathway and that proliferating cell nuclear antigen (PCNA; 176740), a DNA polymerase sliding clamp involved in DNA synthesis and repair, is a substrate. PCNA is monoubiquitinated through RAD6 and RAD18, modified by lys63-linked multiubiquitination, which additionally requires MMS2, UBC13, and RAD5, and is conjugated to SUMO by UBC9. All 3 modifications affect the same lysine residue of PCNA, K164, suggesting that they label PCNA for alternative functions. Hoege et al. (2002) demonstrated that these modifications differentially affect resistance to DNA damage, and that damage-induced PCNA ubiquitination is elementary for DNA repair and occurs at the same conserved residue in yeast and humans. Animal model experiments lend further support to the function of UBE2B. Roest et al. (1996) reported the

phenotype of the first animal mutant in the ubiquitin pathway. Experimental inactivation of the RAD6B gene in mice caused male infertility. Derailment of spermatogenesis became overt during the postmeiotic condensation of chromatin in spermatids. In yeast the gene is not only implicated in postreplication repair and damage-induced mutagenesis but is also required for sporulation and may modulate chromatin structure via histone ubiquitination. The authors stated that the findings in the 'knock-out' mice provided a parallel between yeast sporulation and mammalian spermatogenesis and strongly implicated RAD6-dependent ubiquitination in chromatin remodeling in the human. Since heterozygous male mice and even knockout female mice are completely normal and fertile and thus able to transmit the defect, similar RAD6B mutations may cause male infertility in man. The fact that the RAD6B mice are viable and phenotypically normal is presumably due to functional redundancy with RAD6A (OMIM Ref. No. 312180).

[78675] It is appreciated that the abovementioned animal model for UBE2B is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[78676] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[78677] Hoege, C.; Pfander, B.; Moldovan, G.-L.; Pyrowolakis, G.; Jentsch, S. : RAD6-dependent DNA repair is linked to modification of PCNA by ubiquitin and SUMO. Nature 419: 135-141, 2002. ; and

[78678] Roest, H. P.; van Klaveren, J.; de Wit, J.; van Gurp, C. G.; Koken, M. H. M.; Vermey, M.; van Roijen, J. H.; Hooger-brugge, J. W.; Vreeburg, J. T. M.; Baarends, W. M.; Bootsma, D.; Grootego.

[78679] Further studies establishing the function and utilities of UBE2B are found in John Hopkins OMIM database record ID 179095, and in sited publications numbered 1793-1194 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.FLJ10468 (Accession NM_018101) is another VGAM2314 host target gene. FLJ10468 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10468, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-cleotide sequences of FLJ10468 BINDING SITE, designated

SEQ ID:19872, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78680] Another function of VGAM2314 is therefore inhibition of FLJ10468 (Accession NM_018101). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10468. FLJ14146 (Accession NM_024709) is another VGAM2314 host target gene. FLJ14146 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14146, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14146 BINDING SITE, designated SEQ ID:24028, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78681] Another function of VGAM2314 is therefore inhibition of FLJ14146 (Accession NM_024709). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14146. FLJ20651 (Accession NM_017919) is another VGAM2314 host target gene. FLJ20651 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20651, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20651 BINDING SITE, designated SEQ ID:19573, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78682] Another function of VGAM2314 is therefore inhibition of FLJ20651 (Accession NM_017919). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20651. FLJ21162 (Accession NM_024873) is another VGAM2314 host target gene. FLJ21162 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ21162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21162 BINDING SITE, designated SEQ ID:24305, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78683] Another function of VGAM2314 is therefore inhibition of

FLJ21162 (Accession NM_024873). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21162. KIAA0164 (Accession NM_014739) is another VGAM2314 host target gene. KIAA0164 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0164, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0164 BINDING SITE, designated SEQ ID:16402, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78684] Another function of VGAM2314 is therefore inhibition of KIAA0164 (Accession NM_014739). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0164. KIAA0356 (Accession XM_038655) is another VGAM2314 host target gene. KIAA0356 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0356, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0356 BINDING SITE, designated SEQ ID:32889, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78685] Another function of VGAM2314 is therefore inhibition of KIAA0356 (Accession XM_038655). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0356. KIAA0514 (Accession NM_014696) is another VGAM2314 host target gene. KIAA0514 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0514, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0514 BINDING SITE, designated SEQ ID:16199, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78686] Another function of VGAM2314 is therefore inhibition of KIAA0514 (Accession NM_014696). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0514. KIAA1610 (Accession XM_040622) is another

VGAM2314 host target gene. KIAA1610 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1610, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1610 BINDING SITE, designated SEQ ID:33341, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78687] Another function of VGAM2314 is therefore inhibition of KIAA1610 (Accession XM_040622). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1610. KIAA1954 (Accession XM_085375) is another VGAM2314 host target gene. KIAA1954 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1954, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1954 BINDING SITE, designated SEQ ID:38090, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78688] Another function of VGAM2314 is therefore inhibition of KIAA1954 (Accession XM_085375). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1954. Peroxisomal Biogenesis Factor 12 (PEX12, Accession NM_000286) is another VGAM2314 host target gene. PEX12 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PEX12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEX12 BINDING SITE, designated SEQ ID:5832, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78689] Another function of VGAM2314 is therefore inhibition of Peroxisomal Biogenesis Factor 12 (PEX12, Accession NM_000286). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEX12. RAP2B, Member of RAS Oncogene Family (RAP2B, Accession XM_171061) is another VGAM2314 host target gene. RAP2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by RAP2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAP2B BINDING SITE, designated SEQ ID:45858, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78690] Another function of VGAM2314 is therefore inhibition of RAP2B, Member of RAS Oncogene Family (RAP2B, Accession XM_171061). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP2B. LOC151877 (Accession XM_098132) is another VGAM2314 host target gene. LOC151877 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151877, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151877 BINDING SITE, designated SEQ ID:41392, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78691] Another function of VGAM2314 is therefore inhibition of

LOC151877 (Accession XM_098132). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151877. LOC168489 (Accession XM_095134) is another VGAM2314 host target gene. LOC168489 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC168489, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC168489 BINDING SITE, designated SEQ ID:40249, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78692] Another function of VGAM2314 is therefore inhibition of LOC168489 (Accession XM_095134). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168489. LOC197319 (Accession XM_113862) is another VGAM2314 host target gene. LOC197319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197319, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC197319 BINDING SITE, designated SEQ ID:42474, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78693] Another function of VGAM2314 is therefore inhibition of LOC197319 (Accession XM_113862). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197319. LOC221773 (Accession XM_165802) is another VGAM2314 host target gene. LOC221773 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221773, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221773 BINDING SITE, designated SEQ ID:43758, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78694] Another function of VGAM2314 is therefore inhibition of LOC221773 (Accession XM_165802). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221773. LOC90591 (Accession XM_032811) is an-

other VGAM2314 host target gene. LOC90591 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90591, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90591 BINDING SITE, designated SEQ ID:31757, to the nucleotide sequence of VGAM2314 RNA, herein designated VGAM RNA, also designated SEQ ID:5025.

[78695] Another function of VGAM2314 is therefore inhibition of LOC90591 (Accession XM_032811). Accordingly, utilities of VGAM2314 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90591. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2315 (VGAM2315) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78696] VGAM2315 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2315 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[78697] VGAM2315 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Lumpy Skin Disease Virus. VGAM2315 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78698] VGAM2315 gene encodes a VGAM2315 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2315 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2315 precursor RNA is designated SEQ ID:2301, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2301 is located at position 128712 relative to the genome of Lumpy Skin Disease Virus.

[78699] VGAM2315 precursor RNA folds onto itself, forming VGAM2315 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78700] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2315 folded precursor RNA into VGAM2315 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2315 RNA is designated SEQ ID:5026, and is provided hereinbelow with reference to the sequence listing part.

[78701] VGAM2315 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2315 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2315 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78702] VGAM2315 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2315 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2315 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2315 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2315 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78703] The complementary binding of VGAM2315 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2315 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2315 host target RNA into VGAM2315 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78704] It is appreciated that VGAM2315 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2315 host target genes. The mRNA of each one of this plurality of VGAM2315 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2315 RNA, herein designated VGAM RNA, and which when bound by VGAM2315 RNA causes inhibition of translation of respective one or more VGAM2315 host target proteins.

[78705] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2315 gene, herein designated VGAM GENE, on one or more VGAM2315 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78706] It is yet further appreciated that a function of VGAM2315 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2315 include diagnosis, prevention and treatment of viral infection by Lumpy Skin Disease Virus. Specific functions, and accordingly utilities, of VGAM2315 correlate with, and may be deduced from, the identity of the host target genes which VGAM2315 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78707] Nucleotide sequences of the VGAM2315 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2315 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2315 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2315 are further described hereinbelow with reference to Table 1.

[78708] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2315 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2315 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78709] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2315 gene, herein designated VGAM is inhibition of expression of VGAM2315 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2315 correlate with, and may be deduced from, the identity of the target genes which VGAM2315 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78710] Transient Receptor Potential Cation Channel, Subfamily M, Member 8 (TRPM8, Accession NM_024080) is a VGAM2315 host target gene. TRPM8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRPM8, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPM8 BINDING SITE, designated SEQ ID:23518, to the nucleotide sequence of VGAM2315 RNA, herein designated VGAM RNA, also designated SEQ ID:5026.

[78711] A function of VGAM2315 is therefore inhibition of Transient Receptor Potential Cation Channel, Subfamily M, Member 8 (TRPM8, Accession NM_024080), a gene which is thought to form a receptor-activated calcium permeant cation channel. Accordingly, utilities of VGAM2315 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPM8. The function of TRPM8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM201.UDP-glucose Dehydrogenase (UGDH, Accession NM_003359) is another VGAM2315 host target gene. UGDH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UGDH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of UGDH BINDING SITE, designated SEQ ID:9386, to the nucleotide sequence of VGAM2315 RNA, herein designated VGAM RNA, also designated SEQ ID:5026.

[78712] Another function of VGAM2315 is therefore inhibition of UDP-glucose Dehydrogenase (UGDH, Accession NM_003359), a gene which is an UDP-glucose dehydrogenase. Accordingly, utilities of VGAM2315 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UGDH. The function of UGDH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.FLJ23259 (Accession NM_024727) is another VGAM2315 host target gene. FLJ23259 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23259 BINDING SITE, designated SEQ ID:24063, to the nucleotide sequence of VGAM2315 RNA, herein designated VGAM RNA, also designated SEQ ID:5026.

[78713] Another function of VGAM2315 is therefore inhibition of

FLJ23259 (Accession NM_024727). Accordingly, utilities of VGAM2315 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23259. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2316 (VGAM2316) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78714] VGAM2316 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2316 was detected is described hereinabove with reference to Figs. 1-8.

[78715] VGAM2316 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2316 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78716] VGAM2316 gene encodes a VGAM2316 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2316 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2316 precursor RNA is designated SEQ ID:2302, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2302 is located at position 33473 relative to the genome of Rana Tigrina Ranavirus.

[78717] VGAM2316 precursor RNA folds onto itself, forming VGAM2316 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78718] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2316 folded precursor RNA into VGAM2316 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide se-

quence of VGAM2316 RNA is designated SEQ ID:5027, and is provided hereinbelow with reference to the sequence listing part.

[78719] VGAM2316 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2316 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2316 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78720] VGAM2316 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2316 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2316 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2316 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2316 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78721] The complementary binding of VGAM2316 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2316 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2316 host target RNA into VGAM2316 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78722] It is appreciated that VGAM2316 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2316 host target genes. The mRNA of each one of this plurality of VGAM2316 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2316 RNA, herein designated VGAM RNA, and which when bound by VGAM2316 RNA causes inhibition of translation of respective one or more VGAM2316 host target proteins.

[78723] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2316 gene, herein designated VGAM GENE, on one or more VGAM2316 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78724] It is yet further appreciated that a function of VGAM2316

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2316 correlate with, and may be deduced from, the identity of the host target genes which VGAM2316 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78725] Nucleotide sequences of the VGAM2316 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2316 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2316 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2316 are further described hereinbelow with reference to Table 1.

[78726] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2316 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2316 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78727] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2316 gene, herein designated VGAM is inhibition of expression of VGAM2316 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2316 correlate with, and may be deduced from, the identity of the target genes which VGAM2316 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78728] UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 1 (B4GALT1, Accession NM_001497) is a VGAM2316 host target gene. B4GALT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by B4GALT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B4GALT1 BINDING SITE, designated SEQ ID:7248, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78729] A function of VGAM2316 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 1 (B4GALT1, Accession NM_001497). Accordingly, utilities of VGAM2316 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with B4GALT1. Dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD, Accession NM_004013) is another VGAM2316 host target gene. DMD BINDING SITE1 through DMD BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DMD, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DMD BINDING SITE1 through DMD BINDING SITE3, designated SEQ ID:10200, SEQ ID:10227 and SEQ ID:10239 respectively, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78730] Another function of VGAM2316 is therefore inhibition of Dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD, Accession NM_004013), a gene which muscular dystrophy . Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMD. The function of DMD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM218.Fibroblast Growth Factor Receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) (FGFR2, Accession NM_022972) is another VGAM2316 host target gene. FGFR2 BINDING SITE1 through FGFR2 BINDING SITE6 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FGFR2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGFR2 BINDING SITE1 through FGFR2 BINDING SITE6, designated SEQ ID:23245, SEQ ID:23292, SEQ ID:5642, SEQ ID:23298, SEQ ID:23304 and SEQ ID:13672 respectively, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78731] Another function of VGAM2316 is therefore inhibition of Fibroblast Growth Factor Receptor 2 (bacteria-expressed kinase, keratinocyte growth factor receptor, craniofacial dysostosis 1, Crouzon syndrome, Pfeiffer syndrome, Jackson-Weiss syndrome) (FGFR2, Accession NM_022972). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with FGFR2. PART1 (Accession NM_016590) is another VGAM2316 host target gene. PART1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PART1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PART1 BINDING SITE, designated SEQ ID:18667, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78732] Another function of VGAM2316 is therefore inhibition of PART1 (Accession NM_016590). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PART1. Prostaglandin-endoperoxide Synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1, Accession NM_000962) is another VGAM2316 host target gene. PTGS1 BINDING SITE1 and PTGS1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTGS1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of PTGS1 BINDING SITE1 and PTGS1 BINDING SITE2, designated SEQ ID:6676 and SEQ ID:27897 respectively, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78733] Another function of VGAM2316 is therefore inhibition of Prostaglandin-endoperoxide Synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1, Accession NM_000962), a gene which may play an important role in regulating or promoting cell proliferation in some normal and neoplastically transformed cells. Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGS1. The function of PTGS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1224.FLJ22174 (Accession NM_021945) is another VGAM2316 host target gene. FLJ22174 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22174, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

FLJ22174 BINDING SITE, designated SEQ ID:22468, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78734] Another function of VGAM2316 is therefore inhibition of FLJ22174 (Accession NM_021945). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22174. KIAA0222 (Accession NM_014643) is another VGAM2316 host target gene. KIAA0222 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0222, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0222 BINDING SITE, designated SEQ ID:16048, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78735] Another function of VGAM2316 is therefore inhibition of KIAA0222 (Accession NM_014643). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0222. RAB10, Member RAS Oncogene Family (RAB10, Accession XM_097979) is another VGAM2316 host target

gene. RAB10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB10 BINDING SITE, designated SEQ ID:41282, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78736] Another function of VGAM2316 is therefore inhibition of RAB10, Member RAS Oncogene Family (RAB10, Accession XM_097979). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB10. Sema Domain, Immunoglobulin Domain (Ig), Transmembrane Domain (TM) and Short Cytoplasmic Domain, (semaphorin) 4G (SEMA4G, Accession XM_170638) is another VGAM2316 host target gene. SEMA4G BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SEMA4G, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEMA4G BINDING SITE,

designated SEQ ID:45411, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78737] Another function of VGAM2316 is therefore inhibition of Sema Domain, Immunoglobulin Domain (Ig), Transmembrane Domain (TM) and Short Cytoplasmic Domain, (semaphorin) 4G (SEMA4G, Accession XM_170638). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEMA4G. ZAK (Accession NM_016653) is another VGAM2316 host target gene. ZAK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZAK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZAK BINDING SITE, designated SEQ ID:18776, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78738] Another function of VGAM2316 is therefore inhibition of ZAK (Accession NM_016653). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZAK.

LOC131363 (Accession XM_067344) is another VGAM2316 host target gene. LOC131363 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC131363, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC131363 BINDING SITE, designated SEQ ID:37353, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78739] Another function of VGAM2316 is therefore inhibition of LOC131363 (Accession XM_067344). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC131363. LOC147057 (Accession XM_097166) is another VGAM2316 host target gene. LOC147057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147057 BINDING SITE, designated SEQ ID:40785, to the nucleotide sequence of VGAM2316 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5027.

[78740] Another function of VGAM2316 is therefore inhibition of LOC147057 (Accession XM_097166). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147057. LOC152580 (Accession XM_098240) is another VGAM2316 host target gene. LOC152580 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152580, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152580 BINDING SITE, designated SEQ ID:41521, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78741] Another function of VGAM2316 is therefore inhibition of LOC152580 (Accession XM_098240). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152580. LOC221751 (Accession XM_166370) is another VGAM2316 host target gene. LOC221751 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221751, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221751 BINDING SITE, designated SEQ ID:44191, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78742] Another function of VGAM2316 is therefore inhibition of LOC221751 (Accession XM_166370). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221751. LOC89932 (Accession XM_027341) is another VGAM2316 host target gene. LOC89932 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC89932, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC89932 BINDING SITE, designated SEQ ID:30495, to the nucleotide sequence of VGAM2316 RNA, herein designated VGAM RNA, also designated SEQ ID:5027.

[78743] Another function of VGAM2316 is therefore inhibition of LOC89932 (Accession XM_027341). Accordingly, utilities of VGAM2316 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC89932. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2317 (VGAM2317) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78744] VGAM2317 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2317 was detected is described hereinabove with reference to Figs. 1-8.

[78745] VGAM2317 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2317 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78746] VGAM2317 gene encodes a VGAM2317 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2317 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2317 precursor RNA is desig-

nated SEQ ID:2303, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2303 is located at position 24685 relative to the genome of Rana Tigrina Ranavirus.

[78747] VGAM2317 precursor RNA folds onto itself, forming VGAM2317 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78748] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2317 folded precursor RNA into VGAM2317 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2317 RNA is designated SEQ ID:5028, and is provided hereinbelow with reference to the sequence

listing part.

[78749] VGAM2317 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2317 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2317 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78750] VGAM2317 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2317 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2317 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2317 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2317 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78751] The complementary binding of VGAM2317 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2317 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2317 host target RNA into VGAM2317 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78752] It is appreciated that VGAM2317 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2317 host target genes. The mRNA of each one of this plurality of VGAM2317 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2317 RNA, herein designated VGAM

RNA, and which when bound by VGAM2317 RNA causes inhibition of translation of respective one or more VGAM2317 host target proteins.

[78753] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2317 gene, herein designated VGAM GENE, on one or more VGAM2317 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78754] It is yet further appreciated that a function of VGAM2317 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2317 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2317 correlate with, and may be deduced from, the identity of the host target genes which VGAM2317 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78755] Nucleotide sequences of the VGAM2317 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2317 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2317 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2317 are further described hereinbelow with reference to Table 1.

[78756] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2317 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2317 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78757] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2317 gene, herein designated VGAM is

inhibition of expression of VGAM2317 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2317 correlate with, and may be deduced from, the identity of the target genes which VGAM2317 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78758] Carbohydrate Kinase-like (CARKL, Accession NM_013276) is a VGAM2317 host target gene. CARKL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CARKL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CARKL BINDING SITE, designated SEQ ID:14937, to the nucleotide sequence of VGAM2317 RNA, herein designated VGAM RNA, also designated SEQ ID:5028.

[78759] A function of VGAM2317 is therefore inhibition of Carbohydrate Kinase-like (CARKL, Accession NM_013276), a gene which is a putative carbohydrate kinase and may be a modifier for the cystinosis phenotype. Accordingly, utilities of VGAM2317 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARKL. The function of CARKL and its association

with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM419.Mitogen-activated Protein Kinase Kinase Kinase 11 (MAP3K11, Accession NM_002419) is another VGAM2317 host target gene. MAP3K11 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAP3K11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K11 BINDING SITE, designated SEQ ID:8256, to the nucleotide sequence of VGAM2317 RNA, herein designated VGAM RNA, also designated SEQ ID:5028.

[78760] Another function of VGAM2317 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 11 (MAP3K11, Accession NM_002419), a gene which is a PROTEIN-TYROSINE KINASE. Accordingly, utilities of VGAM2317 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K11. The function of MAP3K11 has been established by previous studies. Using RT-PCR and cDNA library screening, Ing et al. (1994) identified MAP3K11, a novel protein kinase, from human thymus. The deduced open

reading frame, derived from sequencing a 3.5-kb MAP3K11 cDNA, encodes a protein of 847 amino acids with several interesting structural features. These include an SH3 domain in the absence of an SH2 domain, a region containing 2 leucine zippers with an adjacent C-terminal basic region, and a proline rich region. The new kinase showed homology with the mixed-lineage family of protein kinases (MLKs) and shared the unusual leucine zipper-basic motif found in previously identified MLK kinases; Ing et al. (1994) therefore called the protein MLK3. By Northern blot analysis, MAP3K11 mRNA was detected in a wide variety of normal and transformed human cell lines and tissues. SH2 domains refer to src homology 2 domains, which were first identified in the SRC gene family and found in a variety of proteins involved in signal transduction. Proteins bearing an SH3 domain also participate in receptor tyrosine kinase-mediated signal transduction. Using fluorescence in situ hybridization, Ing et al. (1994) mapped the MAP3K11 gene to 11q13.1-q13.3. Courseaux et al. (1996) used a combination of methods to refine maps of the approximately 5-Mb region of 11q13 that includes MEN1 (OMIM Ref. No. 131100). They proposed the following gene order: cen-

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PGA-

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FTH1--UGB--AHNAK--ROM1--MDU1--CHRM1--COX8--EMK1--FKBP2--PLCB3--[PYGM, ZFM1]--FAU--CAPN1--[MAP3K11, RELA]--FOSL1--SEA--CFL1--tel

[78761] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[78762] Courseaux, A.; Grosgeorge, J.; Gaudray, P.; Pannett, A. A. J.; Forbes, S. A.; Williamson, C.; Bassett, D.; Thakker, R. V.; Teh, B. T.; Farnebo, F.; Shepherd, J.; Skogseid, B.; Larsson, C.; Giraud, S.; Zhang, C. X.; Salandre, J.; Calender, A. : Definition of the minimal MEN1 candidate area based on a 5-Mb integrated map of proximal 11q13. Genomics 37: 354-365, 1996. ; and

[78763] Ing, Y. L.; Leung, I. W. L.; Heng, H. H. Q.; Tsui, L.-C.; Lassam, N. J. : MLK-3: identification of a widely-expressed protein kinase bearing an SH3 domain and a leucine zipper-basic regi.

[78764] Further studies establishing the function and utilities of MAP3K11 are found in John Hopkins OMIM database

record ID 600050, and in sited publications numbered 398 and 7725 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.P114-RHO-GEF (Accession NM_015318) is another VGAM2317 host target gene. P114-RHO-GEF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P114-RHO-GEF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P114-RHO-GEF BINDING SITE, designated SEQ ID:17639, to the nucleotide sequence of VGAM2317 RNA, herein designated VGAM RNA, also designated SEQ ID:5028.

[78765] Another function of VGAM2317 is therefore inhibition of P114-RHO-GEF (Accession NM_015318). Accordingly, utilities of VGAM2317 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P114-RHO-GEF. LOC144347 (Accession XM_084832) is another VGAM2317 host target gene. LOC144347 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144347, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144347 BINDING SITE, designated SEQ ID:37722, to the nucleotide sequence of VGAM2317 RNA, herein designated VGAM RNA, also designated SEQ ID:5028.

[78766] Another function of VGAM2317 is therefore inhibition of LOC144347 (Accession XM_084832). Accordingly, utilities of VGAM2317 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144347. LOC146243 (Accession XM_096956) is another VGAM2317 host target gene. LOC146243 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146243, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146243 BINDING SITE, designated SEQ ID:40675, to the nucleotide sequence of VGAM2317 RNA, herein designated VGAM RNA, also designated SEQ ID:5028.

[78767] Another function of VGAM2317 is therefore inhibition of LOC146243 (Accession XM_096956). Accordingly, utilities of VGAM2317 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC146243. LOC255231 (Accession XM_170908) is another VGAM2317 host target gene. LOC255231 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255231 BINDING SITE, designated SEQ ID:45673, to the nucleotide sequence of VGAM2317 RNA, herein designated VGAM RNA, also designated SEQ ID:5028.

[78768] Another function of VGAM2317 is therefore inhibition of LOC255231 (Accession XM_170908). Accordingly, utilities of VGAM2317 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255231. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2318 (VGAM2318) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78769] VGAM2318 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2318 was detected is described hereinabove with reference to Figs. 1-8.

[78770] VGAM2318 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2318 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78771] VGAM2318 gene encodes a VGAM2318 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2318 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2318 precursor RNA is designated SEQ ID:2304, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2304 is located at position 35010 relative to the genome of Rana Tigrina Ranavirus.

[78772] VGAM2318 precursor RNA folds onto itself, forming VGAM2318 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78773] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2318 folded precursor RNA into VGAM2318 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2318 RNA is designated SEQ ID:5029, and is provided hereinbelow with reference to the sequence listing part.

[78774] VGAM2318 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2318 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2318 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78775] VGAM2318 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2318 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2318 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2318 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2318 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78776] The complementary binding of VGAM2318 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2318 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2318 host target RNA into VGAM2318 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78777] It is appreciated that VGAM2318 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2318 host target genes. The mRNA of each one of this plurality of VGAM2318 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2318 RNA, herein designated VGAM RNA, and which when bound by VGAM2318 RNA causes inhibition of translation of respective one or more VGAM2318 host target proteins.

[78778] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2318 gene, herein designated VGAM GENE, on one or more VGAM2318 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78779] It is yet further appreciated that a function of VGAM2318 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2318 correlate with, and may be deduced from, the identity of the host target genes which VGAM2318 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78780] Nucleotide sequences of the VGAM2318 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2318 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2318 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2318 are further described hereinbelow with reference to Table 1.

[78781] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2318 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2318 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78782] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2318 gene, herein designated VGAM is inhibition of expression of VGAM2318 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2318 correlate with, and may be deduced from, the identity of the target genes which VGAM2318 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78783] Dishevelled, Dsh Homolog 3 (Drosophila) (DVL3, Accession NM_004423) is a VGAM2318 host target gene. DVL3 BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by DVL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DVL3 BINDING SITE, designated SEQ ID:10694, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78784] A function of VGAM2318 is therefore inhibition of Dishevelled, Dsh Homolog 3 (Drosophila) (DVL3, Accession NM_004423), a gene which regulates cell proliferation. Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DVL3. The function of DVL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM57.Ephrin-B1 (EFNB1, Accession NM_004429) is another VGAM2318 host target gene. EFNB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EFNB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFNB1 BINDING SITE, designated SEQ

ID:10707, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78785] Another function of VGAM2318 is therefore inhibition of Ephrin-B1 (EFNB1, Accession NM_004429), a gene which is a transmembrane ligand of Eph-related receptor tyrosine kinases, has a role in cell adhesion. Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFNB1. The function of EFNB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM390.LIM Homeobox Protein 5 (LHX5, Accession NM_022363) is another VGAM2318 host target gene. LHX5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LHX5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LHX5 BINDING SITE, designated SEQ ID:22749, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78786] Another function of VGAM2318 is therefore inhibition of

LIM Homeobox Protein 5 (LHX5, Accession NM_022363). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHX5. Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_001879) is another VGAM2318 host target gene. MASP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MASP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MASP1 BINDING SITE, designated SEQ ID:7606, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78787] Another function of VGAM2318 is therefore inhibition of Mannan-binding Lectin Serine Protease 1 (C4/C2 activating component of Ra-reactive factor) (MASP1, Accession NM_001879), a gene which a complement-dependent bactericidal factor . Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MASP1. The function of MASP1 and its association with various diseases and clini-

cal conditions, has been established by previous studies, as described hereinabove with reference to VGAM566.Myogenin (myogenic factor 4) (MYOG, Accession XM_001688) is another VGAM2318 host target gene. MYOG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYOG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYOG BINDING SITE, designated SEQ ID:29847, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78788] Another function of VGAM2318 is therefore inhibition of Myogenin (myogenic factor 4) (MYOG, Accession XM_001688), a gene which can induce myogenesis in a variety of cell types. Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYOG. The function of MYOG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1793.Polypyrimidine Tract Binding Protein 1 (PTBP1,

Accession NM_002819) is another VGAM2318 host target gene. PTBP1 BINDING SITE1 and PTBP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTBP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTBP1 BINDING SITE1 and PTBP1 BINDING SITE2, designated SEQ ID:8684 and SEQ ID:25704 respectively, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78789] Another function of VGAM2318 is therefore inhibition of Polypyrimidine Tract Binding Protein 1 (PTBP1, Accession NM_002819), a gene which is required for pre-mRNA splicing, and acts via the protein degradation ubiquitin-proteasome pathway. Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTBP1. The function of PTBP1 has been established by previous studies. Polypyrimidine tract-binding protein (PTB), also known as heterogeneous nuclear ribonucleoprotein type I (hnRNP I), is a 59.6-kD nuclear protein that binds pre-mRNAs in specific regions of the hnRNA-protein complexes sensitive

to micrococcal nuclease. The hnRNP I protein shows an unusual pattern of nuclear localization (Ghetti et al., 1992). It has been implicated in pre-mRNA splicing. Inclusion of cardiac troponin T (TNNT2; 191045) exon 5 in embryonic muscle requires conserved flanking intronic elements (MSEs). Charlet-B. et al. (2002) found that ETR3 (CUGBP2; 602538), a member of the CELF family, binds U/G motifs in 2 MSEs and directly activates exon inclusion in vitro. They showed that binding and activation by ETR3 are directly antagonized by PTB. The use of dominant-negative mutants demonstrated that endogenous CELF and PTB activities are required for MSE-dependent activation and repression in muscle and nonmuscle cells, respectively. Combined use of CELF and PTB dominant-negative mutants provided an in vivo demonstration that antagonistic splicing activities exist within the same cells.

[78790] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[78791] Ghetti, A.; Pinol-Roma, S.; Michael, W. M.; Morandi, C.; Dreyfuss, G. : HNRNP I, the polypyrimidine tract-binding protein: distinct nuclear localization and association with hnRNAs. Nucleic Acids Res. 20: 3671-3678, 1992. ; and

[78792] Charlet-B., N.; Logan, P.; Singh, G.; Cooper, T. A. : Dynamic antagonism between ETR-3 and PTB regulates cell type-specific alternative splicing. Molec. Cell 9: 649-658, 2002.

[78793] Further studies establishing the function and utilities of PTBP1 are found in John Hopkins OMIM database record ID 600693, and in sited publications numbered 10492-9983 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.ADP-ribosylation Factor GTPase Activating Protein 1 (ARFGAP1, Accession NM_018209) is another VGAM2318 host target gene. ARFGAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARFGAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARFGAP1 BINDING SITE, designated SEQ ID:20108, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78794] Another function of VGAM2318 is therefore inhibition of ADP-ribosylation Factor GTPase Activating Protein 1 (ARFGAP1, Accession NM_018209). Accordingly, utilities

of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARFGAP1. Burkitt Lymphoma Receptor 1, GTP Binding Protein (chemokine (C-X-C motif) Receptor 5) (BLR1, Accession NM_032966) is another VGAM2318 host target gene. BLR1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BLR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BLR1 BINDING SITE, designated SEQ ID:26775, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78795] Another function of VGAM2318 is therefore inhibition of Burkitt Lymphoma Receptor 1, GTP Binding Protein (chemokine (C-X-C motif) Receptor 5) (BLR1, Accession NM_032966). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BLR1. Chromosome 20 Open Reading Frame 110 (C20orf110, Accession XM_086728) is another VGAM2318 host target gene. C20orf110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

C20orf110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf110 BINDING SITE, designated SEQ ID:38837, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78796] Another function of VGAM2318 is therefore inhibition of Chromosome 20 Open Reading Frame 110 (C20orf110, Accession XM_086728). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf110. Collagen, Type IV, Alpha 3 (Goodpasture antigen) Binding Protein (COL4A3BP, Accession NM_005713) is another VGAM2318 host target gene. COL4A3BP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by COL4A3BP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL4A3BP BINDING SITE, designated SEQ ID:12266, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78797] Another function of VGAM2318 is therefore inhibition of Collagen, Type IV, Alpha 3 (Goodpasture antigen) Binding Protein (COL4A3BP, Accession NM_005713). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A3BP. Cathepsin O (CTSO, Accession NM_001334) is another VGAM2318 host target gene. CTSO BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CTSO, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTSO BINDING SITE, designated SEQ ID:7016, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78798] Another function of VGAM2318 is therefore inhibition of Cathepsin O (CTSO, Accession NM_001334). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTSO. FLJ10743 (Accession NM_018201) is another VGAM2318 host target gene. FLJ10743 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10743, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10743 BINDING SITE, designated SEQ ID:20077, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78799] Another function of VGAM2318 is therefore inhibition of FLJ10743 (Accession NM_018201). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10743. FLJ14124 (Accession NM_024868) is another VGAM2318 host target gene. FLJ14124 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14124, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14124 BINDING SITE, designated SEQ ID:24304, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78800] Another function of VGAM2318 is therefore inhibition of FLJ14124 (Accession NM_024868). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ14124. FLJ14824 (Accession NM_032846) is another VGAM2318 host target gene. FLJ14824 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14824, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14824 BINDING SITE, designated SEQ ID:26641, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78801] Another function of VGAM2318 is therefore inhibition of FLJ14824 (Accession NM_032846). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14824. HSU79303 (Accession NM_013301) is another VGAM2318 host target gene. HSU79303 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSU79303, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSU79303 BINDING SITE, designated SEQ ID:14960, to the

nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78802] Another function of VGAM2318 is therefore inhibition of HSU79303 (Accession NM_013301). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSU79303. ICB-1 (Accession NM_004848) is another VGAM2318 host target gene. ICB-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICB-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ICB-1 BINDING SITE, designated SEQ ID:11258, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78803] Another function of VGAM2318 is therefore inhibition of ICB-1 (Accession NM_004848). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICB-1. KIAA0010 (Accession NM_014671) is another VGAM2318 host target gene. KIAA0010 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA

encoded by KIAA0010, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0010 BINDING SITE, designated SEQ ID:16129, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78804] Another function of VGAM2318 is therefore inhibition of KIAA0010 (Accession NM_014671). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0010. KIAA0121 (Accession XM_052386) is another VGAM2318 host target gene. KIAA0121 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0121 BINDING SITE, designated SEQ ID:35969, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78805] Another function of VGAM2318 is therefore inhibition of KIAA0121 (Accession XM_052386). Accordingly, utilities

of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0121. KIAA0194 (Accession XM_038362) is another VGAM2318 host target gene. KIAA0194 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0194, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0194 BINDING SITE, designated SEQ ID:32822, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78806] Another function of VGAM2318 is therefore inhibition of KIAA0194 (Accession XM_038362). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0194. KIAA1691 (Accession XM_166523) is another VGAM2318 host target gene. KIAA1691 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1691, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1691 BINDING SITE, designated SEQ ID:44467, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78807] Another function of VGAM2318 is therefore inhibition of KIAA1691 (Accession XM_166523). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1691. Neuronal Guanine Nucleotide Exchange Factor (NGEF, Accession XM_044799) is another VGAM2318 host target gene. NGEF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NGEF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NGEF BINDING SITE, designated SEQ ID:34276, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78808] Another function of VGAM2318 is therefore inhibition of Neuronal Guanine Nucleotide Exchange Factor (NGEF, Accession XM_044799). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NGEF. REPRIMO

(Accession NM_019845) is another VGAM2318 host target gene. REPRIMO BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by REPRIMO, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of REPRIMO BINDING SITE, designated SEQ ID:21248, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78809] Another function of VGAM2318 is therefore inhibition of REPRIMO (Accession NM_019845). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with REPRIMO. ZF5128 (Accession NM_014347) is another VGAM2318 host target gene. ZF5128 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZF5128, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZF5128 BINDING SITE, designated SEQ ID:15669, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM

RNA, also designated SEQ ID:5029.

[78810] Another function of VGAM2318 is therefore inhibition of ZF5128 (Accession NM_014347). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZF5128. LOC147136 (Accession XM_085716) is another VGAM2318 host target gene. LOC147136 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147136, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147136 BINDING SITE, designated SEQ ID:38302, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78811] Another function of VGAM2318 is therefore inhibition of LOC147136 (Accession XM_085716). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147136. LOC153196 (Accession XM_098323) is another VGAM2318 host target gene. LOC153196 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153196, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153196 BINDING SITE, designated SEQ ID:41589, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78812] Another function of VGAM2318 is therefore inhibition of LOC153196 (Accession XM_098323). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153196. LOC158654 (Accession XM_088632) is another VGAM2318 host target gene. LOC158654 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158654, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158654 BINDING SITE, designated SEQ ID:39877, to the nucleotide sequence of VGAM2318 RNA, herein designated VGAM RNA, also designated SEQ ID:5029.

[78813] Another function of VGAM2318 is therefore inhibition of LOC158654 (Accession XM_088632). Accordingly, utilities of VGAM2318 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC158654. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2319 (VGAM2319) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78814] VGAM2319 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2319 was detected is described hereinabove with reference to Figs. 1-8.

[78815] VGAM2319 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2319 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78816] VGAM2319 gene encodes a VGAM2319 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2319 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2319 precursor RNA is desig-

nated SEQ ID:2305, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2305 is located at position 15762 relative to the genome of Rana Tigrina Ranavirus.

[78817] VGAM2319 precursor RNA folds onto itself, forming VGAM2319 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78818] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2319 folded precursor RNA into VGAM2319 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2319 RNA is designated SEQ ID:5030, and is provided hereinbelow with reference to the sequence

listing part.

[78819] VGAM2319 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2319 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2319 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78820] VGAM2319 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2319 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2319 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2319 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2319 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78821] The complementary binding of VGAM2319 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2319 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2319 host target RNA into VGAM2319 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78822] It is appreciated that VGAM2319 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2319 host target genes. The mRNA of each one of this plurality of VGAM2319 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2319 RNA, herein designated VGAM

RNA, and which when bound by VGAM2319 RNA causes inhibition of translation of respective one or more VGAM2319 host target proteins.

[78823] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2319 gene, herein designated VGAM GENE, on one or more VGAM2319 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78824] It is yet further appreciated that a function of VGAM2319 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2319 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2319 correlate with, and may be deduced from, the identity of the host target genes which VGAM2319 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78825] Nucleotide sequences of the VGAM2319 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2319 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2319 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2319 are further described hereinbelow with reference to Table 1.

[78826] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2319 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2319 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78827] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2319 gene, herein designated VGAM is

inhibition of expression of VGAM2319 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2319 correlate with, and may be deduced from, the identity of the target genes which VGAM2319 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78828] Protein Tyrosine Phosphatase, Non-receptor Type 18 (brain-derived) (PTPN18, Accession NM_014369) is a VGAM2319 host target gene. PTPN18 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPN18, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPN18 BINDING SITE, designated SEQ ID:15704, to the nucleotide sequence of VGAM2319 RNA, herein designated VGAM RNA, also designated SEQ ID:5030.

[78829] A function of VGAM2319 is therefore inhibition of Protein Tyrosine Phosphatase, Non-receptor Type 18 (brain-derived) (PTPN18, Accession NM_014369). Accordingly, utilities of VGAM2319 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPN18. Tumor Necrosis Factor Receptor Super-

family, Member 11a, Activator of NFKB (TNFRSF11A, Accession NM_003839) is another VGAM2319 host target gene. TNFRSF11A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFRSF11A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFRSF11A BINDING SITE, designated SEQ ID:9932, to the nucleotide sequence of VGAM2319 RNA, herein designated VGAM RNA, also designated SEQ ID:5030.

[78830] Another function of VGAM2319 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 11a, Activator of NFKB (TNFRSF11A, Accession NM_003839). Accordingly, utilities of VGAM2319 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF11A. AFAP (Accession NM_021638) is another VGAM2319 host target gene. AFAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AFAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of AFAP BINDING SITE, designated SEQ ID:22293, to the nucleotide sequence of VGAM2319 RNA, herein designated VGAM RNA, also designated SEQ ID:5030.

[78831] Another function of VGAM2319 is therefore inhibition of AFAP (Accession NM_021638). Accordingly, utilities of VGAM2319 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AFAP. LOC221362 (Accession XM_168093) is another VGAM2319 host target gene. LOC221362 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221362, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221362 BINDING SITE, designated SEQ ID:45022, to the nucleotide sequence of VGAM2319 RNA, herein designated VGAM RNA, also designated SEQ ID:5030.

[78832] Another function of VGAM2319 is therefore inhibition of LOC221362 (Accession XM_168093). Accordingly, utilities of VGAM2319 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221362. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2320 (VGAM2320) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78833] VGAM2320 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2320 was detected is described hereinabove with reference to Figs. 1-8.

[78834] VGAM2320 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2320 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78835] VGAM2320 gene encodes a VGAM2320 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2320 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2320 precursor RNA is designated SEQ ID:2306, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2306 is located at position 28526 relative to the

genome of Rana Tigrina Ranavirus.

[78836] VGAM2320 precursor RNA folds onto itself, forming VGAM2320 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78837] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2320 folded precursor RNA into VGAM2320 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2320 RNA is designated SEQ ID:5031, and is provided hereinbelow with reference to the sequence listing part.

[78838] VGAM2320 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2320 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2320 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78839] VGAM2320 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2320 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2320 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2320 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2320 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78840] The complementary binding of VGAM2320 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2320 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2320 host target RNA into VGAM2320 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78841] It is appreciated that VGAM2320 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2320 host target genes. The mRNA of each one of this plurality of VGAM2320 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2320 RNA, herein designated VGAM RNA, and which when bound by VGAM2320 RNA causes inhibition of translation of respective one or more VGAM2320 host target proteins.

[78842] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2320 gene, herein designated VGAM GENE, on one or more VGAM2320 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78843] It is yet further appreciated that a function of VGAM2320 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2320

correlate with, and may be deduced from, the identity of the host target genes which VGAM2320 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78844] Nucleotide sequences of the VGAM2320 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2320 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2320 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2320 are further described hereinbelow with reference to Table 1.

[78845] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2320 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2320 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78846] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2320 gene, herein designated VGAM is inhibition of expression of VGAM2320 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2320 correlate with, and may be deduced

from, the identity of the target genes which VGAM2320 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78847] DEK Oncogene (DNA binding) (DEK, Accession NM_003472) is a VGAM2320 host target gene. DEK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DEK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DEK BINDING SITE, designated SEQ ID:9537, to the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, also designated SEQ ID:5031.

[78848] A function of VGAM2320 is therefore inhibition of DEK Oncogene (DNA binding) (DEK, Accession NM_003472), a gene which interacts in transcriptional regulation and signal transduction. Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DEK. The function of DEK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM795.Hemochromatosis (HFE, Accession NM_139004)

is another VGAM2320 host target gene. HFE BINDING SITE1 through HFE BINDING SITE6 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HFE, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HFE BINDING SITE1 through HFE BINDING SITE6, designated SEQ ID:29098, SEQ ID:29100, SEQ ID:29101, SEQ ID:29102, SEQ ID:29103 and SEQ ID:5984 respectively, to the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, also designated SEQ ID:5031.

[78849] Another function of VGAM2320 is therefore inhibition of Hemochromatosis (HFE, Accession NM_139004). Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HFE. Presenilin 1 (Alzheimer disease 3) (PSEN1, Accession NM_000021) is another VGAM2320 host target gene. PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PSEN1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementar-

ity of the nucleotide sequences of PSEN1 BINDING SITE1 and PSEN1 BINDING SITE2, designated SEQ ID:5456 and SEQ ID:25335 respectively, to the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, also designated SEQ ID:5031.

[78850] Another function of VGAM2320 is therefore inhibition of Presenilin 1 (Alzheimer disease 3) (PSEN1, Accession NM_000021). Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSEN1. FLJ14640 (Accession NM_032816) is another VGAM2320 host target gene. FLJ14640 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ14640, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14640 BINDING SITE, designated SEQ ID:26585, to the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, also designated SEQ ID:5031.

[78851] Another function of VGAM2320 is therefore inhibition of FLJ14640 (Accession NM_032816). Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ14640. FLJ22635 (Accession NM_025092) is another VGAM2320 host target gene. FLJ22635 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22635, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22635 BINDING SITE, designated SEQ ID:24715, to the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, also designated SEQ ID:5031.

[78852] Another function of VGAM2320 is therefore inhibition of FLJ22635 (Accession NM_025092). Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22635. GABA(A) Receptor-associated Protein Like 1 (GABARAPL1, Accession NM_031412) is another VGAM2320 host target gene. GABARAPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

GABARAPL1 BINDING SITE, designated SEQ ID:25389, to the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, also designated SEQ ID:5031.

[78853] Another function of VGAM2320 is therefore inhibition of GABA(A) Receptor-associated Protein Like 1 (GABARAPL1, Accession NM_031412). Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL1. KIAA0441 (Accession NM_014797) is another VGAM2320 host target gene. KIAA0441 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0441, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0441 BINDING SITE, designated SEQ ID:16708, to the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, also designated SEQ ID:5031.

[78854] Another function of VGAM2320 is therefore inhibition of KIAA0441 (Accession NM_014797). Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0441. KIAA0494 (Accession NM_014774) is another

VGAM2320 host target gene. KIAA0494 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0494, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0494 BINDING SITE, designated SEQ ID:16587, to the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, also designated SEQ ID:5031.

[78855] Another function of VGAM2320 is therefore inhibition of KIAA0494 (Accession NM_014774). Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0494. MGC27277 (Accession NM_144989) is another VGAM2320 host target gene. MGC27277 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC27277, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC27277 BINDING SITE, designated SEQ ID:29592, to the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, also designated SEQ ID:5031.

[78856] Another function of VGAM2320 is therefore inhibition of MGC27277 (Accession NM_144989). Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC27277. LOC129530 (Accession XM_059362) is another VGAM2320 host target gene. LOC129530 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC129530, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC129530 BINDING SITE, designated SEQ ID:36971, to the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, also designated SEQ ID:5031.

[78857] Another function of VGAM2320 is therefore inhibition of LOC129530 (Accession XM_059362). Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129530. LOC145678 (Accession XM_096832) is another VGAM2320 host target gene. LOC145678 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145678, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145678 BINDING SITE, designated SEQ ID:40555, to the nucleotide sequence of VGAM2320 RNA, herein designated VGAM RNA, also designated SEQ ID:5031.

[78858] Another function of VGAM2320 is therefore inhibition of LOC145678 (Accession XM_096832). Accordingly, utilities of VGAM2320 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145678. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2321 (VGAM2321) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78859] VGAM2321 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2321 was detected is described hereinabove with reference to Figs. 1-8.

[78860] VGAM2321 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2321 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[78861] VGAM2321 gene encodes a VGAM2321 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2321 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2321 precursor RNA is designated SEQ ID:2307, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2307 is located at position 24842 relative to the genome of Rana Tigrina Ranavirus.

[78862] VGAM2321 precursor RNA folds onto itself, forming VGAM2321 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78863] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2321 folded precursor RNA into VGAM2321

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2321 RNA is designated SEQ ID:5032, and is provided hereinbelow with reference to the sequence listing part.

[78864] VGAM2321 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2321 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2321 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78865] VGAM2321 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2321 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2321 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2321 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2321 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78866] The complementary binding of VGAM2321 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2321 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2321 host target RNA into VGAM2321 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[78867] It is appreciated that VGAM2321 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2321 host target genes. The mRNA of each one of this plurality of VGAM2321 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2321 RNA, herein designated VGAM RNA, and which when bound by VGAM2321 RNA causes inhibition of translation of respective one or more VGAM2321 host target proteins.

[78868] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2321 gene, herein designated VGAM GENE, on one or more VGAM2321 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78869] It is yet further appreciated that a function of VGAM2321 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2321 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2321 correlate with, and may be deduced from, the identity of the host target genes which VGAM2321 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78870] Nucleotide sequences of the VGAM2321 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2321 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2321 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2321 are further described hereinbelow with reference to Table 1.

[78871] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2321 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2321 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78872] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2321 gene, herein designated VGAM is inhibition of expression of VGAM2321 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2321 correlate with, and may be deduced from, the identity of the target genes which VGAM2321 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78873] CD4 Antigen (p55) (CD4, Accession NM_000616) is a VGAM2321 host target gene. CD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD4 BINDING SITE, designated SEQ ID:6218, to the nucleotide sequence of VGAM2321 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5032.

[78874] A function of VGAM2321 is therefore inhibition of CD4 Antigen (p55) (CD4, Accession NM_000616), a gene which is T-cell surface glycoprotein and has role in cell-cell interactions and may act in signal transduction. Accordingly, utilities of VGAM2321 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD4. The function of CD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.V-maf Musculoaponeurotic Fibrosarcoma Oncogene Homolog K (avian) (MAFK, Accession NM_002360) is another VGAM2321 host target gene. MAFK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAFK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAFK BINDING SITE, designated SEQ ID:8172, to the nucleotide sequence of VGAM2321 RNA, herein designated VGAM RNA, also designated SEQ ID:5032.

[78875] Another function of VGAM2321 is therefore inhibition of V-maf Musculoaponeurotic Fibrosarcoma Oncogene Ho-

molog K (avian) (MAFK, Accession NM_002360), a gene which is involved in regulation of transcription at NEF2 sites. Accordingly, utilities of VGAM2321 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAFK. The function of MAFK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1505.Multiple Endocrine Neoplasia I (MEN1, Accession NM_130803) is another VGAM2321 host target gene. MEN1 BINDING SITE1 and MEN1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MEN1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEN1 BINDING SITE1 and MEN1 BINDING SITE2, designated SEQ ID:28298 and SEQ ID:28302 respectively, to the nucleotide sequence of VGAM2321 RNA, herein designated VGAM RNA, also designated SEQ ID:5032.

[78876] Another function of VGAM2321 is therefore inhibition of Multiple Endocrine Neoplasia I (MEN1, Accession NM_130803). Accordingly, utilities of VGAM2321 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with MEN1. Usher Syndrome 3A (USH3A, Accession NM_052995) is another VGAM2321 host target gene. USH3A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by USH3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USH3A BINDING SITE, designated SEQ ID:27562, to the nucleotide sequence of VGAM2321 RNA, herein designated VGAM RNA, also designated SEQ ID:5032.

[78877] Another function of VGAM2321 is therefore inhibition of Usher Syndrome 3A (USH3A, Accession NM_052995). Accordingly, utilities of VGAM2321 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USH3A. Glucocorticoid Modulatory Element Binding Protein 2 (GMEB2, Accession NM_012384) is another VGAM2321 host target gene. GMEB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GMEB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of GMEB2 BINDING SITE, designated SEQ ID:14738, to the nucleotide sequence of VGAM2321 RNA, herein designated VGAM RNA, also designated SEQ ID:5032.

[78878] Another function of VGAM2321 is therefore inhibition of Glucocorticoid Modulatory Element Binding Protein 2 (GMEB2, Accession NM_012384). Accordingly, utilities of VGAM2321 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GMEB2. R3H Domain (binds single-stranded nucleic acids) Containing (R3HDM, Accession NM_015361) is another VGAM2321 host target gene. R3HDM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by R3HDM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of R3HDM BINDING SITE, designated SEQ ID:17662, to the nucleotide sequence of VGAM2321 RNA, herein designated VGAM RNA, also designated SEQ ID:5032.

[78879] Another function of VGAM2321 is therefore inhibition of R3H Domain (binds single-stranded nucleic acids) Containing (R3HDM, Accession NM_015361). Accordingly,

utilities of VGAM2321 include diagnosis, prevention and treatment of diseases and clinical conditions associated with R3HDM. LOC145216 (Accession XM_096730) is another VGAM2321 host target gene. LOC145216 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145216, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145216 BINDING SITE, designated SEQ ID:40509, to the nucleotide sequence of VGAM2321 RNA, herein designated VGAM RNA, also designated SEQ ID:5032.

[78880] Another function of VGAM2321 is therefore inhibition of LOC145216 (Accession XM_096730). Accordingly, utilities of VGAM2321 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145216. LOC148697 (Accession XM_086276) is another VGAM2321 host target gene. LOC148697 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148697, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC148697 BINDING SITE, designated SEQ ID:38572, to the nucleotide sequence of VGAM2321 RNA, herein designated VGAM RNA, also designated SEQ ID:5032.

[78881] Another function of VGAM2321 is therefore inhibition of LOC148697 (Accession XM_086276). Accordingly, utilities of VGAM2321 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148697. LOC152580 (Accession XM_098240) is another VGAM2321 host target gene. LOC152580 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152580, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152580 BINDING SITE, designated SEQ ID:41523, to the nucleotide sequence of VGAM2321 RNA, herein designated VGAM RNA, also designated SEQ ID:5032.

[78882] Another function of VGAM2321 is therefore inhibition of LOC152580 (Accession XM_098240). Accordingly, utilities of VGAM2321 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152580. LOC254431 (Accession XM_173024) is another VGAM2321 host target gene. LOC254431 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254431, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254431 BINDING SITE, designated SEQ ID:46292, to the nucleotide sequence of VGAM2321 RNA, herein designated VGAM RNA, also designated SEQ ID:5032.

[78883] Another function of VGAM2321 is therefore inhibition of LOC254431 (Accession XM_173024). Accordingly, utilities of VGAM2321 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254431. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2322 (VGAM2322) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78884] VGAM2322 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2322 was detected is described hereinabove with reference to Figs. 1-8.

[78885] VGAM2322 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2322 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78886] VGAM2322 gene encodes a VGAM2322 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2322 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2322 precursor RNA is designated SEQ ID:2308, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2308 is located at position 49980 relative to the genome of Rana Tigrina Ranavirus.

[78887] VGAM2322 precursor RNA folds onto itself, forming VGAM2322 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[78888] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2322 folded precursor RNA into VGAM2322 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2322 RNA is designated SEQ ID:5033, and is provided hereinbelow with reference to the sequence listing part.

[78889] VGAM2322 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2322 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2322 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78890] VGAM2322 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2322 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2322 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2322 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2322 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78891] The complementary binding of VGAM2322 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2322 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2322 host target RNA into VGAM2322 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78892] It is appreciated that VGAM2322 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2322 host target genes. The mRNA of each one of this plurality of VGAM2322 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2322 RNA, herein designated VGAM RNA, and which when bound by VGAM2322 RNA causes inhibition of translation of respective one or more VGAM2322 host target proteins.

[78893] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2322 gene, herein designated VGAM GENE, on one or more VGAM2322 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78894] It is yet further appreciated that a function of VGAM2322 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2322 correlate with, and may be deduced from, the identity of the host target genes which VGAM2322 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78895] Nucleotide sequences of the VGAM2322 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2322 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2322 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2322 are further described hereinbelow with reference to Table 1.

[78896] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2322 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2322 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78897] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2322 gene, herein designated VGAM is inhibition of expression of VGAM2322 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2322 correlate with, and may be deduced from, the identity of the target genes which VGAM2322 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78898] APG5 Autophagy 5-like (S. cerevisiae) (APG5L, Accession NM_004849) is a VGAM2322 host target gene. APG5L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APG5L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of APG5L BINDING SITE, designated SEQ ID:11261, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78899] A function of VGAM2322 is therefore inhibition of APG5 Autophagy 5-like (S. cerevisiae) (APG5L, Accession NM_004849), a gene which conjugates to apg12 and associates with isolation membrane to form cup-shaped isolation membrane and autophagosome. Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APG5L. The function of APG5L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM492.UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 5 (B4GALT5, Accession NM_004776) is another VGAM2322 host target gene. B4GALT5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by B4GALT5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B4GALT5 BINDING SITE, designated SEQ

ID:11171, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78900] Another function of VGAM2322 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 5 (B4GALT5, Accession NM_004776). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT5. Early Growth Response 2 (Krox-20 homolog, Drosophila) (EGR2, Accession NM_000399) is another VGAM2322 host target gene. EGR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EGR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGR2 BINDING SITE, designated SEQ ID:5970, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78901] Another function of VGAM2322 is therefore inhibition of Early Growth Response 2 (Krox-20 homolog, Drosophila) (EGR2, Accession NM_000399), a gene which binds to two specific dna sites located in the promoter region of hox-

1.4. Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGR2. The function of EGR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM234.FUS1 (Accession NM_007275) is another VGAM2322 host target gene. FUS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FUS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FUS1 BINDING SITE, designated SEQ ID:14136, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78902] Another function of VGAM2322 is therefore inhibition of FUS1 (Accession NM_007275), a gene which may function as a tumor suppressor. Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUS1. The function of FUS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM1246.Potassium Channel, Subfamily K, Member 4 (KCNK4, Accession NM_033310) is another VGAM2322 host target gene. KCNK4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCNK4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNK4 BINDING SITE, designated SEQ ID:27150, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78903] Another function of VGAM2322 is therefore inhibition of Potassium Channel, Subfamily K, Member 4 (KCNK4, Accession NM_033310). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK4. MUS81 (Accession NM_025128) is another VGAM2322 host target gene. MUS81 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MUS81, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MUS81 BINDING SITE, designated SEQ

ID:24771, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78904] Another function of VGAM2322 is therefore inhibition of MUS81 (Accession NM_025128). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MUS81. Nijmegen Breakage Syndrome 1 (nibrin) (NBS1, Accession XM_045343) is another VGAM2322 host target gene. NBS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NBS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NBS1 BINDING SITE, designated SEQ ID:34437, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78905] Another function of VGAM2322 is therefore inhibition of Nijmegen Breakage Syndrome 1 (nibrin) (NBS1, Accession XM_045343), a gene which may be involved in repair of DNA double-strand breaks. Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NBS1.

The function of NBS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM450.Numb Homolog (Drosophila) (NUMB, Accession NM_003744) is another VGAM2322 host target gene. NUMB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUMB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUMB BINDING SITE, designated SEQ ID:9832, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78906] Another function of VGAM2322 is therefore inhibition of Numb Homolog (Drosophila) (NUMB, Accession NM_003744), a gene which may act in generating asymmetric cell division during neurogenesisand is strongly similar to murine Numb. Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUMB. The function of NUMB has been established by previous studies. During Drosophila neurogenesis, differential partitioning of the 'Numb' (dNumb) gene product is necessary

for daughter cells to adopt distinct fates. Numb is thought to act by causing a bias in the cell-cell interaction mediated by Notch (see OMIM Ref. No. JAG2; 602570). Zhong et al. (1996) isolated cDNAs encoding mouse Numb (mNumb). The N-terminal region of the deduced 593-amino acid mouse protein contains a predicted phosphotyrosine-binding domain and shares 63% identity with dNumb. The C-terminal half shows little similarity with dNumb and includes a proline-rich segment with potential SH3-binding sites. Immunofluorescence experiments revealed that mNumb is asymmetrically localized to the apical membrane of dividing ventricular neural progenitors during mouse cortical neurogenesis. However, unlike dNumb, there was no correlation between cleavage planes and mNumb localization at the apical cell membrane in anaphase ventricular cells. Zhong et al. (1996) expressed mNumb in Drosophila embryos and found that it localized asymmetrically in dividing neural precursors and rescued the Numb mutant phenotype. Yeast 2-hybrid assays and in vitro binding experiments demonstrated that mNumb can physically interact with the intracellular domain of mouse Notch1 (OMIM Ref. No. 190198). The authors concluded that shared molecular mechanisms

generate asymmetric cell divisions during neurogenesis of vertebrates and invertebrates. Salcini et al. (1997) reported that both the NUMB and NUMB-like (NUMBL; 604018) proteins bind to the EH protein-protein interaction domain found in EPS15 (OMIM Ref. No. 600051) and other proteins. Coimmunoprecipitation studies demonstrated that NUMB and EPS15 are associated in vivo. This association appears to be mediated by an interaction between the EH domain of EPS15 and an asn-pro-phe (NPF) motif located near the C terminus of NUMB.

[78907] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[78908] Salcini, A. E.; Confalonieri, S.; Doria, M.; Santolini, E.; Tassi, E.; Minenkova, O.; Cesareni, G.; Pelicci, P. G.; Di Fiore, P. P. : Binding specificity and in vivo targets of the EH domain, a novel protein-protein interaction module. Genes Dev. 11: 2239-2249, 1997. ; and

[78909] Zhong, W.; Feder, J. N.; Jiang, M.-M.; Jan, L. Y.; Jan, Y. N. : Asymmetric localization of a mammalian Numb homolog during mouse cortical neurogenesis. Neuron 17: 43-53, 1996.

[78910] Further studies establishing the function and utilities of

NUMB are found in John Hopkins OMIM database record ID 603728, and in sited publications numbered 7012-5839 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Oligophrenin 1 (OPHN1, Accession NM_002547) is another VGAM2322 host target gene. OPHN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OPHN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OPHN1 BINDING SITE, designated SEQ ID:8398, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78911] Another function of VGAM2322 is therefore inhibition of Oligophrenin 1 (OPHN1, Accession NM_002547). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OPHN1. Protein Kinase C, Mu (PRKCM, Accession NM_002742) is another VGAM2322 host target gene. PRKCM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKCM, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKCM BINDING SITE, designated SEQ ID:8613, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78912] Another function of VGAM2322 is therefore inhibition of Protein Kinase C, Mu (PRKCM, Accession NM_002742). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKCM. Retinoid X Receptor, Alpha (RXRA, Accession NM_002957) is another VGAM2322 host target gene. RXRA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RXRA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RXRA BINDING SITE, designated SEQ ID:8868, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78913] Another function of VGAM2322 is therefore inhibition of Retinoid X Receptor, Alpha (RXRA, Accession NM_002957), a gene which activates genes required for vitamin A

metabolism, binds 9-cis retinoic acid. Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RXRA. The function of RXRA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM349.SIP (Accession NM_014412) is another VGAM2322 host target gene. SIP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIP BINDING SITE, designated SEQ ID:15756, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78914] Another function of VGAM2322 is therefore inhibition of SIP (Accession NM_014412). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIP. Zinc-fingers and Homeoboxes 1 (ZHX1, Accession NM_007222) is another VGAM2322 host target gene. ZHX1 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by ZHX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZHX1 BINDING SITE, designated SEQ ID:14090, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78915] Another function of VGAM2322 is therefore inhibition of Zinc-fingers and Homeoboxes 1 (ZHX1, Accession NM_007222). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZHX1. FLJ20257 (Accession NM_019606) is another VGAM2322 host target gene. FLJ20257 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20257, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20257 BINDING SITE, designated SEQ ID:21219, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78916] Another function of VGAM2322 is therefore inhibition of

FLJ20257 (Accession NM_019606). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20257. FLJ21865 (Accession NM_022759) is another VGAM2322 host target gene. FLJ21865 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21865, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21865 BINDING SITE, designated SEQ ID:22999, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78917] Another function of VGAM2322 is therefore inhibition of FLJ21865 (Accession NM_022759). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21865. FLJ22160 (Accession NM_024585) is another VGAM2322 host target gene. FLJ22160 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ22160 BINDING SITE, designated SEQ ID:23821, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78918] Another function of VGAM2322 is therefore inhibition of FLJ22160 (Accession NM_024585). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22160. KIAA1328 (Accession XM_029429) is another VGAM2322 host target gene. KIAA1328 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1328, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1328 BINDING SITE, designated SEQ ID:30887, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78919] Another function of VGAM2322 is therefore inhibition of KIAA1328 (Accession XM_029429). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1328. KIAA1354 (Accession XM_027604) is another

VGAM2322 host target gene. KIAA1354 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1354, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1354 BINDING SITE, designated SEQ ID:30539, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78920] Another function of VGAM2322 is therefore inhibition of KIAA1354 (Accession XM_027604). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1354. KIAA1554 (Accession XM_170834) is another VGAM2322 host target gene. KIAA1554 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1554, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1554 BINDING SITE, designated SEQ ID:45611, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78921] Another function of VGAM2322 is therefore inhibition of KIAA1554 (Accession XM_170834). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1554. OS4 (Accession NM_005730) is another VGAM2322 host target gene. OS4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OS4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OS4 BINDING SITE, designated SEQ ID:12288, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78922] Another function of VGAM2322 is therefore inhibition of OS4 (Accession NM_005730). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OS4. Oxysterol Binding Protein-like 3 (OSBPL3, Accession NM_015550) is another VGAM2322 host target gene. OSBPL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL3, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL3 BINDING SITE, designated SEQ ID:17812, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78923] Another function of VGAM2322 is therefore inhibition of Oxysterol Binding Protein-like 3 (OSBPL3, Accession NM_015550). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL3. PRO0365 (Accession NM_014126) is another VGAM2322 host target gene. PRO0365 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0365, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0365 BINDING SITE, designated SEQ ID:15384, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78924] Another function of VGAM2322 is therefore inhibition of PRO0365 (Accession NM_014126). Accordingly, utilities of

VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0365. RAB20, Member RAS Oncogene Family (RAB20, Accession NM_017817) is another VGAM2322 host target gene. RAB20 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB20, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB20 BINDING SITE, designated SEQ ID:19465, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78925] Another function of VGAM2322 is therefore inhibition of RAB20, Member RAS Oncogene Family (RAB20, Accession NM_017817). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB20. TRIP-Br2 (Accession NM_014755) is another VGAM2322 host target gene. TRIP-Br2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIP-Br2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of TRIP-Br2 BINDING SITE, designated SEQ ID:16480, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78926] Another function of VGAM2322 is therefore inhibition of TRIP-Br2 (Accession NM_014755). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIP-Br2. LOC118978 (Accession XM_071677) is another VGAM2322 host target gene. LOC118978 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC118978, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC118978 BINDING SITE, designated SEQ ID:37412, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78927] Another function of VGAM2322 is therefore inhibition of LOC118978 (Accession XM_071677). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC118978. LOC159110 (Accession XM_088753) is another VGAM2322 host target gene. LOC159110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC159110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159110 BINDING SITE, designated SEQ ID:39943, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78928] Another function of VGAM2322 is therefore inhibition of LOC159110 (Accession XM_088753). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159110. LOC159116 (Accession XM_088752) is another VGAM2322 host target gene. LOC159116 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC159116, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159116 BINDING SITE, designated SEQ ID:39941, to the nucleotide sequence of VGAM2322 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5033.

[78929] Another function of VGAM2322 is therefore inhibition of LOC159116 (Accession XM_088752). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159116. LOC203221 (Accession XM_116795) is another VGAM2322 host target gene. LOC203221 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203221, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203221 BINDING SITE, designated SEQ ID:43126, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78930] Another function of VGAM2322 is therefore inhibition of LOC203221 (Accession XM_116795). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203221. LOC90844 (Accession XM_034434) is another VGAM2322 host target gene. LOC90844 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90844, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90844 BINDING SITE, designated SEQ ID:32118, to the nucleotide sequence of VGAM2322 RNA, herein designated VGAM RNA, also designated SEQ ID:5033.

[78931] Another function of VGAM2322 is therefore inhibition of LOC90844 (Accession XM_034434). Accordingly, utilities of VGAM2322 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90844. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2323 (VGAM2323) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78932] VGAM2323 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2323 was detected is described hereinabove with reference to Figs. 1-8.

[78933] VGAM2323 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus.

VGAM2323 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78934] VGAM2323 gene encodes a VGAM2323 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2323 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2323 precursor RNA is designated SEQ ID:2309, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2309 is located at position 27691 relative to the genome of Rana Tigrina Ranavirus.

[78935] VGAM2323 precursor RNA folds onto itself, forming VGAM2323 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78936] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2323 folded precursor RNA into VGAM2323 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2323 RNA is designated SEQ ID:5034, and is provided hereinbelow with reference to the sequence listing part.

[78937] VGAM2323 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2323 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2323 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78938] VGAM2323 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2323 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2323 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2323 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2323 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78939] The complementary binding of VGAM2323 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2323 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2323 host target RNA into VGAM2323 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78940] It is appreciated that VGAM2323 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2323 host target genes. The mRNA of each one of this plurality of VGAM2323 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2323 RNA, herein designated VGAM RNA, and which when bound by VGAM2323 RNA causes inhibition of translation of respective one or more VGAM2323 host target proteins.

[78941] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2323 gene, herein designated VGAM GENE, on one or more VGAM2323 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78942] It is yet further appreciated that a function of VGAM2323 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2323 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2323 correlate with, and may be deduced from, the identity of the host target genes which VGAM2323 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78943] Nucleotide sequences of the VGAM2323 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2323 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2323 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2323 are further described hereinbelow with reference to Table 1.

[78944] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2323 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2323 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78945] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2323 gene, herein designated VGAM is inhibition of expression of VGAM2323 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2323 correlate with, and may be deduced from, the identity of the target genes which VGAM2323 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78946] KIAA0620 (Accession XM_030707) is a VGAM2323 host target gene. KIAA0620 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0620, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0620 BINDING SITE, designated SEQ ID:31120, to the nucleotide sequence of

VGAM2323 RNA, herein designated VGAM RNA, also designated SEQ ID:5034.

[78947] A function of VGAM2323 is therefore inhibition of KIAA0620 (Accession XM_030707). Accordingly, utilities of VGAM2323 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0620. KIAA1023 (Accession NM_017604) is another VGAM2323 host target gene. KIAA1023 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1023, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1023 BINDING SITE, designated SEQ ID:19087, to the nucleotide sequence of VGAM2323 RNA, herein designated VGAM RNA, also designated SEQ ID:5034.

[78948] Another function of VGAM2323 is therefore inhibition of KIAA1023 (Accession NM_017604). Accordingly, utilities of VGAM2323 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1023. LOC127534 (Accession XM_060532) is another VGAM2323 host target gene. LOC127534 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC127534, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127534 BINDING SITE, designated SEQ ID:37164, to the nucleotide sequence of VGAM2323 RNA, herein designated VGAM RNA, also designated SEQ ID:5034.

[78949] Another function of VGAM2323 is therefore inhibition of LOC127534 (Accession XM_060532). Accordingly, utilities of VGAM2323 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127534. LOC155179 (Accession XM_088169) is another VGAM2323 host target gene. LOC155179 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155179, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155179 BINDING SITE, designated SEQ ID:39554, to the nucleotide sequence of VGAM2323 RNA, herein designated VGAM RNA, also designated SEQ ID:5034.

[78950] Another function of VGAM2323 is therefore inhibition of LOC155179 (Accession XM_088169). Accordingly, utilities

of VGAM2323 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155179. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2324 (VGAM2324) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78951] VGAM2324 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2324 was detected is described hereinabove with reference to Figs. 1-8.

[78952] VGAM2324 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2324 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78953] VGAM2324 gene encodes a VGAM2324 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2324 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2324 precursor RNA is designated SEQ ID:2310, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2310 is located at position 26882 relative to the genome of Rana Tigrina Ranavirus.

[78954] VGAM2324 precursor RNA folds onto itself, forming VGAM2324 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[78955] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2324 folded precursor RNA into VGAM2324 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2324 RNA is designated SEQ ID:5035, and

is provided hereinbelow with reference to the sequence listing part.

[78956] VGAM2324 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2324 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2324 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78957] VGAM2324 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2324 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2324 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2324 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2324 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78958] The complementary binding of VGAM2324 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2324 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2324 host target RNA into VGAM2324 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78959] It is appreciated that VGAM2324 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2324 host target genes. The mRNA of each one of this plurality of VGAM2324 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2324 RNA, herein designated VGAM RNA, and which when bound by VGAM2324 RNA causes inhibition of translation of respective one or more VGAM2324 host target proteins.

[78960] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2324 gene, herein designated VGAM GENE, on one or more VGAM2324 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78961] It is yet further appreciated that a function of VGAM2324 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2324 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2324 correlate with, and may be deduced from, the identity of the host target genes which VGAM2324 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78962] Nucleotide sequences of the VGAM2324 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2324 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2324 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2324 are further described hereinbelow with reference to Table 1.

[78963] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2324 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2324 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78964] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2324 gene, herein designated VGAM is inhibition of expression of VGAM2324 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2324 correlate with, and may be deduced from, the identity of the target genes which VGAM2324 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78965] FLJ20298 (Accession NM_017752) is a VGAM2324 host target gene. FLJ20298 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20298, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20298 BINDING SITE, designated SEQ ID:19363, to the nucleotide sequence of VGAM2324 RNA, herein designated VGAM RNA, also designated SEQ ID:5035.

[78966] A function of VGAM2324 is therefore inhibition of FLJ20298 (Accession NM_017752). Accordingly, utilities of VGAM2324 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20298. LOC152445 (Accession XM_098231) is another VGAM2324 host target gene. LOC152445 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152445 BINDING SITE, designated SEQ ID:41508, to the nucleotide sequence of VGAM2324 RNA, herein designated VGAM RNA, also designated SEQ ID:5035.

[78967] Another function of VGAM2324 is therefore inhibition of LOC152445 (Accession XM_098231). Accordingly, utilities of VGAM2324 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152445. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2325 (VGAM2325) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78968] VGAM2325 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2325 was detected is described hereinabove with reference to Figs. 1-8.

[78969] VGAM2325 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2325 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78970] VGAM2325 gene encodes a VGAM2325 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2325 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2325 precursor RNA is designated SEQ ID:2311, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2311 is located at position 28131 relative to the genome of Rana Tigrina Ranavirus.

[78971] VGAM2325 precursor RNA folds onto itself, forming VGAM2325 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[78972] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2325 folded precursor RNA into VGAM2325 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2325 RNA is designated SEQ ID:5036, and is provided hereinbelow with reference to the sequence listing part.

[78973] VGAM2325 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2325 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2325 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[78974] VGAM2325 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2325 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2325 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2325 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2325 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[78975] The complementary binding of VGAM2325 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2325 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2325 host target RNA into VGAM2325 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[78976] It is appreciated that VGAM2325 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2325 host target genes. The mRNA of each one of this plurality of VGAM2325 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2325 RNA, herein designated VGAM RNA, and which when bound by VGAM2325 RNA causes inhibition of translation of respective one or more VGAM2325 host target proteins.

[78977] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2325 gene, herein designated VGAM GENE, on one or more VGAM2325 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[78978] It is yet further appreciated that a function of VGAM2325 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2325 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2325 correlate with, and may be deduced from, the identity of the host target genes which VGAM2325 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[78979] Nucleotide sequences of the VGAM2325 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2325 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2325 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2325 are further described hereinbelow with reference to Table 1.

[78980] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2325 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2325 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[78981] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2325 gene, herein designated VGAM is inhibition of expression of VGAM2325 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2325 correlate with, and may be deduced from, the identity of the target genes which VGAM2325 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[78982] BCLG (Accession NM_030766) is a VGAM2325 host target gene. BCLG BINDING SITE1 through BCLG BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by BCLG, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the comple-

mentarity of the nucleotide sequences of BCLG BINDING SITE1 through BCLG BINDING SITE3, designated SEQ ID:25050, SEQ ID:28966 and SEQ ID:28968 respectively, to the nucleotide sequence of VGAM2325 RNA, herein designated VGAM RNA, also designated SEQ ID:5036.

[78983] A function of VGAM2325 is therefore inhibition of BCLG (Accession NM_030766). Accordingly, utilities of VGAM2325 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCLG. LIM Domain Binding 2 (LDB2, Accession NM_001290) is another VGAM2325 host target gene. LDB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LDB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LDB2 BINDING SITE, designated SEQ ID:6969, to the nucleotide sequence of VGAM2325 RNA, herein designated VGAM RNA, also designated SEQ ID:5036.

[78984] Another function of VGAM2325 is therefore inhibition of LIM Domain Binding 2 (LDB2, Accession NM_001290), a gene which physically interacts with the LIM domains of nuclear proteins. Accordingly, utilities of VGAM2325 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with LDB2. The function of LDB2 has been established by previous studies. Genes encoding LIM domain-binding factors were initially isolated in a screen for proteins that physically interact with the LIM domains of nuclear proteins. These proteins are capable of binding to a variety of transcription factors and are likely to function at enhancers to bring together diverse transcription factors and form higher order activation complexes or to block formation of such complexes (Jurata and Gill, 1997). The family of genes encoding LIM domain-binding factors includes 2 members isolated from the mouse, Clim1 (Bach et al., 1997) and Clim2/Lbd1/Nli (Agulnick et al., 1996; Jurata et al., 1996; Bach et al., 1997) and their homologs cloned from the frog, chicken, and fly. The fact that LIM domain-binding factors are likely to be involved in the coordination of the transcriptional activity of many diverse factors might implicate them in human phenotypes characterized by multiple affected sites. Semina et al. (1998) cloned the human genes CLIM1 and CLIM2 (OMIM Ref. No. 603451). They identified human sequences homologous to the mouse gene encoding Nli/Lbd1 in the EST database. Human sequences ho-

mologous to both Clim1 and Clim2 proteins were found. To obtain full-length cDNA clones for both genes, they screened a human craniofacial cDNA library with the corresponding human clones. The CLIM1 composite cDNA was found to be 2,351 bp long; the CLIM2 composite cDNA was found to be 1,953 bp long. The genes encode proteins of similar size, 373 and 375 amino acids, respectively. The proteins show a very high degree of identity with their homologs from other species as well as with each other. Using the Genebridge 4 radiation hybrid panel, Semina et al. (1998) mapped the CLIM1 and CLIM2 genes. CLIM1 was localized to 4p16-p15 and the map position was refined to 4p15 with a regional mapping panel for human chromosome 4. CLIM2 was localized to 10q24-q25; this region shares homology with the distal region of mouse chromosome 19, where the mouse gene Lbd1 was mapped by Yamashita et al. (1998).

[78985] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[78986] Semina, E. V.; Altherr, M. R.; Murray, J. C. : Cloning and chromosomal localization of two novel human genes encoding LIM-domain binding factors CLIM1 and

CLIM2/LDB1/NL1. Mammalian Genome 9: 921-924, 1998. ; and

[78987] Yamashita, T.; Agulnick, A. D.; Copeland, N. G.; Gilbert, D. J.; Jenkins, N. A.; Westphal, H. : Genomic structure and chromosomal localization of the mouse LIM domain-binding protein 1 g.

[78988] Further studies establishing the function and utilities of LDB2 are found in John Hopkins OMIM database record ID 603450, and in sited publications numbered 5977-5982 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Podocalyxin-like (PODXL, Accession NM_005397) is another VGAM2325 host target gene. PODXL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PODXL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PODXL BINDING SITE, designated SEQ ID:11872, to the nucleotide sequence of VGAM2325 RNA, herein designated VGAM RNA, also designated SEQ ID:5036.

[78989] Another function of VGAM2325 is therefore inhibition of Podocalyxin-like (PODXL, Accession NM_005397), a gene

which is an antiadhesin. Accordingly, utilities of VGAM2325 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PODXL. The function of PODXL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM247.TR2 (Accession XM_051264) is another VGAM2325 host target gene. TR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TR2 BINDING SITE, designated SEQ ID:35793, to the nucleotide sequence of VGAM2325 RNA, herein designated VGAM RNA, also designated SEQ ID:5036.

[78990] Another function of VGAM2325 is therefore inhibition of TR2 (Accession XM_051264), a gene which maintains high levels of reduced glutathione in the cytosol (by similarity). Accordingly, utilities of VGAM2325 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TR2. The function of TR2 and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to VGAM125.Chromosome 20 Open Reading Frame 18 (C20orf18, Accession NM_031228) is another VGAM2325 host target gene. C20orf18 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf18, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf18 BINDING SITE, designated SEQ ID:25275, to the nucleotide sequence of VGAM2325 RNA, herein designated VGAM RNA, also designated SEQ ID:5036.

[78991] Another function of VGAM2325 is therefore inhibition of Chromosome 20 Open Reading Frame 18 (C20orf18, Accession NM_031228). Accordingly, utilities of VGAM2325 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf18. Dynactin 4 (p62) (DCTN4, Accession XM_041993) is another VGAM2325 host target gene. DCTN4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCTN4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCTN4 BINDING SITE, designated SEQ ID:33666, to the nucleotide sequence of VGAM2325 RNA, herein designated VGAM RNA, also designated SEQ ID:5036.

[78992] Another function of VGAM2325 is therefore inhibition of Dynactin 4 (p62) (DCTN4, Accession XM_041993). Accordingly, utilities of VGAM2325 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCTN4. KIAA1855 (Accession XM_166453) is another VGAM2325 host target gene. KIAA1855 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1855, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1855 BINDING SITE, designated SEQ ID:44353, to the nucleotide sequence of VGAM2325 RNA, herein designated VGAM RNA, also designated SEQ ID:5036.

[78993] Another function of VGAM2325 is therefore inhibition of KIAA1855 (Accession XM_166453). Accordingly, utilities of VGAM2325 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1855. LOC158402 (Accession XM_098936) is another VGAM2325 host target gene. LOC158402 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158402, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158402 BINDING SITE, designated SEQ ID:41977, to the nucleotide sequence of VGAM2325 RNA, herein designated VGAM RNA, also designated SEQ ID:5036.

[78994] Another function of VGAM2325 is therefore inhibition of LOC158402 (Accession XM_098936). Accordingly, utilities of VGAM2325 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158402. LOC56963 (Accession XM_049372) is another VGAM2325 host target gene. LOC56963 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC56963, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56963 BINDING SITE, designated SEQ ID:35400, to the

nucleotide sequence of VGAM2325 RNA, herein designated VGAM RNA, also designated SEQ ID:5036.

[78995] Another function of VGAM2325 is therefore inhibition of LOC56963 (Accession XM_049372). Accordingly, utilities of VGAM2325 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56963. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2326 (VGAM2326) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[78996] VGAM2326 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2326 was detected is described hereinabove with reference to Figs. 1-8.

[78997] VGAM2326 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2326 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[78998] VGAM2326 gene encodes a VGAM2326 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2326 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2326 precursor RNA is designated SEQ ID:2312, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2312 is located at position 37660 relative to the genome of Rana Tigrina Ranavirus.

[78999] VGAM2326 precursor RNA folds onto itself, forming VGAM2326 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79000] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2326 folded precursor RNA into VGAM2326 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2326 RNA is designated SEQ ID:5037, and is provided hereinbelow with reference to the sequence listing part.

[79001] VGAM2326 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2326 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2326 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79002] VGAM2326 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2326 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2326 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2326 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2326 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79003] The complementary binding of VGAM2326 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2326 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2326 host target RNA into VGAM2326 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79004] It is appreciated that VGAM2326 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2326 host target genes. The mRNA of each one of this plurality of VGAM2326 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2326 RNA, herein designated VGAM RNA, and which when bound by VGAM2326 RNA causes inhibition of translation of respective one or more VGAM2326 host target proteins.

[79005] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2326 gene, herein designated VGAM GENE, on one or more VGAM2326 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79006] It is yet further appreciated that a function of VGAM2326 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2326 correlate with, and may be deduced from, the identity of the host target genes which VGAM2326 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79007] Nucleotide sequences of the VGAM2326 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2326 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2326 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2326 are further described hereinbelow with reference to Table 1.

[79008] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2326 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2326 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79009] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2326 gene, herein designated VGAM is inhibition of expression of VGAM2326 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2326 correlate with, and may be deduced from, the identity of the target genes which VGAM2326 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79010] B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6, Accession NM_138931) is a VGAM2326 host target gene. BCL6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BCL6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL6 BINDING SITE, designated SEQ ID:29057, to the nucleotide sequence of VGAM2326 RNA, herein designated VGAM RNA, also designated SEQ ID:5037.

[79011] A function of VGAM2326 is therefore inhibition of B-cell CLL/lymphoma 6 (zinc finger protein 51) (BCL6, Accession

NM_138931), a gene which is involved in the generation and maintenance of both T and B cells during immune responses. Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL6. The function of BCL6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM481.Staufen, RNA Binding Protein (Drosophila) (STAU, Accession NM_017454) is another VGAM2326 host target gene. STAU BINDING SITE1 through STAU BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by STAU, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAU BINDING SITE1 through STAU BINDING SITE4, designated SEQ ID:18925, SEQ ID:10941, SEQ ID:18913 and SEQ ID:18919 respectively, to the nucleotide sequence of VGAM2326 RNA, herein designated VGAM RNA, also designated SEQ ID:5037.

[79012] Another function of VGAM2326 is therefore inhibition of Staufen, RNA Binding Protein (Drosophila) (STAU, Acces-

sion NM_017454), a gene which may play a role in specific positioning of mrnas at given sites in the cell and in stimulating their translation at the site. Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAU. The function of STAU and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM916.Huntingtin-associated Protein Interacting Protein (duo) (HAPIP, Accession NM_003947) is another VGAM2326 host target gene. HAPIP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HAPIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HAPIP BINDING SITE, designated SEQ ID:10065, to the nucleotide sequence of VGAM2326 RNA, herein designated VGAM RNA, also designated SEQ ID:5037.

[79013] Another function of VGAM2326 is therefore inhibition of Huntingtin-associated Protein Interacting Protein (duo) (HAPIP, Accession NM_003947). Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with HAPIP. KIAA0092 (Accession NM_014679) is another VGAM2326 host target gene. KIAA0092 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0092 BINDING SITE, designated SEQ ID:16151, to the nucleotide sequence of VGAM2326 RNA, herein designated VGAM RNA, also designated SEQ ID:5037.

[79014] Another function of VGAM2326 is therefore inhibition of KIAA0092 (Accession NM_014679). Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0092. KIAA0217 (Accession XM_040265) is another VGAM2326 host target gene. KIAA0217 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0217, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0217 BINDING SITE, designated SEQ ID:33282, to the

nucleotide sequence of VGAM2326 RNA, herein designated VGAM RNA, also designated SEQ ID:5037.

[79015] Another function of VGAM2326 is therefore inhibition of KIAA0217 (Accession XM_040265). Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0217. LIM Domain Kinase 2 (LIMK2, Accession NM_016733) is another VGAM2326 host target gene. LIMK2 BINDING SITE1 and LIMK2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LIMK2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIMK2 BINDING SITE1 and LIMK2 BINDING SITE2, designated SEQ ID:18785 and SEQ ID:12095 respectively, to the nucleotide sequence of VGAM2326 RNA, herein designated VGAM RNA, also designated SEQ ID:5037.

[79016] Another function of VGAM2326 is therefore inhibition of LIM Domain Kinase 2 (LIMK2, Accession NM_016733). Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIMK2. LOC150225 (Accession

XM_097870) is another VGAM2326 host target gene. LOC150225 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150225, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150225 BINDING SITE, designated SEQ ID:41185, to the nucleotide sequence of VGAM2326 RNA, herein designated VGAM RNA, also designated SEQ ID:5037.

[79017] Another function of VGAM2326 is therefore inhibition of LOC150225 (Accession XM_097870). Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150225. LOC158191 (Accession XM_088505) is another VGAM2326 host target gene. LOC158191 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158191, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158191 BINDING SITE, designated SEQ ID:39757, to the nucleotide sequence of VGAM2326 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5037.

[79018] Another function of VGAM2326 is therefore inhibition of LOC158191 (Accession XM_088505). Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158191. LOC196446 (Accession XM_113722) is another VGAM2326 host target gene. LOC196446 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196446, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196446 BINDING SITE, designated SEQ ID:42372, to the nucleotide sequence of VGAM2326 RNA, herein designated VGAM RNA, also designated SEQ ID:5037.

[79019] Another function of VGAM2326 is therefore inhibition of LOC196446 (Accession XM_113722). Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196446. LOC222182 (Accession XM_168471) is another VGAM2326 host target gene. LOC222182 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222182, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222182 BINDING SITE, designated SEQ ID:45195, to the nucleotide sequence of VGAM2326 RNA, herein designated VGAM RNA, also designated SEQ ID:5037.

[79020] Another function of VGAM2326 is therefore inhibition of LOC222182 (Accession XM_168471). Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222182. LOC90841 (Accession XM_034427) is another VGAM2326 host target gene. LOC90841 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90841 BINDING SITE, designated SEQ ID:32111, to the nucleotide sequence of VGAM2326 RNA, herein designated VGAM RNA, also designated SEQ ID:5037.

[79021] Another function of VGAM2326 is therefore inhibition of LOC90841 (Accession XM_034427). Accordingly, utilities of VGAM2326 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC90841. LOC91056 (Accession XM_170662) is another VGAM2326 host target gene. LOC91056 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91056, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91056 BINDING SITE, designated SEQ ID:45438, to the nucleotide sequence of VGAM2326 RNA, herein designated VGAM RNA, also designated SEQ ID:5037.

[79022] Another function of VGAM2326 is therefore inhibition of LOC91056 (Accession XM_170662). Accordingly, utilities of VGAM2326 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91056. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2327 (VGAM2327) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79023] VGAM2327 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2327 was detected is described hereinabove with reference to Figs. 1-8.

[79024] VGAM2327 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2327 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79025] VGAM2327 gene encodes a VGAM2327 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2327 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2327 precursor RNA is designated SEQ ID:2313, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2313 is located at position 30986 relative to the genome of Rana Tigrina Ranavirus.

[79026] VGAM2327 precursor RNA folds onto itself, forming VGAM2327 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79027] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2327 folded precursor RNA into VGAM2327 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 90%) nucleotide sequence of VGAM2327 RNA is designated SEQ ID:5038, and is provided hereinbelow with reference to the sequence listing part.

[79028] VGAM2327 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2327 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2327 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79029] VGAM2327 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2327 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2327 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2327 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2327 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79030] The complementary binding of VGAM2327 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2327 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2327 host target RNA into VGAM2327 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79031] It is appreciated that VGAM2327 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2327 host target genes. The mRNA of each one of this plurality of VGAM2327 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2327 RNA, herein designated VGAM RNA, and which when bound by VGAM2327 RNA causes inhibition of translation of respective one or more VGAM2327 host target proteins.

[79032] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2327 gene, herein designated VGAM GENE, on one or more VGAM2327 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79033] It is yet further appreciated that a function of VGAM2327 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2327 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2327 correlate with, and may be deduced from, the identity of the host target genes which VGAM2327 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79034] Nucleotide sequences of the VGAM2327 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2327 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2327 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2327 are further described hereinbelow with reference to Table 1.

[79035] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2327 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2327 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79036] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2327 gene, herein designated VGAM is inhibition of expression of VGAM2327 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2327 correlate with, and may be deduced from, the identity of the target genes which VGAM2327 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79037] G Protein-coupled Receptor 61 (GPR61, Accession XM_086232) is a VGAM2327 host target gene. GPR61 BINDING SITE is HOST TARGET binding site found in the

5` untranslated region of mRNA encoded by GPR61, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR61 BINDING SITE, designated SEQ ID:38562, to the nucleotide sequence of VGAM2327 RNA, herein designated VGAM RNA, also designated SEQ ID:5038.

[79038] A function of VGAM2327 is therefore inhibition of G Protein-coupled Receptor 61 (GPR61, Accession XM_086232), a gene which transduces extracellular signals through heterotrimeric G proteins. Accordingly, utilities of VGAM2327 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR61. The function of GPR61 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Phospholipid Scramblase 1 (PLSCR1, Accession NM_021105) is another VGAM2327 host target gene. PLSCR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLSCR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of PLSCR1 BINDING SITE, designated SEQ ID:22085, to the nucleotide sequence of VGAM2327 RNA, herein designated VGAM RNA, also designated SEQ ID:5038.

[79039] Another function of VGAM2327 is therefore inhibition of Phospholipid Scramblase 1 (PLSCR1, Accession NM_021105), a gene which involves in the initiation of fibrin clot formation and in the recognition of apoptotic and injured cells by the reticuloendothelial system. Accordingly, utilities of VGAM2327 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLSCR1. The function of PLSCR1 has been established by previous studies. Quantitative immunoblotting revealed that PL scramblase levels are approximately 10-fold higher in platelets than in erythrocytes, which Zhou et al. (1997) stated was consistent with the apparent increased enzyme activity of the platelet plasma membrane. Using Northern blot analysis, the authors demonstrated that PL scramblase was expressed as 1.6- and 2.6-kb mRNAs in all tissues and cell lines tested. Independently, Kasukabe et al. (1998) identified PL scramblase as the human homolog of mouse MmTRA1b (Mm1 cell-derived transplantability-associated gene 1b), the

gene encoding a truncated leukemogenesis-associated cDNA, MmTRA1a. Human and mouse MmTRA1b are 78% identical. Sequence analysis revealed that the predicted human protein contains 3 leucine repeats and a proline-rich N-terminal domain with 3 motifs which may act as docking sites for SH3 motifs. Kasukabe et al. (1998) noted that mouse MmTRA1b was distinct from a putative mouse PL scramblase homolog identified by Zhou et al. (1998). The mouse protein described by Zhou et al. (1998) shares 75% and 71% identity with mouse MmTRA1b and human PL scramblase, respectively

[79040] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[79041] Kasukabe, T.; Kobayashi, H.; Kaneko, Y.; Okabe-Kado, J.; Honma, Y. : Identity of human normal counterpart (MmTRA1b) of mouse leukemogenesis-associated gene (MmTRA1a) product as a plasma membrane phospholipid scramblase and chromosome mapping of the human Mm-TRA1b/phospholipid scramblase gene. Biochem. Biophys. Res. Commun. 249: 449-455, 1998. ; and

[79042] Zhou, Q.; Zhao, J.; Stout, J. G.; Luhm, R. A.; Wiedmer, T.; Sims, P. J. : Molecular cloning of human plasma membrane

phospholipid scramblase: a protein mediating transbilayer movement of pl.

[79043] Further studies establishing the function and utilities of PLSCR1 are found in John Hopkins OMIM database record ID 604170, and in sited publications numbered 8704-5061 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Solute Carrier Family 21 (prostaglandin transporter), Member 2 (SLC21A2, Accession NM_005630) is another VGAM2327 host target gene. SLC21A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC21A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC21A2 BINDING SITE, designated SEQ ID:12154, to the nucleotide sequence of VGAM2327 RNA, herein designated VGAM RNA, also designated SEQ ID:5038.

[79044] Another function of VGAM2327 is therefore inhibition of Solute Carrier Family 21 (prostaglandin transporter), Member 2 (SLC21A2, Accession NM_005630), a gene which is a Prostaglandin transporter. Accordingly, utilities of VGAM2327 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with SLC21A2. The function of SLC21A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM83.FLJ10702 (Accession NM_018184) is another VGAM2327 host target gene. FLJ10702 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10702, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10702 BINDING SITE, designated SEQ ID:20024, to the nucleotide sequence of VGAM2327 RNA, herein designated VGAM RNA, also designated SEQ ID:5038.

[79045] Another function of VGAM2327 is therefore inhibition of FLJ10702 (Accession NM_018184). Accordingly, utilities of VGAM2327 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10702. FLJ12287 (Accession NM_022367) is another VGAM2327 host target gene. FLJ12287 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12287, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12287 BINDING SITE, designated SEQ ID:22753, to the nucleotide sequence of VGAM2327 RNA, herein designated VGAM RNA, also designated SEQ ID:5038.

[79046] Another function of VGAM2327 is therefore inhibition of FLJ12287 (Accession NM_022367). Accordingly, utilities of VGAM2327 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12287. MGC20253 (Accession NM_144583) is another VGAM2327 host target gene. MGC20253 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC20253, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC20253 BINDING SITE, designated SEQ ID:29396, to the nucleotide sequence of VGAM2327 RNA, herein designated VGAM RNA, also designated SEQ ID:5038.

[79047] Another function of VGAM2327 is therefore inhibition of MGC20253 (Accession NM_144583). Accordingly, utilities of VGAM2327 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC20253. PR Domain Containing 10 (PRDM10, Accession NM_020228) is another VGAM2327 host target gene. PRDM10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRDM10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRDM10 BINDING SITE, designated SEQ ID:21495, to the nucleotide sequence of VGAM2327 RNA, herein designated VGAM RNA, also designated SEQ ID:5038.

[79048] Another function of VGAM2327 is therefore inhibition of PR Domain Containing 10 (PRDM10, Accession NM_020228). Accordingly, utilities of VGAM2327 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDM10. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2328 (VGAM2328) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79049] VGAM2328 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2328 was detected is described hereinabove with reference to Figs. 1-8.

[79050] VGAM2328 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rana Tigrina Ranavirus. VGAM2328 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79051] VGAM2328 gene encodes a VGAM2328 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2328 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2328 precursor RNA is designated SEQ ID:2314, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2314 is located at position 16752 relative to the genome of Rana Tigrina Ranavirus.

[79052] VGAM2328 precursor RNA folds onto itself, forming VGAM2328 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79053] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2328 folded precursor RNA into VGAM2328 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2328 RNA is designated SEQ ID:5039, and is provided hereinbelow with reference to the sequence listing part.

[79054] VGAM2328 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2328 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2328 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[79055] VGAM2328 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2328 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2328 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2328 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2328 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79056] The complementary binding of VGAM2328 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2328 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2328 host target RNA into VGAM2328 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79057] It is appreciated that VGAM2328 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2328 host target genes. The mRNA of each one of this plurality of VGAM2328 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2328 RNA, herein designated VGAM RNA, and which when bound by VGAM2328 RNA causes inhibition of translation of respective one or more VGAM2328 host target proteins.

[79058] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2328 gene, herein designated VGAM GENE, on one or more VGAM2328 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79059] It is yet further appreciated that a function of VGAM2328 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of viral infection by Rana Tigrina Ranavirus. Specific functions, and accordingly utilities, of VGAM2328 correlate with, and may be deduced from, the identity of the host target genes which VGAM2328 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79060] Nucleotide sequences of the VGAM2328 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2328 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2328 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2328 are further described hereinbelow with reference to Table 1.

[79061] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2328 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2328 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79062] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2328 gene, herein designated VGAM is inhibition of expression of VGAM2328 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2328 correlate with, and may be deduced from, the identity of the target genes which VGAM2328 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79063] A Kinase (PRKA) Anchor Protein 13 (AKAP13, Accession NM_144767) is a VGAM2328 host target gene. AKAP13

BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AKAP13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP13 BINDING SITE, designated SEQ ID:29559, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79064] A function of VGAM2328 is therefore inhibition of A Kinase (PRKA) Anchor Protein 13 (AKAP13, Accession NM_144767), a gene which regulates subcellular localization of type II cAMP-dependent PKA. Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP13. The function of AKAP13 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM17.Distal-less Homeobox 4 (DLX4, Accession NM_138281) is another VGAM2328 host target gene. DLX4 BINDING SITE1 and DLX4 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DLX4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II

or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLX4 BINDING SITE1 and DLX4 BINDING SITE2, designated SEQ ID:28694 and SEQ ID:7646 respectively, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79065] Another function of VGAM2328 is therefore inhibition of Distal-less Homeobox 4 (DLX4, Accession NM_138281), a gene which may regulate gene expression, morphogenesis, and differentiation. Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLX4. The function of DLX4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1929.Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog 2 (mouse) (MEIS2, Accession NM_020149) is another VGAM2328 host target gene. MEIS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MEIS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

MEIS2 BINDING SITE, designated SEQ ID:21349, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79066] Another function of VGAM2328 is therefore inhibition of Meis1, Myeloid Ecotropic Viral Integration Site 1 Homolog 2 (mouse) (MEIS2, Accession NM_020149), a gene which may regulate gene expression and control cell differentiation. Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEIS2. The function of MEIS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1244.Norrie Disease (pseudoglioma) (NDP, Accession NM_000266) is another VGAM2328 host target gene. NDP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NDP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDP BINDING SITE, designated SEQ ID:5810, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79067] Another function of VGAM2328 is therefore inhibition of Norrie Disease (pseudoglioma) (NDP, Accession NM_000266), a gene which may be involved in a pathway that regulates neural cell differentiation and proliferation. Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDP. The function of NDP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM113.Nuclear Factor Related to Kappa B Binding Protein (NFRKB, Accession NM_006165) is another VGAM2328 host target gene. NFRKB BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NFRKB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFRKB BINDING SITE, designated SEQ ID:12824, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79068] Another function of VGAM2328 is therefore inhibition of Nuclear Factor Related to Kappa B Binding Protein (NFRKB,

Accession NM_006165). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFRKB. UC28 (Accession NM_021635) is another VGAM2328 host target gene. UC28 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UC28, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UC28 BINDING SITE, designated SEQ ID:22282, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79069] Another function of VGAM2328 is therefore inhibition of UC28 (Accession NM_021635). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UC28. C1q and Tumor Necrosis Factor Related Protein 7 (C1QTNF7, Accession NM_031911) is another VGAM2328 host target gene. C1QTNF7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1QTNF7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1QTNF7 BINDING SITE, designated SEQ ID:25668, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79070] Another function of VGAM2328 is therefore inhibition of C1q and Tumor Necrosis Factor Related Protein 7 (C1QTNF7, Accession NM_031911). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QTNF7. KIAA1416 (Accession XM_098762) is another VGAM2328 host target gene. KIAA1416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1416 BINDING SITE, designated SEQ ID:41805, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79071] Another function of VGAM2328 is therefore inhibition of KIAA1416 (Accession XM_098762). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1416. KIAA1493 (Accession XM_034415) is another VGAM2328 host target gene. KIAA1493 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1493, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1493 BINDING SITE, designated SEQ ID:32096, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79072] Another function of VGAM2328 is therefore inhibition of KIAA1493 (Accession XM_034415). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1493. KIAA1524 (Accession XM_056015) is another VGAM2328 host target gene. KIAA1524 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1524, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1524 BINDING SITE, designated SEQ ID:36361, to the

nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79073] Another function of VGAM2328 is therefore inhibition of KIAA1524 (Accession XM_056015). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1524. KIAA1904 (Accession XM_056282) is another VGAM2328 host target gene. KIAA1904 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1904, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1904 BINDING SITE, designated SEQ ID:36384, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79074] Another function of VGAM2328 is therefore inhibition of KIAA1904 (Accession XM_056282). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1904. TUSP (Accession NM_020245) is another VGAM2328 host target gene. TUSP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by TUSP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUSP BINDING SITE, designated SEQ ID:21538, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79075] Another function of VGAM2328 is therefore inhibition of TUSP (Accession NM_020245). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUSP. LOC128989 (Accession XM_059310) is another VGAM2328 host target gene. LOC128989 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC128989, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC128989 BINDING SITE, designated SEQ ID:36942, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79076] Another function of VGAM2328 is therefore inhibition of LOC128989 (Accession XM_059310). Accordingly, utilities

of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128989. LOC146455 (Accession XM_085471) is another VGAM2328 host target gene. LOC146455 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146455, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146455 BINDING SITE, designated SEQ ID:38157, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79077] Another function of VGAM2328 is therefore inhibition of LOC146455 (Accession XM_085471). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146455. LOC150282 (Accession XM_086852) is another VGAM2328 host target gene. LOC150282 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150282, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC150282 BINDING SITE, designated SEQ ID:38919, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79078] Another function of VGAM2328 is therefore inhibition of LOC150282 (Accession XM_086852). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150282. LOC219731 (Accession XM_167596) is another VGAM2328 host target gene. LOC219731 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219731, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219731 BINDING SITE, designated SEQ ID:44719, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79079] Another function of VGAM2328 is therefore inhibition of LOC219731 (Accession XM_167596). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219731. LOC254024 (Accession XM_171285) is another VGAM2328 host target gene. LOC254024 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254024, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254024 BINDING SITE, designated SEQ ID:46040, to the nucleotide sequence of VGAM2328 RNA, herein designated VGAM RNA, also designated SEQ ID:5039.

[79080] Another function of VGAM2328 is therefore inhibition of LOC254024 (Accession XM_171285). Accordingly, utilities of VGAM2328 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254024. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2329 (VGAM2329) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79081] VGAM2329 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2329 was detected is described hereinabove with reference to Figs. 1-8.

[79082] VGAM2329 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2329 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79083] VGAM2329 gene encodes a VGAM2329 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2329 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2329 precursor RNA is designated SEQ ID:2315, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2315 is located at position 39739 relative to the genome of Equine Herpesvirus 2.

[79084] VGAM2329 precursor RNA folds onto itself, forming VGAM2329 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[79085] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2329 folded precursor RNA into VGAM2329 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2329 RNA is designated SEQ ID:5040, and is provided hereinbelow with reference to the sequence listing part.

[79086] VGAM2329 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2329 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2329 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79087] VGAM2329 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2329 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2329 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2329 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2329 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79088] The complementary binding of VGAM2329 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2329 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2329 host target RNA into VGAM2329 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79089] It is appreciated that VGAM2329 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2329 host target genes. The mRNA of each one of this plurality of VGAM2329 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2329 RNA, herein designated VGAM RNA, and which when bound by VGAM2329 RNA causes inhibition of translation of respective one or more VGAM2329 host target proteins.

[79090] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2329 gene, herein designated VGAM GENE, on one or more VGAM2329 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79091] It is yet further appreciated that a function of VGAM2329 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2329 correlate with, and may be deduced from, the identity of the host target genes which VGAM2329 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79092] Nucleotide sequences of the VGAM2329 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2329 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2329 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2329 are further described hereinbelow with reference to Table 1.

[79093] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2329 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2329 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79094] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2329 gene, herein designated VGAM is inhibition of expression of VGAM2329 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2329 correlate with, and may be deduced from, the identity of the target genes which VGAM2329 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79095] APM1 (Accession NM_004797) is a VGAM2329 host target gene. APM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of APM1 BINDING SITE, designated SEQ ID:11205, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79096] A function of VGAM2329 is therefore inhibition of APM1 (Accession NM_004797). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APM1. UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 3 (B4GALT3, Accession NM_003779) is another VGAM2329 host target gene. B4GALT3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by B4GALT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B4GALT3 BINDING SITE, designated SEQ ID:9863, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79097] Another function of VGAM2329 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 3 (B4GALT3, Accession NM_003779). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with B4GALT3. Cysteine Knot Superfamily 1, BMP Antagonist 1 (CKTSF1B1, Accession NM_013372) is another VGAM2329 host target gene. CKTSF1B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CKTSF1B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CKTSF1B1 BINDING SITE, designated SEQ ID:15020, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79098] Another function of VGAM2329 is therefore inhibition of Cysteine Knot Superfamily 1, BMP Antagonist 1 (CKTSF1B1, Accession NM_013372), a gene which blocks signaling of bone morphogenetic protein (BMP) . Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CKTSF1B1. The function of CKTSF1B1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM28.Potassium Inwardly-rectifying Channel, Subfamily J, Member 3 (KCNJ3, Accession NM_002239) is another VGAM2329 host target gene.

KCNJ3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNJ3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNJ3 BINDING SITE, designated SEQ ID:8021, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79099] Another function of VGAM2329 is therefore inhibition of Potassium Inwardly-rectifying Channel, Subfamily J, Member 3 (KCNJ3, Accession NM_002239), a gene which is a potassium inwardly-rectifying channel. Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ3. The function of KCNJ3 has been established by previous studies. Inwardly rectifying potassium channels control the excitability of neuronal cells by allowing potassium ion influx through a nonvoltage-gated mechanism. See 602208. Stoffel et al. (1994) screened a rat insulinoma cell line cDNA library with a human IRK1 (OMIM Ref. No. 600681) probe. A cDNA, designated RINm5F by them, was shown to be highly expressed in atrial myocardium and brain. The same sequence was reported by

Kubo et al. (1993) and was designated GIRK1. It was shown to be a G protein-coupled muscarinic potassium channel related to ROMK1 (OMIM Ref. No. 600359) and IRK1. Stoffel et al. (1994) isolated and partially characterized the human GIRK1 gene which was assigned to chromosome 2 using a somatic cell hybrid DNA panel and localized it to 2q24.1 by fluorescence in situ hybridization. A polymorphic dinucleotide repeat sequence was found in the GIRK1 genomic clones and used to map the locus genetically. Schoots et al. (1996) cloned the complete human GIRK1 gene by probing a cerebellum cDNA library with the rat gene. The cDNA encodes a predicted 501-amino acid protein whose sequence is 99% identical to that of rat GIRK1. Northern blot analysis showed that human GIRK1 is expressed as 2 mRNAs (4.3 kb and 6.2 kb) that are most abundant in brain, but are also seen in kidney and heart. In Xenopus oocytes that coexpressed GIRK1 and the rat serotonin receptor 5-HT-1A (OMIM Ref. No. 109760), serotonin evoked inward potassium currents. Schoots et al. (1997) found that the KCNJ3 gene, which they referred to as Kir3.1, contains 3 exons and spans more than 45 kb

[79100] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[79101] Kubo, Y.; Reuveny, E.; Slesinger, P. A.; Jan, Y. N.; Jan, L. Y. : Primary structure and functional expression of a rat G-protein-coupled muscarinic potassium channel. Nature 364: 802-806, 1993. ; and

[79102] Schoots, O.; Voskoglou, T.; Van Tol, H. H. M. : Genomic organization and promoter analysis of the human G-protein-coupled K+ channel Kir3.1 (KCNJ3/HGIRK1). Genomics 39: 279-288, 1997.

[79103] Further studies establishing the function and utilities of KCNJ3 are found in John Hopkins OMIM database record ID 601534, and in sited publications numbered 7203-7206 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Membrane Metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME, Accession NM_007289) is another VGAM2329 host target gene. MME BINDING SITE1 through MME BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MME, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MME BINDING SITE1

through MME BINDING SITE4, designated SEQ ID:14157, SEQ ID:14153, SEQ ID:14149 and SEQ ID:6601 respectively, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79104] Another function of VGAM2329 is therefore inhibition of Membrane Metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10) (MME, Accession NM_007289), a gene which is thermolysin-like specificity. Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MME. The function of MME and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1332.RAN Binding Protein 2 (RANBP2, Accession NM_006267) is another VGAM2329 host target gene. RANBP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RANBP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RANBP2 BINDING SITE, designated SEQ ID:12947, to the nucleotide

sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79105] Another function of VGAM2329 is therefore inhibition of RAN Binding Protein 2 (RANBP2, Accession NM_006267), a gene which is thought to control a variety of cellular functions through its interactions with other proteins. Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RANBP2. The function of RANBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1337.Ribosomal Protein L10 (RPL10, Accession NM_006013) is another VGAM2329 host target gene. RPL10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPL10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPL10 BINDING SITE, designated SEQ ID:12621, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79106] Another function of VGAM2329 is therefore inhibition of

Ribosomal Protein L10 (RPL10, Accession NM_006013), a gene which may be a component of the 60S ribosomal subunit. Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPL10. The function of RPL10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM476.T-cell Acute Lymphocytic Leukemia 1 (TAL1, Accession NM_003189) is another VGAM2329 host target gene. TAL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TAL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAL1 BINDING SITE, designated SEQ ID:9167, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79107] Another function of VGAM2329 is therefore inhibition of T-cell Acute Lymphocytic Leukemia 1 (TAL1, Accession NM_003189), a gene which may help control cell growth and differentiation. Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with TAL1. The function of TAL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM172.Tumor Necrosis Factor Receptor Superfamily, Member 1B (TNFRSF1B, Accession NM_001066) is another VGAM2329 host target gene. TNFRSF1B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFRSF1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFRSF1B BINDING SITE, designated SEQ ID:6733, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79108] Another function of VGAM2329 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 1B (TNFRSF1B, Accession NM_001066), a gene which mediates proinflammatory cellular responses. Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF1B. The function of TNFRSF1B and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to VGAM939.Chromosome 1 Open Reading Frame 24 (C1orf24, Accession NM_052966) is another VGAM2329 host target gene. C1orf24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1orf24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf24 BINDING SITE, designated SEQ ID:27525, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79109] Another function of VGAM2329 is therefore inhibition of Chromosome 1 Open Reading Frame 24 (C1orf24, Accession NM_052966). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1orf24. DKFZP564O123 (Accession XM_002810) is another VGAM2329 host target gene. DKFZP564O123 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O123, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of DKFZP564O123 BINDING SITE, designated SEQ ID:29904, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79110] Another function of VGAM2329 is therefore inhibition of DKFZP564O123 (Accession XM_002810). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564O123. KIAA1560 (Accession XM_034422) is another VGAM2329 host target gene. KIAA1560 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1560, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1560 BINDING SITE, designated SEQ ID:32097, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79111] Another function of VGAM2329 is therefore inhibition of KIAA1560 (Accession XM_034422). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1560. MGC3222 (Accession NM_024334) is another VGAM2329 host target gene. MGC3222 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC3222, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC3222 BINDING SITE, designated SEQ ID:23640, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79112] Another function of VGAM2329 is therefore inhibition of MGC3222 (Accession NM_024334). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3222. Peroxisomal Membrane Protein 4, 24kDa (PXMP4, Accession NM_007238) is another VGAM2329 host target gene. PXMP4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PXMP4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PXMP4 BINDING SITE, designated SEQ ID:14110, to the nucleotide sequence of

VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79113] Another function of VGAM2329 is therefore inhibition of Peroxisomal Membrane Protein 4, 24kDa (PXMP4, Accession NM_007238). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PXMP4. Rab11-FIP2 (Accession NM_014904) is another VGAM2329 host target gene. Rab11-FIP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Rab11-FIP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rab11-FIP2 BINDING SITE, designated SEQ ID:17093, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79114] Another function of VGAM2329 is therefore inhibition of Rab11-FIP2 (Accession NM_014904). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Rab11-FIP2. Rabip4R (Accession NM_017987) is another VGAM2329 host target gene. Rabip4R BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Rabip4R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rabip4R BINDING SITE, designated SEQ ID:19714, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79115] Another function of VGAM2329 is therefore inhibition of Rabip4R (Accession NM_017987). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Rabip4R. Rho-related BTB Domain Containing 1 (RHOBTB1, Accession XM_166144) is another VGAM2329 host target gene. RHOBTB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RHOBTB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RHOBTB1 BINDING SITE, designated SEQ ID:43948, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79116] Another function of VGAM2329 is therefore inhibition of Rho-related BTB Domain Containing 1 (RHOBTB1, Accession XM_166144). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHOBTB1. Solute Carrier Family 1 (glutamate transporter), Member 7 (SLC1A7, Accession NM_006671) is another VGAM2329 host target gene. SLC1A7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC1A7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC1A7 BINDING SITE, designated SEQ ID:13487, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79117] Another function of VGAM2329 is therefore inhibition of Solute Carrier Family 1 (glutamate transporter), Member 7 (SLC1A7, Accession NM_006671). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC1A7. SMT3 Suppressor of Mif Two 3 Homolog 2 (yeast) (SMT3H2, Accession NM_006937) is another VGAM2329

host target gene. SMT3H2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMT3H2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMT3H2 BINDING SITE, designated SEQ ID:13818, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79118] Another function of VGAM2329 is therefore inhibition of SMT3 Suppressor of Mif Two 3 Homolog 2 (yeast) (SMT3H2, Accession NM_006937). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMT3H2. LOC112687 (Accession XM_053145) is another VGAM2329 host target gene. LOC112687 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC112687, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112687 BINDING SITE, designated SEQ ID:36063, to the nucleotide sequence of VGAM2329 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5040.

[79119] Another function of VGAM2329 is therefore inhibition of LOC112687 (Accession XM_053145). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112687. LOC143154 (Accession XM_084441) is another VGAM2329 host target gene. LOC143154 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143154, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143154 BINDING SITE, designated SEQ ID:37583, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79120] Another function of VGAM2329 is therefore inhibition of LOC143154 (Accession XM_084441). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143154. LOC144262 (Accession XM_084793) is another VGAM2329 host target gene. LOC144262 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144262, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144262 BINDING SITE, designated SEQ ID:37703, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79121] Another function of VGAM2329 is therefore inhibition of LOC144262 (Accession XM_084793). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144262. LOC151632 (Accession XM_098098) is another VGAM2329 host target gene. LOC151632 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151632, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151632 BINDING SITE, designated SEQ ID:41380, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79122] Another function of VGAM2329 is therefore inhibition of LOC151632 (Accession XM_098098). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC151632. LOC152271 (Accession XM_087419) is another VGAM2329 host target gene. LOC152271 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152271 BINDING SITE, designated SEQ ID:39237, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79123] Another function of VGAM2329 is therefore inhibition of LOC152271 (Accession XM_087419). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152271. LOC158434 (Accession XM_098939) is another VGAM2329 host target gene. LOC158434 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158434, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158434 BINDING SITE, designated SEQ ID:41980, to

the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79124] Another function of VGAM2329 is therefore inhibition of LOC158434 (Accession XM_098939). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158434. LOC158662 (Accession XM_088633) is another VGAM2329 host target gene. LOC158662 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158662, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158662 BINDING SITE, designated SEQ ID:39879, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79125] Another function of VGAM2329 is therefore inhibition of LOC158662 (Accession XM_088633). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158662. LOC200904 (Accession XM_117291) is another VGAM2329 host target gene. LOC200904 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC200904, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200904 BINDING SITE, designated SEQ ID:43359, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79126] Another function of VGAM2329 is therefore inhibition of LOC200904 (Accession XM_117291). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200904. LOC201824 (Accession XM_114384) is another VGAM2329 host target gene. LOC201824 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201824, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201824 BINDING SITE, designated SEQ ID:42919, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79127] Another function of VGAM2329 is therefore inhibition of LOC201824 (Accession XM_114384). Accordingly, utilities

of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201824. LOC203083 (Accession XM_117496) is another VGAM2329 host target gene. LOC203083 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203083, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203083 BINDING SITE, designated SEQ ID:43476, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79128] Another function of VGAM2329 is therefore inhibition of LOC203083 (Accession XM_117496). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203083. LOC219294 (Accession XM_167566) is another VGAM2329 host target gene. LOC219294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC219294 BINDING SITE, designated SEQ ID:44684, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79129] Another function of VGAM2329 is therefore inhibition of LOC219294 (Accession XM_167566). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219294. LOC219300 (Accession XM_168749) is another VGAM2329 host target gene. LOC219300 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219300, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219300 BINDING SITE, designated SEQ ID:45287, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79130] Another function of VGAM2329 is therefore inhibition of LOC219300 (Accession XM_168749). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219300. LOC219919 (Accession XM_167785) is another VGAM2329 host target gene. LOC219919 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219919, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219919 BINDING SITE, designated SEQ ID:44798, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79131] Another function of VGAM2329 is therefore inhibition of LOC219919 (Accession XM_167785). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219919. LOC254176 (Accession XM_173215) is another VGAM2329 host target gene. LOC254176 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254176, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254176 BINDING SITE, designated SEQ ID:46473, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79132] Another function of VGAM2329 is therefore inhibition of

LOC254176 (Accession XM_173215). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254176. LOC255327 (Accession XM_171236) is another VGAM2329 host target gene. LOC255327 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255327, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255327 BINDING SITE, designated SEQ ID:46021, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79133] Another function of VGAM2329 is therefore inhibition of LOC255327 (Accession XM_171236). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255327. LOC256594 (Accession XM_173127) is another VGAM2329 host target gene. LOC256594 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256594, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC256594 BINDING SITE, designated SEQ ID:46376, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79134] Another function of VGAM2329 is therefore inhibition of LOC256594 (Accession XM_173127). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256594. LOC51301 (Accession NM_016591) is another VGAM2329 host target gene. LOC51301 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51301 BINDING SITE, designated SEQ ID:18668, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79135] Another function of VGAM2329 is therefore inhibition of LOC51301 (Accession NM_016591). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51301. LOC90826 (Accession XM_034321) is another

VGAM2329 host target gene. LOC90826 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90826, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90826 BINDING SITE, designated SEQ ID:32047, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79136] Another function of VGAM2329 is therefore inhibition of LOC90826 (Accession XM_034321). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90826. LOC93206 (Accession XM_049838) is another VGAM2329 host target gene. LOC93206 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93206, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93206 BINDING SITE, designated SEQ ID:35514, to the nucleotide sequence of VGAM2329 RNA, herein designated VGAM RNA, also designated SEQ ID:5040.

[79137] Another function of VGAM2329 is therefore inhibition of LOC93206 (Accession XM_049838). Accordingly, utilities of VGAM2329 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93206. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2330 (VGAM2330) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79138] VGAM2330 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2330 was detected is described hereinabove with reference to Figs. 1-8.

[79139] VGAM2330 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2330 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79140] VGAM2330 gene encodes a VGAM2330 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2330 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2330 precursor RNA is designated SEQ ID:2316, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2316 is located at position 1147 relative to the genome of Equine Herpesvirus 2.

[79141] VGAM2330 precursor RNA folds onto itself, forming VGAM2330 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79142] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2330 folded precursor RNA into VGAM2330 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2330 RNA is designated SEQ ID:5041, and is provided hereinbelow with reference to the sequence listing part.

[79143] VGAM2330 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2330 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2330 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79144] VGAM2330 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2330 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2330 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2330 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2330 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79145] The complementary binding of VGAM2330 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2330 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2330 host target RNA into VGAM2330 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79146] It is appreciated that VGAM2330 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2330 host target genes. The mRNA of each one of this plurality of VGAM2330 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2330 RNA, herein designated VGAM RNA, and which when bound by VGAM2330 RNA causes inhibition of translation of respective one or more VGAM2330 host target proteins.

[79147] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2330 gene, herein designated VGAM GENE, on one or more VGAM2330 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79148] It is yet further appreciated that a function of VGAM2330 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2330 correlate with, and may be deduced from, the identity of the host target genes which VGAM2330 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79149] Nucleotide sequences of the VGAM2330 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2330 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2330 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2330 are further described hereinbelow with reference to Table 1.

[79150] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2330 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2330 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[79151] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2330 gene, herein designated VGAM is inhibition of expression of VGAM2330 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2330 correlate with, and may be deduced from, the identity of the target genes which VGAM2330 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79152] AF5Q31 (Accession NM_014423) is a VGAM2330 host target gene. AF5Q31 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AF5Q31, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AF5Q31 BINDING SITE, designated SEQ ID:15778, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79153] A function of VGAM2330 is therefore inhibition of AF5Q31 (Accession NM_014423). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

AF5Q31. Centromere Protein B, 80kDa (CENPB, Accession XM_045451) is another VGAM2330 host target gene. CENPB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CENPB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CENPB BINDING SITE, designated SEQ ID:34465, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79154] Another function of VGAM2330 is therefore inhibition of Centromere Protein B, 80kDa (CENPB, Accession XM_045451), a gene which is the major centromere antigen . Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENPB. The function of CENPB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Cysteine and Glycine-rich Protein 1 (CSRP1, Accession NM_004078) is another VGAM2330 host target gene. CSRP1 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by CSRP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSRP1 BINDING SITE, designated SEQ ID:10279, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79155] Another function of VGAM2330 is therefore inhibition of Cysteine and Glycine-rich Protein 1 (CSRP1, Accession NM_004078), a gene which could play a role in neuronal development. Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSRP1. The function of CSRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM743.EphA8 (EPHA8, Accession NM_020526) is another VGAM2330 host target gene. EPHA8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPHA8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPHA8 BIND-

ING SITE, designated SEQ ID:21750, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79156] Another function of VGAM2330 is therefore inhibition of EphA8 (EPHA8, Accession NM_020526), a gene which Eph-related receptor tyrosine kinase A8. Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPHA8. The function of EPHA8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM494.Glutamate Decarboxylase 1 (brain, 67kDa) (GAD1, Accession NM_000817) is another VGAM2330 host target gene. GAD1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GAD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAD1 BINDING SITE, designated SEQ ID:6480, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79157] Another function of VGAM2330 is therefore inhibition of

Glutamate Decarboxylase 1 (brain, 67kDa) (GAD1, Accession NM_000817), a gene which catalyzes the conversion of glutamic acid to gamma-aminobutyric acid. Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAD1. The function of GAD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM691.Homeo Box C9 (HOXC9, Accession XM_028620) is another VGAM2330 host target gene. HOXC9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HOXC9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOXC9 BINDING SITE, designated SEQ ID:30719, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79158] Another function of VGAM2330 is therefore inhibition of Homeo Box C9 (HOXC9, Accession XM_028620). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with HOXC9. Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)) (KAI1, Accession NM_002231) is another VGAM2330 host target gene. KAI1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KAI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KAI1 BINDING SITE, designated SEQ ID:8012, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79159] Another function of VGAM2330 is therefore inhibition of Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody IA4)) (KAI1, Accession NM_002231), a gene which associates with cd4 or cd8 and delivers costimulatory signals for the tcr/cd3 pathway. Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KAI1. The function of KAI1 has been established by previous studies. As noted, KAI1 is capable of inhibiting the metastatic process in experimental animals. The ex-

pression of the KAI1 gene is also downregulated during tumor progression of prostate, breast, lung, bladder, and pancreatic cancers in humans, and this downregulation appears to be at the level of transcription or posttranscription. Mashimo et al. (1998) found that the tumor suppressor gene p53 (TP53; 191170) can directly activate the KAI1 gene by interacting with the 5-prime upstream region. The p53 responding region is located approximately 860 bases upstream of the transcriptional initiation site, and contains a typical tandem repeat of the p53 consensus binding sequence. Mutations of this sequence abolish the responsiveness to p53 and also the ability to bind to p53 protein. Immunohistochemical analysis of 177 samples of human prostate tumors showed that the expression of the KAI1 gene correlated strongly with that of the p53 gene and that the loss of these 2 markers resulted in poor survival of patients. The data indicated a direct relationship between p53 and KAI1 genes and suggested that the loss of p53 function, which is commonly observed in many types of cancer, leads to downregulation of the KAI1 gene, which may result in progression of metastases Baek et al. (2002) demonstrated that interleukin-1-beta (IL1B; 147720) causes nuclear export of a

specific NCOR (OMIM Ref. No. 600849) corepressor complex, resulting in derepression of a specific subset of nuclear factor-kappa-B (NFKB; OMIM Ref. No. 164011)-regulated genes. These genes are exemplified by the tetraspanin KAI1, which regulates membrane receptor function. Nuclear export of the NCOR/TAB2 (OMIM Ref. No. 605101)/HDAC3 (OMIM Ref. No. 605166) complex by IL1B is temporally linked to selective recruitment of a TIP60 (OMIM Ref. No. 601409) coactivator complex. KAI1 is also directly activated by a ternary complex, dependent on the acetyltransferase activity of TIP60, that consists of the presenilin-dependent C-terminal cleavage product of the beta amyloid precursor protein (APP; 104760), FE65 (OMIM Ref. No. 602709), and TIP60, identifying a specific in vivo gene target of an APP-dependent transcription complex in the brain

[79160] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[79161] Mashimo, T.; Watabe, M.; Hirota, S.; Hosobe, S.; Miura, K.; Tegtmeyer, P. J.; Rinker-Shaeffer, C. W.; Watabe, K. : The expression of the KAI1 gene, a tumor metastasis suppressor, is directly activated by p53. Proc. Nat. Acad. Sci. 95:

11307-11311, 1998. ; and

[79162] Baek, S. H.; Ohgi, K. A.; Rose, D. W.; Koo, E. H.; Glass, C. K.; Rosenfeld, M. G. : Exchange of N-CoR corepressor and Tip60 coactivator complexes links gene expression by NF-kappa-B and.

[79163] Further studies establishing the function and utilities of KAI1 are found in John Hopkins OMIM database record ID 600623, and in sited publications numbered 481, 6562-6564, 1635-1636, 6565-656 and 5081 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Paired Box Gene 2 (PAX2, Accession NM_003987) is another VGAM2330 host target gene. PAX2 BINDING SITE1 and PAX2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PAX2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAX2 BINDING SITE1 and PAX2 BINDING SITE2, designated SEQ ID:10139 and SEQ ID:10145 respectively, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79164] Another function of VGAM2330 is therefore inhibition of

Paired Box Gene 2 (PAX2, Accession NM_003987), a gene which involves in kidney cell differentiation. Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAX2. The function of PAX2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM407.PCTAIRE Protein Kinase 1 (PCTK1, Accession NM_033019) is another VGAM2330 host target gene. PCTK1 BINDING SITE1 through PCTK1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCTK1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCTK1 BINDING SITE1 through PCTK1 BINDING SITE3, designated SEQ ID:26914, SEQ ID:12873 and SEQ ID:12875 respectively, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79165] Another function of VGAM2330 is therefore inhibition of PCTAIRE Protein Kinase 1 (PCTK1, Accession NM_033019), a gene which may play a role in signal transduction cas-

cades in terminally differentiated cells. Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCTK1. The function of PCTK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM75.Profilin 2 (PFN2, Accession NM_002628) is another VGAM2330 host target gene. PFN2 BINDING SITE1 and PFN2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PFN2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PFN2 BINDING SITE1 and PFN2 BINDING SITE2, designated SEQ ID:8489 and SEQ ID:12745 respectively, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79166] Another function of VGAM2330 is therefore inhibition of Profilin 2 (PFN2, Accession NM_002628). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PFN2. Serine (or cysteine) Proteinase Inhibitor, Clade

B (ovalbumin), Member 9 (SERPINB9, Accession NM_004155) is another VGAM2330 host target gene. SERPINB9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SERPINB9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERPINB9 BINDING SITE, designated SEQ ID:10363, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79167] Another function of VGAM2330 is therefore inhibition of Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 9 (SERPINB9, Accession NM_004155), a gene which may be a serpin serine protease inhibitor that interacts with granzyme B (GZMB). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINB9. The function of SERPINB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM60.V-ski Sarcoma Viral Oncogene Homolog (avian) (SKI, Accession

NM_003036) is another VGAM2330 host target gene. SKI BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SKI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SKI BINDING SITE, designated SEQ ID:8989, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79168] Another function of VGAM2330 is therefore inhibition of V-ski Sarcoma Viral Oncogene Homolog (avian) (SKI, Accession NM_003036). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SKI. Tafazzin (cardiomyopathy, dilated 3A (X-linked); Endocardial Fibroelastosis 2; Barth Syndrome) (TAZ, Accession NM_000116) is another VGAM2330 host target gene. TAZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAZ BINDING SITE, designated SEQ ID:5588, to the nu-

cleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79169] Another function of VGAM2330 is therefore inhibition of Tafazzin (cardiomyopathy, dilated 3A (X-linked); Endocardial Fibroelastosis 2; Barth Syndrome) (TAZ, Accession NM_000116). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAZ. Translocase of Inner Mitochondrial Membrane 23 Homolog (yeast) (TIMM23, Accession XM_011891) is another VGAM2330 host target gene. TIMM23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIMM23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIMM23 BINDING SITE, designated SEQ ID:30197, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79170] Another function of VGAM2330 is therefore inhibition of Translocase of Inner Mitochondrial Membrane 23 Homolog (yeast) (TIMM23, Accession XM_011891), a gene which translocates nuclear-encoded proteins into the mi-

tochondrion. Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIMM23. The function of TIMM23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Chromosome 4 Open Reading Frame 6 (C4orf6, Accession NM_005750) is another VGAM2330 host target gene. C4orf6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C4orf6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C4orf6 BINDING SITE, designated SEQ ID:12311, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79171] Another function of VGAM2330 is therefore inhibition of Chromosome 4 Open Reading Frame 6 (C4orf6, Accession NM_005750). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C4orf6. DKFZP434K1772 (Accession XM_041936) is another VGAM2330 host target

gene. DKFZP434K1772 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434K1772, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434K1772 BINDING SITE, designated SEQ ID:33633, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79172] Another function of VGAM2330 is therefore inhibition of DKFZP434K1772 (Accession XM_041936). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434K1772. DKFZP564D172 (Accession NM_032042) is another VGAM2330 host target gene. DKFZP564D172 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564D172, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564D172 BINDING SITE, designated SEQ ID:25750, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5041.

[79173] Another function of VGAM2330 is therefore inhibition of DKFZP564D172 (Accession NM_032042). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564D172. E74-like Factor 4 (ets domain transcription factor) (ELF4, Accession NM_001421) is another VGAM2330 host target gene. ELF4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELF4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELF4 BINDING SITE, designated SEQ ID:7122, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79174] Another function of VGAM2330 is therefore inhibition of E74-like Factor 4 (ets domain transcription factor) (ELF4, Accession NM_001421). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELF4. FLJ10206 (Accession NM_018025) is another VGAM2330 host target gene. FLJ10206 BINDING SITE is HOST TARGET

binding site found in the 5` untranslated region of mRNA encoded by FLJ10206, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10206 BINDING SITE, designated SEQ ID:19767, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79175] Another function of VGAM2330 is therefore inhibition of FLJ10206 (Accession NM_018025). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10206. FLJ13710 (Accession NM_024817) is another VGAM2330 host target gene. FLJ13710 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13710, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13710 BINDING SITE, designated SEQ ID:24205, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79176] Another function of VGAM2330 is therefore inhibition of

FLJ13710 (Accession NM_024817). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13710. KIAA0022 (Accession NM_014880) is another VGAM2330 host target gene. KIAA0022 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0022, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0022 BINDING SITE, designated SEQ ID:17027, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79177] Another function of VGAM2330 is therefore inhibition of KIAA0022 (Accession NM_014880). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0022. KIAA0173 (Accession NM_014640) is another VGAM2330 host target gene. KIAA0173 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0173, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0173 BINDING SITE, designated SEQ ID:16039, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79178] Another function of VGAM2330 is therefore inhibition of KIAA0173 (Accession NM_014640). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0173. KIAA0515 (Accession XM_033380) is another VGAM2330 host target gene. KIAA0515 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0515, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0515 BINDING SITE, designated SEQ ID:31922, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79179] Another function of VGAM2330 is therefore inhibition of KIAA0515 (Accession XM_033380). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0515. KIAA0774 (Accession XM_166270) is another

VGAM2330 host target gene. KIAA0774 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0774, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0774 BINDING SITE, designated SEQ ID:44090, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79180] Another function of VGAM2330 is therefore inhibition of KIAA0774 (Accession XM_166270). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0774. KIAA0819 (Accession XM_032996) is another VGAM2330 host target gene. KIAA0819 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0819, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0819 BINDING SITE, designated SEQ ID:31807, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79181] Another function of VGAM2330 is therefore inhibition of KIAA0819 (Accession XM_032996). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0819. KIAA1437 (Accession XM_026998) is another VGAM2330 host target gene. KIAA1437 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1437, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1437 BINDING SITE, designated SEQ ID:30387, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79182] Another function of VGAM2330 is therefore inhibition of KIAA1437 (Accession XM_026998). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1437. MGC20470 (Accession NM_145053) is another VGAM2330 host target gene. MGC20470 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC20470, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC20470 BINDING SITE, designated SEQ ID:29685, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79183] Another function of VGAM2330 is therefore inhibition of MGC20470 (Accession NM_145053). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC20470. MGC4796 (Accession XM_029031) is another VGAM2330 host target gene. MGC4796 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4796, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4796 BINDING SITE, designated SEQ ID:30831, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79184] Another function of VGAM2330 is therefore inhibition of MGC4796 (Accession XM_029031). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC4796. PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335) is another VGAM2330 host target gene. PRPF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRPF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRPF8 BINDING SITE, designated SEQ ID:30681, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79185] Another function of VGAM2330 is therefore inhibition of PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRPF8. RAB40C, Member RAS Oncogene Family (RAB40C, Accession NM_021168) is another VGAM2330 host target gene. RAB40C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB40C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of RAB40C BINDING SITE, designated SEQ ID:22146, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79186] Another function of VGAM2330 is therefore inhibition of RAB40C, Member RAS Oncogene Family (RAB40C, Accession NM_021168). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB40C. RER1 (Accession NM_007033) is another VGAM2330 host target gene. RER1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RER1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RER1 BINDING SITE, designated SEQ ID:13903, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79187] Another function of VGAM2330 is therefore inhibition of RER1 (Accession NM_007033). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RER1. Syndecan 3 (N-syndecan) (SDC3, Accession NM_014654)

is another VGAM2330 host target gene. SDC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SDC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDC3 BINDING SITE, designated SEQ ID:16090, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79188] Another function of VGAM2330 is therefore inhibition of Syndecan 3 (N-syndecan) (SDC3, Accession NM_014654). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDC3. LOC116411 (Accession XM_058095) is another VGAM2330 host target gene. LOC116411 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC116411, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC116411 BINDING SITE, designated SEQ ID:36569, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5041.

[79189] Another function of VGAM2330 is therefore inhibition of LOC116411 (Accession XM_058095). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116411. LOC129880 (Accession XM_059383) is another VGAM2330 host target gene. LOC129880 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC129880, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC129880 BINDING SITE, designated SEQ ID:36983, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79190] Another function of VGAM2330 is therefore inhibition of LOC129880 (Accession XM_059383). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC129880. LOC149422 (Accession XM_086527) is another VGAM2330 host target gene. LOC149422 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149422, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149422 BINDING SITE, designated SEQ ID:38744, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79191] Another function of VGAM2330 is therefore inhibition of LOC149422 (Accession XM_086527). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149422. LOC154043 (Accession XM_087831) is another VGAM2330 host target gene. LOC154043 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154043, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154043 BINDING SITE, designated SEQ ID:39459, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79192] Another function of VGAM2330 is therefore inhibition of LOC154043 (Accession XM_087831). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC154043. LOC155382 (Accession XM_098713) is another VGAM2330 host target gene. LOC155382 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155382, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155382 BINDING SITE, designated SEQ ID:41766, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79193] Another function of VGAM2330 is therefore inhibition of LOC155382 (Accession XM_098713). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155382. LOC158364 (Accession XM_088546) is another VGAM2330 host target gene. LOC158364 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158364, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158364 BINDING SITE, designated SEQ ID:39816, to

the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79194] Another function of VGAM2330 is therefore inhibition of LOC158364 (Accession XM_088546). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158364. LOC170393 (Accession XM_096327) is another VGAM2330 host target gene. LOC170393 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC170393, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC170393 BINDING SITE, designated SEQ ID:40312, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79195] Another function of VGAM2330 is therefore inhibition of LOC170393 (Accession XM_096327). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170393. LOC202868 (Accession XM_117477) is another VGAM2330 host target gene. LOC202868 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC202868, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202868 BINDING SITE, designated SEQ ID:43449, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79196] Another function of VGAM2330 is therefore inhibition of LOC202868 (Accession XM_117477). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202868. LOC219649 (Accession XM_167562) is another VGAM2330 host target gene. LOC219649 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219649, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219649 BINDING SITE, designated SEQ ID:44665, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79197] Another function of VGAM2330 is therefore inhibition of LOC219649 (Accession XM_167562). Accordingly, utilities

of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219649. LOC253664 (Accession XM_170673) is another VGAM2330 host target gene. LOC253664 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253664, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253664 BINDING SITE, designated SEQ ID:45451, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79198] Another function of VGAM2330 is therefore inhibition of LOC253664 (Accession XM_170673). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253664. LOC256306 (Accession XM_172976) is another VGAM2330 host target gene. LOC256306 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256306, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC256306 BINDING SITE, designated SEQ ID:46238, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79199] Another function of VGAM2330 is therefore inhibition of LOC256306 (Accession XM_172976). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256306. LOC90198 (Accession XM_029882) is another VGAM2330 host target gene. LOC90198 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90198, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90198 BINDING SITE, designated SEQ ID:30959, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79200] Another function of VGAM2330 is therefore inhibition of LOC90198 (Accession XM_029882). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90198. LOC90249 (Accession XM_030300) is another VGAM2330 host target gene. LOC90249 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90249, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90249 BINDING SITE, designated SEQ ID:31009, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79201] Another function of VGAM2330 is therefore inhibition of LOC90249 (Accession XM_030300). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90249. LOC91064 (Accession XM_035806) is another VGAM2330 host target gene. LOC91064 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91064, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91064 BINDING SITE, designated SEQ ID:32341, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79202] Another function of VGAM2330 is therefore inhibition of

LOC91064 (Accession XM_035806). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91064. LOC91355 (Accession XM_037825) is another VGAM2330 host target gene. LOC91355 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91355, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91355 BINDING SITE, designated SEQ ID:32703, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79203] Another function of VGAM2330 is therefore inhibition of LOC91355 (Accession XM_037825). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91355. LOC92697 (Accession XM_046715) is another VGAM2330 host target gene. LOC92697 BINDING SITE1 and LOC92697 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC92697, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of LOC92697 BINDING SITE1 and LOC92697 BINDING SITE2, designated SEQ ID:34802 and SEQ ID:34803 respectively, to the nucleotide sequence of VGAM2330 RNA, herein designated VGAM RNA, also designated SEQ ID:5041.

[79204] Another function of VGAM2330 is therefore inhibition of LOC92697 (Accession XM_046715). Accordingly, utilities of VGAM2330 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92697. Placental Growth Factor, Vascular Endothelial Growth Factor-related Protein (PGF, Accession NM_002632) is another VGAM2331 host target gene. PGF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PGF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PGF BINDING SITE, designated SEQ ID:8490, to the nucleotide sequence of VGAM2331 RNA, herein designated VGAM RNA, also designated SEQ ID:5042.

[79205] Another function of VGAM2331 is therefore inhibition of Placental Growth Factor, Vascular Endothelial Growth Fac-

tor-related Protein (PGF, Accession NM_002632), a gene which is a growth factor active in angiogenesis, and endothelial cell growth, stimulating cell proliferation and migration. it binds to receptor vegfr-1/fl. Accordingly, utilities of VGAM2331 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PGF. The function of PGF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1420.Organic Cationic Transporter-like 3 (ORCTL3, Accession NM_004256) is another VGAM2331 host target gene. ORCTL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ORCTL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ORCTL3 BINDING SITE, designated SEQ ID:10442, to the nucleotide sequence of VGAM2331 RNA, herein designated VGAM RNA, also designated SEQ ID:5042.

[79206] Another function of VGAM2331 is therefore inhibition of Organic Cationic Transporter-like 3 (ORCTL3, Accession NM_004256). Accordingly, utilities of VGAM2331 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with ORCTL3. LOC202459 (Accession NM_145303) is another VGAM2331 host target gene. LOC202459 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202459, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202459 BINDING SITE, designated SEQ ID:29815, to the nucleotide sequence of VGAM2331 RNA, herein designated VGAM RNA, also designated SEQ ID:5042.

[79207] Another function of VGAM2331 is therefore inhibition of LOC202459 (Accession NM_145303). Accordingly, utilities of VGAM2331 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202459. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2332 (VGAM2332) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79208] VGAM2332 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2332 was detected is described hereinabove with reference to Figs. 1-8.

[79209] VGAM2332 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2332 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79210] VGAM2332 gene encodes a VGAM2332 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2332 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2332 precursor RNA is designated SEQ ID:2318, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2318 is located at position 21991 relative to the genome of Equine Herpesvirus 2.

[79211] VGAM2332 precursor RNA folds onto itself, forming VGAM2332 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79212] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2332 folded precursor RNA into VGAM2332 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2332 RNA is designated SEQ ID:5043, and is provided hereinbelow with reference to the sequence listing part.

[79213] VGAM2332 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2332 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2332 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[79214] VGAM2332 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2332 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2332 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2332 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2332 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79215] The complementary binding of VGAM2332 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2332 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2332 host target RNA into VGAM2332 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79216] It is appreciated that VGAM2332 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2332 host target genes. The mRNA of each one of this plurality of VGAM2332 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2332 RNA, herein designated VGAM RNA, and which when bound by VGAM2332 RNA causes inhibition of translation of respective one or more VGAM2332 host target proteins.

[79217] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2332 gene, herein designated VGAM GENE, on one or more VGAM2332 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79218] It is yet further appreciated that a function of VGAM2332 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2332 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2332 correlate with, and may be deduced from, the identity of the host target genes which VGAM2332 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79219] Nucleotide sequences of the VGAM2332 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2332 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2332 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2332 are further described hereinbelow with reference to Table 1.

[79220] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2332 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2332 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79221] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2332 gene, herein designated VGAM is inhibition of expression of VGAM2332 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2332 correlate with, and may be deduced from, the identity of the target genes which VGAM2332 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79222] 5-hydroxytryptamine (serotonin) Receptor 6 (HTR6, Accession NM_000871) is a VGAM2332 host target gene.

HTR6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HTR6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HTR6 BINDING SITE, designated SEQ ID:6547, to the nucleotide sequence of VGAM2332 RNA, herein designated VGAM RNA, also designated SEQ ID:5043.

[79223] A function of VGAM2332 is therefore inhibition of 5-hydroxytryptamine (serotonin) Receptor 6 (HTR6, Accession NM_000871), a gene which stimulates adenylate cyclase. Accordingly, utilities of VGAM2332 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR6. The function of HTR6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM326.FLJ10043 (Accession NM_017979) is another VGAM2332 host target gene. FLJ10043 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10043, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of FLJ10043 BINDING SITE, designated SEQ ID:19708, to the nucleotide sequence of VGAM2332 RNA, herein designated VGAM RNA, also designated SEQ ID:5043.

[79224] Another function of VGAM2332 is therefore inhibition of FLJ10043 (Accession NM_017979). Accordingly, utilities of VGAM2332 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10043. FLJ20694 (Accession NM_017928) is another VGAM2332 host target gene. FLJ20694 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20694, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20694 BINDING SITE, designated SEQ ID:19605, to the nucleotide sequence of VGAM2332 RNA, herein designated VGAM RNA, also designated SEQ ID:5043.

[79225] Another function of VGAM2332 is therefore inhibition of FLJ20694 (Accession NM_017928). Accordingly, utilities of VGAM2332 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20694. KIAA0798 (Accession NM_014650) is another

VGAM2332 host target gene. KIAA0798 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0798, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0798 BINDING SITE, designated SEQ ID:16066, to the nucleotide sequence of VGAM2332 RNA, herein designated VGAM RNA, also designated SEQ ID:5043.

[79226] Another function of VGAM2332 is therefore inhibition of KIAA0798 (Accession NM_014650). Accordingly, utilities of VGAM2332 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0798. KLK15 (Accession NM_138563) is another VGAM2332 host target gene. KLK15 BINDING SITE1 and KLK15 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KLK15, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLK15 BINDING SITE1 and KLK15 BINDING SITE2, designated SEQ ID:28862 and SEQ ID:23264 respectively, to the nucleotide sequence of VGAM2332 RNA,

herein designated VGAM RNA, also designated SEQ ID:5043.

[79227] Another function of VGAM2332 is therefore inhibition of KLK15 (Accession NM_138563). Accordingly, utilities of VGAM2332 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLK15. LOC121838 (Accession XM_071772) is another VGAM2332 host target gene. LOC121838 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC121838, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC121838 BINDING SITE, designated SEQ ID:37418, to the nucleotide sequence of VGAM2332 RNA, herein designated VGAM RNA, also designated SEQ ID:5043.

[79228] Another function of VGAM2332 is therefore inhibition of LOC121838 (Accession XM_071772). Accordingly, utilities of VGAM2332 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC121838. LOC220739 (Accession XM_167548) is another VGAM2332 host target gene. LOC220739 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC220739, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220739 BINDING SITE, designated SEQ ID:44654, to the nucleotide sequence of VGAM2332 RNA, herein designated VGAM RNA, also designated SEQ ID:5043.

[79229] Another function of VGAM2332 is therefore inhibition of LOC220739 (Accession XM_167548). Accordingly, utilities of VGAM2332 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220739. LOC222066 (Accession XM_166582) is another VGAM2332 host target gene. LOC222066 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222066, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222066 BINDING SITE, designated SEQ ID:44555, to the nucleotide sequence of VGAM2332 RNA, herein designated VGAM RNA, also designated SEQ ID:5043.

[79230] Another function of VGAM2332 is therefore inhibition of LOC222066 (Accession XM_166582). Accordingly, utilities

of VGAM2332 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222066. LOC254685 (Accession XM_172876) is another VGAM2332 host target gene. LOC254685 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254685, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254685 BINDING SITE, designated SEQ ID:46152, to the nucleotide sequence of VGAM2332 RNA, herein designated VGAM RNA, also designated SEQ ID:5043.

[79231] Another function of VGAM2332 is therefore inhibition of LOC254685 (Accession XM_172876). Accordingly, utilities of VGAM2332 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254685. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2333 (VGAM2333) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79232] VGAM2333 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2333 was detected is described hereinabove with reference to Figs. 1-8.

[79233] VGAM2333 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2333 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79234] VGAM2333 gene encodes a VGAM2333 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2333 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2333 precursor RNA is designated SEQ ID:2319, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2319 is located at position 36149 relative to the genome of Equine Herpesvirus 2.

[79235] VGAM2333 precursor RNA folds onto itself, forming VGAM2333 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79236] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2333 folded precursor RNA into VGAM2333 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2333 RNA is designated SEQ ID:5044, and is provided hereinbelow with reference to the sequence listing part.

[79237] VGAM2333 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2333 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2333 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[79238] VGAM2333 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2333 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2333 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2333 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2333 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79239] The complementary binding of VGAM2333 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2333 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2333 host target RNA into VGAM2333 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79240] It is appreciated that VGAM2333 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2333 host target genes. The mRNA of each one of this plurality of VGAM2333 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2333 RNA, herein designated VGAM RNA, and which when bound by VGAM2333 RNA causes inhibition of translation of respective one or more VGAM2333 host target proteins.

[79241] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2333 gene, herein designated VGAM GENE, on one or more VGAM2333 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79242] It is yet further appreciated that a function of VGAM2333 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2333 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2333 correlate with, and may be deduced from, the identity of the host target genes which VGAM2333 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79243] Nucleotide sequences of the VGAM2333 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2333 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2333 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2333 are further described hereinbelow with reference to Table 1.

[79244] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2333 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2333 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79245] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2333 gene, herein designated VGAM is inhibition of expression of VGAM2333 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2333 correlate with, and may be deduced from, the identity of the target genes which VGAM2333 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79246] GLI-Kruppel Family Member GLI2 (GLI2, Accession NM_030379) is a VGAM2333 host target gene. GLI2 BIND-

ING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GLI2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GLI2 BINDING SITE, designated SEQ ID:24937, to the nucleotide sequence of VGAM2333 RNA, herein designated VGAM RNA, also designated SEQ ID:5044.

[79247] A function of VGAM2333 is therefore inhibition of GLI-Kruppel Family Member GLI2 (GLI2, Accession NM_030379), a gene which may promote tax-dependent transcription of T-cell leukemia virus type 1 genes. Accordingly, utilities of VGAM2333 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLI2. The function of GLI2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM465.Solute Carrier Family 19 (thiamine transporter), Member 2 (SLC19A2, Accession XM_044421) is another VGAM2333 host target gene. SLC19A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC19A2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC19A2 BINDING SITE, designated SEQ ID:34193, to the nucleotide sequence of VGAM2333 RNA, herein designated VGAM RNA, also designated SEQ ID:5044.

[79248] Another function of VGAM2333 is therefore inhibition of Solute Carrier Family 19 (thiamine transporter), Member 2 (SLC19A2, Accession XM_044421). Accordingly, utilities of VGAM2333 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC19A2. FLJ11210 (Accession XM_005298) is another VGAM2333 host target gene. FLJ11210 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11210, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11210 BINDING SITE, designated SEQ ID:29973, to the nucleotide sequence of VGAM2333 RNA, herein designated VGAM RNA, also designated SEQ ID:5044.

[79249] Another function of VGAM2333 is therefore inhibition of FLJ11210 (Accession XM_005298). Accordingly, utilities of

VGAM2333 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11210. FLJ22167 (Accession NM_024533) is another VGAM2333 host target gene. FLJ22167 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22167, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22167 BINDING SITE, designated SEQ ID:23744, to the nucleotide sequence of VGAM2333 RNA, herein designated VGAM RNA, also designated SEQ ID:5044.

[79250] Another function of VGAM2333 is therefore inhibition of FLJ22167 (Accession NM_024533). Accordingly, utilities of VGAM2333 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22167. KIAA0285 (Accession NM_014807) is another VGAM2333 host target gene. KIAA0285 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0285, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0285 BINDING SITE, designated SEQ ID:16755, to the nucleotide sequence of VGAM2333 RNA, herein designated VGAM RNA, also designated SEQ ID:5044.

[79251] Another function of VGAM2333 is therefore inhibition of KIAA0285 (Accession NM_014807). Accordingly, utilities of VGAM2333 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0285. KIAA0635 (Accession NM_014645) is another VGAM2333 host target gene. KIAA0635 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0635, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0635 BINDING SITE, designated SEQ ID:16057, to the nucleotide sequence of VGAM2333 RNA, herein designated VGAM RNA, also designated SEQ ID:5044.

[79252] Another function of VGAM2333 is therefore inhibition of KIAA0635 (Accession NM_014645). Accordingly, utilities of VGAM2333 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0635. KIAA1656 (Accession XM_038022) is another VGAM2333 host target gene. KIAA1656 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1656, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1656 BINDING SITE, designated SEQ ID:32737, to the nucleotide sequence of VGAM2333 RNA, herein designated VGAM RNA, also designated SEQ ID:5044.

[79253] Another function of VGAM2333 is therefore inhibition of KIAA1656 (Accession XM_038022). Accordingly, utilities of VGAM2333 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1656. LIG-1 (Accession XM_033712) is another VGAM2333 host target gene. LIG-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIG-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIG-1 BINDING SITE, designated SEQ ID:31956, to the nucleotide sequence of VGAM2333 RNA, herein designated VGAM RNA, also designated SEQ ID:5044.

[79254] Another function of VGAM2333 is therefore inhibition of

LIG-1 (Accession XM_033712). Accordingly, utilities of VGAM2333 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIG-1. PFTAIRE Protein Kinase 1 (PFTK1, Accession NM_012395) is another VGAM2333 host target gene. PFTK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PFTK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PFTK1 BINDING SITE, designated SEQ ID:14750, to the nucleotide sequence of VGAM2333 RNA, herein designated VGAM RNA, also designated SEQ ID:5044.

[79255] Another function of VGAM2333 is therefore inhibition of PFTAIRE Protein Kinase 1 (PFTK1, Accession NM_012395). Accordingly, utilities of VGAM2333 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PFTK1. LOC255565 (Accession XM_170811) is another VGAM2333 host target gene. LOC255565 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255565, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255565 BINDING SITE, designated SEQ ID:45592, to the nucleotide sequence of VGAM2333 RNA, herein designated VGAM RNA, also designated SEQ ID:5044.

[79256] Another function of VGAM2333 is therefore inhibition of LOC255565 (Accession XM_170811). Accordingly, utilities of VGAM2333 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255565. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2334 (VGAM2334) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79257] VGAM2334 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2334 was detected is described hereinabove with reference to Figs. 1-8.

[79258] VGAM2334 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2334 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[79259] VGAM2334 gene encodes a VGAM2334 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2334 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2334 precursor RNA is designated SEQ ID:2320, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2320 is located at position 40967 relative to the genome of Equine Herpesvirus 2.

[79260] VGAM2334 precursor RNA folds onto itself, forming VGAM2334 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79261] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2334 folded precursor RNA into VGAM2334

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2334 RNA is designated SEQ ID:5045, and is provided hereinbelow with reference to the sequence listing part.

[79262] VGAM2334 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2334 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2334 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79263] VGAM2334 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2334 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2334 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2334 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2334 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79264] The complementary binding of VGAM2334 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2334 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2334 host target RNA into VGAM2334 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[79265] It is appreciated that VGAM2334 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2334 host target genes. The mRNA of each one of this plurality of VGAM2334 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2334 RNA, herein designated VGAM RNA, and which when bound by VGAM2334 RNA causes inhibition of translation of respective one or more VGAM2334 host target proteins.

[79266] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2334 gene, herein designated VGAM GENE, on one or more VGAM2334 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79267] It is yet further appreciated that a function of VGAM2334 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2334 correlate with, and may be deduced from, the identity of the host target genes which VGAM2334 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79268] Nucleotide sequences of the VGAM2334 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2334 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2334 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2334 are further described hereinbelow with reference to Table 1.

[79269] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2334 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2334 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79270] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2334 gene, herein designated VGAM is inhibition of expression of VGAM2334 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2334 correlate with, and may be deduced from, the identity of the target genes which VGAM2334 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79271] Eukaryotic Translation Initiation Factor 3, Subunit 10 Theta, 150/170kDa (EIF3S10, Accession XM_049795) is a VGAM2334 host target gene. EIF3S10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF3S10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF3S10 BINDING SITE, designated SEQ ID:35499, to the nucleotide

sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79272] A function of VGAM2334 is therefore inhibition of Eukaryotic Translation Initiation Factor 3, Subunit 10 Theta, 150/170kDa (EIF3S10, Accession XM_049795), a gene which binds to the 40s ribosome and promotes the binding of methionyl-trnai and mrna. Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF3S10. The function of EIF3S10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM882.Gap Junction Protein, Beta 3, 31kDa (connexin 31) (GJB3, Accession NM_024009) is another VGAM2334 host target gene. GJB3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GJB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GJB3 BINDING SITE, designated SEQ ID:23435, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79273] Another function of VGAM2334 is therefore inhibition of Gap Junction Protein, Beta 3, 31kDa (connexin 31) (GJB3, Accession NM_024009). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GJB3. Guanine Nucleotide Binding Protein (G protein), Alpha 15 (Gq class) (GNA15, Accession XM_009220) is another VGAM2334 host target gene. GNA15 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GNA15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNA15 BINDING SITE, designated SEQ ID:30102, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79274] Another function of VGAM2334 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Alpha 15 (Gq class) (GNA15, Accession XM_009220). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNA15. Huntingtin Interacting Protein 1 (HIP1, Accession NM_005338) is another VGAM2334 host target

gene. HIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIP1 BINDING SITE, designated SEQ ID:11810, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79275] Another function of VGAM2334 is therefore inhibition of Huntingtin Interacting Protein 1 (HIP1, Accession NM_005338), a gene which is a membrane protein and interacts with huntingtin. Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIP1. The function of HIP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM474.Human Immunodeficiency Virus Type I Enhancer Binding Protein 3 (HIVEP3, Accession NM_024503) is another VGAM2334 host target gene. HIVEP3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HIVEP3, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIVEP3 BINDING SITE, designated SEQ ID:23697, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79276] Another function of VGAM2334 is therefore inhibition of Human Immunodeficiency Virus Type I Enhancer Binding Protein 3 (HIVEP3, Accession NM_024503), a gene which is required for transcriptional activation of glucose- repressible alcohol dehydrogenase (adh2). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIVEP3. The function of HIVEP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1781.Serine/threonine Kinase 10 (STK10, Accession NM_005990) is another VGAM2334 host target gene. STK10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STK10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STK10 BINDING SITE, des-

ignated SEQ ID:12612, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79277] Another function of VGAM2334 is therefore inhibition of Serine/threonine Kinase 10 (STK10, Accession NM_005990), a gene which can act on substrates such as myelin basic protein and histone iia on serine and threonine residues. Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK10. The function of STK10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.A Kinase (PRKA) Anchor Protein 7 (AKAP7, Accession NM_004842) is another VGAM2334 host target gene. AKAP7 BINDING SITE1 through AKAP7 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AKAP7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP7 BINDING SITE1 through AKAP7 BINDING SITE3, designated SEQ ID:11252, SEQ ID:18515 and SEQ ID:28905 respectively,

to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79278] Another function of VGAM2334 is therefore inhibition of A Kinase (PRKA) Anchor Protein 7 (AKAP7, Accession NM_004842). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP7. Chromosome 5 Open Reading Frame 7 (C5orf7, Accession XM_033576) is another VGAM2334 host target gene. C5orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C5orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5orf7 BINDING SITE, designated SEQ ID:31939, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79279] Another function of VGAM2334 is therefore inhibition of Chromosome 5 Open Reading Frame 7 (C5orf7, Accession XM_033576). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf7. FLJ10081 (Accession NM_017991) is another VGAM2334 host target

gene. FLJ10081 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10081, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10081 BINDING SITE, designated SEQ ID:19721, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79280] Another function of VGAM2334 is therefore inhibition of FLJ10081 (Accession NM_017991). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10081. FLJ13491 (Accession NM_024623) is another VGAM2334 host target gene. FLJ13491 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13491, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13491 BINDING SITE, designated SEQ ID:23885, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79281] Another function of VGAM2334 is therefore inhibition of FLJ13491 (Accession NM_024623). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13491. FLJ21308 (Accession NM_024615) is another VGAM2334 host target gene. FLJ21308 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ21308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21308 BINDING SITE, designated SEQ ID:23877, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79282] Another function of VGAM2334 is therefore inhibition of FLJ21308 (Accession NM_024615). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21308. FLJ21918 (Accession NM_024939) is another VGAM2334 host target gene. FLJ21918 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21918, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21918 BINDING SITE, designated SEQ ID:24481, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79283] Another function of VGAM2334 is therefore inhibition of FLJ21918 (Accession NM_024939). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21918. FLJ22173 (Accession NM_025041) is another VGAM2334 host target gene. FLJ22173 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22173, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22173 BINDING SITE, designated SEQ ID:24634, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79284] Another function of VGAM2334 is therefore inhibition of FLJ22173 (Accession NM_025041). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ22173. KIAA1155 (Accession XM_030864) is another VGAM2334 host target gene. KIAA1155 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1155, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1155 BINDING SITE, designated SEQ ID:31193, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79285] Another function of VGAM2334 is therefore inhibition of KIAA1155 (Accession XM_030864). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1155. KIAA1560 (Accession XM_034422) is another VGAM2334 host target gene. KIAA1560 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1560, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1560 BINDING SITE, designated SEQ ID:32098, to the nucleotide sequence of VGAM2334 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5045.

[79286] Another function of VGAM2334 is therefore inhibition of KIAA1560 (Accession XM_034422). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1560. KIAA1764 (Accession XM_045086) is another VGAM2334 host target gene. KIAA1764 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1764, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1764 BINDING SITE, designated SEQ ID:34351, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79287] Another function of VGAM2334 is therefore inhibition of KIAA1764 (Accession XM_045086). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1764. KIAA1936 (Accession XM_056082) is another VGAM2334 host target gene. KIAA1936 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1936, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1936 BINDING SITE, designated SEQ ID:36362, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79288] Another function of VGAM2334 is therefore inhibition of KIAA1936 (Accession XM_056082). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1936. LOC150605 (Accession XM_097927) is another VGAM2334 host target gene. LOC150605 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150605, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150605 BINDING SITE, designated SEQ ID:41227, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79289] Another function of VGAM2334 is therefore inhibition of LOC150605 (Accession XM_097927). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC150605. LOC157858 (Accession XM_098833) is another VGAM2334 host target gene. LOC157858 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157858, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157858 BINDING SITE, designated SEQ ID:41864, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79290] Another function of VGAM2334 is therefore inhibition of LOC157858 (Accession XM_098833). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157858. LOC254057 (Accession XM_173085) is another VGAM2334 host target gene. LOC254057 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254057 BINDING SITE, designated SEQ ID:46341, to

the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79291] Another function of VGAM2334 is therefore inhibition of LOC254057 (Accession XM_173085). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254057. LOC90485 (Accession XM_032059) is another VGAM2334 host target gene. LOC90485 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90485, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90485 BINDING SITE, designated SEQ ID:31552, to the nucleotide sequence of VGAM2334 RNA, herein designated VGAM RNA, also designated SEQ ID:5045.

[79292] Another function of VGAM2334 is therefore inhibition of LOC90485 (Accession XM_032059). Accordingly, utilities of VGAM2334 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90485. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2335 (VGAM2335) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79293] VGAM2335 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2335 was detected is described hereinabove with reference to Figs. 1-8.

[79294] VGAM2335 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2335 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79295] VGAM2335 gene encodes a VGAM2335 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2335 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2335 precursor RNA is designated SEQ ID:2321, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2321 is located at position 42087 relative to the genome of Equine Herpesvirus 2.

[79296] VGAM2335 precursor RNA folds onto itself, forming VGAM2335 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79297] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2335 folded precursor RNA into VGAM2335 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2335 RNA is designated SEQ ID:5046, and is provided hereinbelow with reference to the sequence listing part.

[79298] VGAM2335 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2335 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2335 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79299] VGAM2335 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2335 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2335 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2335 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2335 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79300] The complementary binding of VGAM2335 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2335 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2335 host target RNA into VGAM2335 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79301] It is appreciated that VGAM2335 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2335 host target genes. The mRNA of each one of this plurality of VGAM2335 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2335 RNA, herein designated VGAM RNA, and which when bound by VGAM2335 RNA causes inhibition of translation of respective one or more VGAM2335 host target proteins.

[79302] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2335 gene, herein designated VGAM GENE, on one or more VGAM2335 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79303] It is yet further appreciated that a function of VGAM2335 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2335 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2335 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2335 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79304] Nucleotide sequences of the VGAM2335 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2335 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2335 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2335 are further described hereinbelow with reference to Table 1.

[79305] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2335 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2335 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79306] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2335 gene, herein designated VGAM is inhibition of expression of VGAM2335 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2335 correlate with, and may be deduced from, the identity of the target genes which VGAM2335

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79307] CARPX (Accession NM_020178) is a VGAM2335 host target gene. CARPX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CARPX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CARPX BINDING SITE, designated SEQ ID:21396, to the nucleotide sequence of VGAM2335 RNA, herein designated VGAM RNA, also designated SEQ ID:5046.

[79308] A function of VGAM2335 is therefore inhibition of CARPX (Accession NM_020178), a gene which is alpha-carbonic anhydrases-related protein. Accordingly, utilities of VGAM2335 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARPX. The function of CARPX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM904.PLAB (Accession XM_038098) is another VGAM2335 host target gene. PLAB BINDING SITE is HOST TARGET binding site found in the 5` untranslated region

of mRNA encoded by PLAB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLAB BINDING SITE, designated SEQ ID:32753, to the nucleotide sequence of VGAM2335 RNA, herein designated VGAM RNA, also designated SEQ ID:5046.

[79309] Another function of VGAM2335 is therefore inhibition of PLAB (Accession XM_038098), a gene which regulates tissue differentiation and maintenance. Accordingly, utilities of VGAM2335 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAB. The function of PLAB has been established by previous studies. Bone morphogenetic proteins (e.g., BMP5; 112265) are members of the transforming growth factor-beta (see OMIM Ref. No. TGFB1; 190180) superfamily and regulate tissue differentiation and maintenance. They are synthesized as precursor molecules that are processed at a dibasic cleavage site to release C-terminal domains containing a characteristic motif of 7 conserved cysteines in the mature protein. By screening a full-length cDNA library constructed from a fibrosarcoma cell line for secretory proteins, Yokoyama-Kobayashi et al. (1997) isolated

a cDNA encoding a 308-amino acid protein related to TGFB. Northern blot analysis detected strongest expression of a 1.35-kb transcript in placenta, with lower levels in prostate and colon and some expression in kidney. By searching an EST database for TGFB/BMP-related sequences, Hromas et al. (1997) identified a cDNA encoding an identical protein, which they called PLAB (placental BMP). Through analysis of hematopoietic progenitor proliferation, they found that PLAB reduces the growth of granulocytes and macrophages. By searching an EST database, followed by screening a placental cDNA library, Paralkar et al. (1998) isolated a cDNA encoding PLAB, which they called PDF (prostate-derived factor). Western blot analysis showed that PDF is expressed as a 16-kD protein under reducing conditions. In situ hybridization and immunohistochemical analysis demonstrated that PDF is expressed at high levels in cells of the terminal villi in placenta and in the epithelium of prostate but not in other accessory male genital glands. Using subtraction cloning in a monocyte/macrophage cell line, Bootcov et al. (1997) isolated a cDNA encoding PLAB, which they called MIC1 (macrophage-inhibiting cytokine-1). Sequence analysis predicted that the mature secreted MIC1 protein contains

224 amino acids. Northern blot analysis showed that MIC1 is not expressed in undifferentiated cells but is progressively upregulated upon differentiation with retinoic acid followed by phorbol ester or cytokine (e.g., TNFA; 191160) treatment. Exposure of macrophages to MIC1 or TGFB1, followed by stimulation with lipopolysaccharide, suppressed the production of TNFA. Unlike most TGFB superfamily members, in which the amino acid sequence is completely conserved, MIC1 shares only 70% amino acid identity with its rodent counterparts (Bottner et al., 1999). Using FISH, Bottner et al. (1999) mapped the MIC1 gene to 19p13.2-p13.1.

[79310] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[79311] Paralkar, V. M.; Vail, A. L.; Grasser, W. A.; Brown, T. A.; Xu, H.; Vukicevic, S.; Ke, H. Z.; Qi, H.; Owen, T. A.; Thompson, D. D. : Cloning and characterization of a novel member of the transforming growth factor-beta/bone morphogenetic protein family. J. Biol. Chem. 273: 13760-13767, 1998. ; and

[79312] Yokoyama-Kobayashi, M.; Saeki, M.; Sekine, S.; Kato, S. : Human cDNA encoding a novel TGF-beta superfamily pro-

tein highly expressed in placenta. J. Biochem. 122: 622-626, 1997.

[79313] Further studies establishing the function and utilities of PLAB are found in John Hopkins OMIM database record ID 605312, and in sited publications numbered 7446-745 and 7454-7452 listed in the bibliography section herein-below, which are also hereby incorporated by refer-ence.FLJ21916 (Accession NM_023112) is another VGAM2335 host target gene. FLJ21916 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21916, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-ING SITE II or BINDING SITE III. Table 2 illustrates the com-plementarity of the nucleotide sequences of FLJ21916 BINDING SITE, designated SEQ ID:23379, to the nucleotide sequence of VGAM2335 RNA, herein designated VGAM RNA, also designated SEQ ID:5046.

[79314] Another function of VGAM2335 is therefore inhibition of FLJ21916 (Accession NM_023112). Accordingly, utilities of VGAM2335 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21916. FLJ23233 (Accession NM_024691) is another VGAM2335 host target gene. FLJ23233 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23233, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23233 BINDING SITE, designated SEQ ID:24000, to the nucleotide sequence of VGAM2335 RNA, herein designated VGAM RNA, also designated SEQ ID:5046.

[79315] Another function of VGAM2335 is therefore inhibition of FLJ23233 (Accession NM_024691). Accordingly, utilities of VGAM2335 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23233. Ring Finger Protein (C3HC4 type) 8 (RNF8, Accession NM_003958) is another VGAM2335 host target gene. RNF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF8 BINDING SITE, designated SEQ ID:10094, to the nucleotide sequence of VGAM2335 RNA, herein designated VGAM RNA, also designated SEQ ID:5046.

[79316] Another function of VGAM2335 is therefore inhibition of

Ring Finger Protein (C3HC4 type) 8 (RNF8, Accession NM_003958). Accordingly, utilities of VGAM2335 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF8. LOC149461 (Accession XM_086547) is another VGAM2335 host target gene. LOC149461 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149461, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149461 BINDING SITE, designated SEQ ID:38762, to the nucleotide sequence of VGAM2335 RNA, herein designated VGAM RNA, also designated SEQ ID:5046.

[79317] Another function of VGAM2335 is therefore inhibition of LOC149461 (Accession XM_086547). Accordingly, utilities of VGAM2335 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149461. LOC152018 (Accession XM_098156) is another VGAM2335 host target gene. LOC152018 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152018, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152018 BINDING SITE, designated SEQ ID:41420, to the nucleotide sequence of VGAM2335 RNA, herein designated VGAM RNA, also designated SEQ ID:5046.

[79318] Another function of VGAM2335 is therefore inhibition of LOC152018 (Accession XM_098156). Accordingly, utilities of VGAM2335 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152018. LOC164684 (Accession XM_092926) is another VGAM2335 host target gene. LOC164684 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC164684, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164684 BINDING SITE, designated SEQ ID:40160, to the nucleotide sequence of VGAM2335 RNA, herein designated VGAM RNA, also designated SEQ ID:5046.

[79319] Another function of VGAM2335 is therefore inhibition of LOC164684 (Accession XM_092926). Accordingly, utilities of VGAM2335 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC164684. LOC203083 (Accession XM_117496) is another VGAM2335 host target gene. LOC203083 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203083, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203083 BINDING SITE, designated SEQ ID:43477, to the nucleotide sequence of VGAM2335 RNA, herein designated VGAM RNA, also designated SEQ ID:5046.

[79320] Another function of VGAM2335 is therefore inhibition of LOC203083 (Accession XM_117496). Accordingly, utilities of VGAM2335 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203083. LOC254176 (Accession XM_173215) is another VGAM2335 host target gene. LOC254176 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254176, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254176 BINDING SITE, designated SEQ ID:46474, to the nucleotide sequence of VGAM2335 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5046.

[79321] Another function of VGAM2335 is therefore inhibition of LOC254176 (Accession XM_173215). Accordingly, utilities of VGAM2335 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254176. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2336 (VGAM2336) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79322] VGAM2336 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2336 was detected is described hereinabove with reference to Figs. 1-8.

[79323] VGAM2336 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2336 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79324] VGAM2336 gene encodes a VGAM2336 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2336 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2336 precursor RNA is designated SEQ ID:2322, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2322 is located at position 40488 relative to the genome of Equine Herpesvirus 2.

[79325] VGAM2336 precursor RNA folds onto itself, forming VGAM2336 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79326] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2336 folded precursor RNA into VGAM2336 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2336 RNA is designated SEQ ID:5047, and is provided hereinbelow with reference to the sequence listing part.

[79327] VGAM2336 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2336 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2336 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79328] VGAM2336 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2336 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2336 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2336 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2336 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79329] The complementary binding of VGAM2336 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2336 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2336 host target RNA into VGAM2336 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79330] It is appreciated that VGAM2336 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2336 host target genes. The mRNA of

each one of this plurality of VGAM2336 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2336 RNA, herein designated VGAM RNA, and which when bound by VGAM2336 RNA causes inhibition of translation of respective one or more VGAM2336 host target proteins.

[79331] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2336 gene, herein designated VGAM GENE, on one or more VGAM2336 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[79332] It is yet further appreciated that a function of VGAM2336 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2336 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2336 correlate with, and may be deduced from, the identity of the host target genes which VGAM2336 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79333] Nucleotide sequences of the VGAM2336 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2336 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2336 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2336 are further described hereinbelow with reference to Table 1.

[79334] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2336 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2336 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79335] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2336 gene, herein designated VGAM is inhibition of expression of VGAM2336 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2336 correlate with, and may be deduced from, the identity of the target genes which VGAM2336 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79336] ATPase, Aminophospholipid Transporter-like, Class I, Type 8A, Member 2 (ATP8A2, Accession XM_167916) is a VGAM2336 host target gene. ATP8A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP8A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP8A2 BINDING SITE, designated SEQ ID:44922, to the nucleotide sequence of VGAM2336 RNA, herein designated VGAM RNA, also designated SEQ ID:5047.

[79337] A function of VGAM2336 is therefore inhibition of ATPase, Aminophospholipid Transporter-like, Class I, Type 8A,

Member 2 (ATP8A2, Accession XM_167916). Accordingly, utilities of VGAM2336 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8A2. KIAA0218 (Accession NM_014760) is another VGAM2336 host target gene. KIAA0218 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0218, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0218 BINDING SITE, designated SEQ ID:16517, to the nucleotide sequence of VGAM2336 RNA, herein designated VGAM RNA, also designated SEQ ID:5047.

[79338] Another function of VGAM2336 is therefore inhibition of KIAA0218 (Accession NM_014760). Accordingly, utilities of VGAM2336 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0218. KIAA0570 (Accession NM_014709) is another VGAM2336 host target gene. KIAA0570 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0570, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0570 BINDING SITE, designated SEQ ID:16255, to the nucleotide sequence of VGAM2336 RNA, herein designated VGAM RNA, also designated SEQ ID:5047.

[79339] Another function of VGAM2336 is therefore inhibition of KIAA0570 (Accession NM_014709). Accordingly, utilities of VGAM2336 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0570. Rho-related BTB Domain Containing 2 (RHOBTB2, Accession XM_027679) is another VGAM2336 host target gene. RHOBTB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RHOBTB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RHOBTB2 BINDING SITE, designated SEQ ID:30560, to the nucleotide sequence of VGAM2336 RNA, herein designated VGAM RNA, also designated SEQ ID:5047.

[79340] Another function of VGAM2336 is therefore inhibition of Rho-related BTB Domain Containing 2 (RHOBTB2, Accession XM_027679). Accordingly, utilities of VGAM2336 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with RHOBTB2. LOC149910 (Accession XM_086699) is another VGAM2336 host target gene. LOC149910 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149910, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149910 BINDING SITE, designated SEQ ID:38826, to the nucleotide sequence of VGAM2336 RNA, herein designated VGAM RNA, also designated SEQ ID:5047.

[79341] Another function of VGAM2336 is therefore inhibition of LOC149910 (Accession XM_086699). Accordingly, utilities of VGAM2336 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149910. LOC151361 (Accession XM_098048) is another VGAM2336 host target gene. LOC151361 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151361, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151361 BINDING SITE, designated SEQ ID:41330, to

the nucleotide sequence of VGAM2336 RNA, herein designated VGAM RNA, also designated SEQ ID:5047.

[79342] Another function of VGAM2336 is therefore inhibition of LOC151361 (Accession XM_098048). Accordingly, utilities of VGAM2336 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151361. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2337 (VGAM2337) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79343] VGAM2337 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2337 was detected is described hereinabove with reference to Figs. 1-8.

[79344] VGAM2337 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2337 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79345] VGAM2337 gene encodes a VGAM2337 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2337 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2337 precursor RNA is designated SEQ ID:2323, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2323 is located at position 42439 relative to the genome of Equine Herpesvirus 2.

[79346] VGAM2337 precursor RNA folds onto itself, forming VGAM2337 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79347] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2337 folded precursor RNA into VGAM2337 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2337 RNA is designated SEQ ID:5048, and is provided hereinbelow with reference to the sequence listing part.

[79348] VGAM2337 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2337 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2337 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79349] VGAM2337 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2337 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2337 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2337 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2337 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79350] The complementary binding of VGAM2337 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2337 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2337 host target RNA into VGAM2337 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79351] It is appreciated that VGAM2337 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2337 host target genes. The mRNA of each one of this plurality of VGAM2337 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2337 RNA, herein designated VGAM RNA, and which when bound by VGAM2337 RNA causes inhibition of translation of respective one or more VGAM2337 host target proteins.

[79352] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2337 gene, herein designated VGAM GENE, on one or more VGAM2337 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79353] It is yet further appreciated that a function of VGAM2337 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2337 correlate with, and may be deduced from, the identity of the host target genes which VGAM2337 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79354] Nucleotide sequences of the VGAM2337 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2337 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2337 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2337 are further described hereinbelow with reference to Table 1.

[79355] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2337 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2337 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79356] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2337 gene, herein designated VGAM is inhibition of expression of VGAM2337 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2337 correlate with, and may be deduced from, the identity of the target genes which VGAM2337 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79357] BRCA1 Associated Protein-1 (ubiquitin carboxy-terminal hydrolase) (BAP1, Accession NM_004656) is a VGAM2337 host target gene. BAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAP1 BINDING SITE, designated SEQ ID:11023, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79358] A function of VGAM2337 is therefore inhibition of BRCA1

Associated Protein-1 (ubiquitin carboxy-terminal hydrolase) (BAP1, Accession NM_004656). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAP1. Ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2, Accession NM_015838) is another VGAM2337 host target gene. FCN2 BINDING SITE1 and FCN2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FCN2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FCN2 BINDING SITE1 and FCN2 BINDING SITE2, designated SEQ ID:17951 and SEQ ID:17953 respectively, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79359] Another function of VGAM2337 is therefore inhibition of Ficolin (collagen/fibrinogen domain containing lectin) 2 (hucolin) (FCN2, Accession NM_015838), a gene which is involved in phagocytosis of pathogens. Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FCN2. The function of FCN2 and its association with

various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM493.BIKE (Accession NM_017593) is another VGAM2337 host target gene. BIKE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BIKE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIKE BINDING SITE, designated SEQ ID:19040, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79360] Another function of VGAM2337 is therefore inhibition of BIKE (Accession NM_017593). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIKE. Burkitt Lymphoma Receptor 1, GTP Binding Protein (chemokine (C-X-C motif) Receptor 5) (BLR1, Accession NM_032966) is another VGAM2337 host target gene. BLR1 BINDING SITE1 and BLR1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by BLR1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BLR1 BINDING SITE1 and BLR1 BINDING SITE2, designated SEQ ID:26774 and SEQ ID:7445 respectively, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79361] Another function of VGAM2337 is therefore inhibition of Burkitt Lymphoma Receptor 1, GTP Binding Protein (chemokine (C-X-C motif) Receptor 5) (BLR1, Accession NM_032966). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BLR1. CUB and Sushi Multiple Domains 1 (CSMD1, Accession XM_054838) is another VGAM2337 host target gene. CSMD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSMD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSMD1 BINDING SITE, designated SEQ ID:36191, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79362] Another function of VGAM2337 is therefore inhibition of

CUB and Sushi Multiple Domains 1 (CSMD1, Accession XM_054838). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSMD1. FLJ20435 (Accession NM_017821) is another VGAM2337 host target gene. FLJ20435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20435 BINDING SITE, designated SEQ ID:19469, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79363] Another function of VGAM2337 is therefore inhibition of FLJ20435 (Accession NM_017821). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20435. MAD4 (Accession NM_006454) is another VGAM2337 host target gene. MAD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAD4 BINDING SITE, designated SEQ ID:13170, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79364] Another function of VGAM2337 is therefore inhibition of MAD4 (Accession NM_006454). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAD4. MGC2721 (Accession NM_032737) is another VGAM2337 host target gene. MGC2721 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2721, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2721 BINDING SITE, designated SEQ ID:26463, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79365] Another function of VGAM2337 is therefore inhibition of MGC2721 (Accession NM_032737). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC2721. Nucleoredoxin (NXN, Accession NM_022463) is another VGAM2337 host target gene. NXN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NXN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NXN BINDING SITE, designated SEQ ID:22808, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79366] Another function of VGAM2337 is therefore inhibition of Nucleoredoxin (NXN, Accession NM_022463). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXN. Purinergic Receptor P2X-like 1, Orphan Receptor (P2RXL1, Accession NM_005446) is another VGAM2337 host target gene. P2RXL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P2RXL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P2RXL1 BINDING SITE, designated SEQ ID:11929, to the nucleotide se-

quence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79367] Another function of VGAM2337 is therefore inhibition of Purinergic Receptor P2X-like 1, Orphan Receptor (P2RXL1, Accession NM_005446). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RXL1. TACTILE (Accession NM_005816) is another VGAM2337 host target gene. TACTILE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TACTILE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TACTILE BINDING SITE, designated SEQ ID:12410, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79368] Another function of VGAM2337 is therefore inhibition of TACTILE (Accession NM_005816). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TACTILE. Zinc Finger Protein 213 (ZNF213, Accession XM_036493) is another VGAM2337 host target gene.

ZNF213 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF213, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF213 BINDING SITE, designated SEQ ID:32463, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also designated SEQ ID:5048.

[79369] Another function of VGAM2337 is therefore inhibition of Zinc Finger Protein 213 (ZNF213, Accession XM_036493). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF213. LOC257482 (Accession XM_168544) is another VGAM2337 host target gene. LOC257482 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257482, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257482 BINDING SITE, designated SEQ ID:45236, to the nucleotide sequence of VGAM2337 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5048.

[79370] Another function of VGAM2337 is therefore inhibition of LOC257482 (Accession XM_168544). Accordingly, utilities of VGAM2337 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257482. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2338 (VGAM2338) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79371] VGAM2338 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2338 was detected is described hereinabove with reference to Figs. 1-8.

[79372] VGAM2338 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2338 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79373] VGAM2338 gene encodes a VGAM2338 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2338 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2338 precursor RNA is designated SEQ ID:2324, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2324 is located at position 36402 relative to the genome of Equine Herpesvirus 2.

[79374] VGAM2338 precursor RNA folds onto itself, forming VGAM2338 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79375] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2338 folded precursor RNA into VGAM2338 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2338 RNA is designated SEQ ID:5049, and is provided hereinbelow with reference to the sequence listing part.

[79376] VGAM2338 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2338 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2338 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79377] VGAM2338 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2338 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2338 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2338 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2338 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79378] The complementary binding of VGAM2338 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2338 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2338 host target RNA into VGAM2338 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79379] It is appreciated that VGAM2338 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2338 host target genes. The mRNA of

each one of this plurality of VGAM2338 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2338 RNA, herein designated VGAM RNA, and which when bound by VGAM2338 RNA causes inhibition of translation of respective one or more VGAM2338 host target proteins.

[79380] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2338 gene, herein designated VGAM GENE, on one or more VGAM2338 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[79381] It is yet further appreciated that a function of VGAM2338 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2338 correlate with, and may be deduced from, the identity of the host target genes which VGAM2338 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79382] Nucleotide sequences of the VGAM2338 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2338 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2338 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2338 are further described hereinbelow with reference to Table 1.

[79383] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2338 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2338 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79384] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2338 gene, herein designated VGAM is inhibition of expression of VGAM2338 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2338 correlate with, and may be deduced from, the identity of the target genes which VGAM2338 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79385] Aquaporin 1 (channel-forming integral protein, 28kDa) (AQP1, Accession NM_000385) is a VGAM2338 host target gene. AQP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AQP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AQP1 BINDING SITE, designated SEQ ID:5960, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79386] A function of VGAM2338 is therefore inhibition of Aquaporin 1 (channel-forming integral protein, 28kDa) (AQP1, Accession NM_000385). Accordingly, utilities of

VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP1. UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 6 (B4GALT6, Accession XM_008799) is another VGAM2338 host target gene. B4GALT6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by B4GALT6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B4GALT6 BINDING SITE, designated SEQ ID:30092, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79387] Another function of VGAM2338 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 6 (B4GALT6, Accession XM_008799). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT6. B-cell CLL/lymphoma 2 (BCL2, Accession NM_000633) is another VGAM2338 host target gene. BCL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL2, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL2 BINDING SITE, designated SEQ ID:6252, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79388] Another function of VGAM2338 is therefore inhibition of B-cell CLL/lymphoma 2 (BCL2, Accession NM_000633). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL2. Calcium-sensing Receptor (hypocalciuric hypercalcemia 1, severe neonatal hyperparathyroidism) (CASR, Accession NM_000388) is another VGAM2338 host target gene. CASR BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CASR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASR BINDING SITE, designated SEQ ID:5961, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79389] Another function of VGAM2338 is therefore inhibition of Calcium-sensing Receptor (hypocalciuric hypercalcemia 1,

severe neonatal hyperparathyroidism) (CASR, Accession NM_000388). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASR. CERD4 (Accession NM_012074) is another VGAM2338 host target gene. CERD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CERD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CERD4 BINDING SITE, designated SEQ ID:14351, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79390] Another function of VGAM2338 is therefore inhibition of CERD4 (Accession NM_012074). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CERD4. Diacylglycerol O-acyltransferase Homolog 2 (mouse) (DGAT2, Accession NM_032564) is another VGAM2338 host target gene. DGAT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DGAT2, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGAT2 BINDING SITE, designated SEQ ID:26289, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79391] Another function of VGAM2338 is therefore inhibition of Diacylglycerol O-acyltransferase Homolog 2 (mouse) (DGAT2, Accession NM_032564). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGAT2. Inositol Hexaphosphate Kinase 3 (IHPK3, Accession NM_054111) is another VGAM2338 host target gene. IHPK3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IHPK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IHPK3 BINDING SITE, designated SEQ ID:27659, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79392] Another function of VGAM2338 is therefore inhibition of Inositol Hexaphosphate Kinase 3 (IHPK3, Accession

NM_054111). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IHPK3. Interleukin 17E (IL17E, Accession NM_022789) is another VGAM2338 host target gene. IL17E BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IL17E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL17E BINDING SITE, designated SEQ ID:23070, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79393] Another function of VGAM2338 is therefore inhibition of Interleukin 17E (IL17E, Accession NM_022789), a gene which induces activation of nf-kappab and stimulates production of the proinflammatory chemokine il-8. Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL17E. The function of IL17E has been established by previous studies. By genomic DNA sequence analysis, Lee et al. (2001) identified a cDNA encoding IL17E. Sequence analysis predicted that the 177-amino

acid protein shares 16 to 20% identity with IL17, IL17B (OMIM Ref. No. 604627), and IL17C (OMIM Ref. No. 604628). These proteins share 20 to 30% identity in the C terminus, and all contain 4 conserved cysteine residues. Although Northern blot analysis revealed no IL17E expression, RT-PCR detected low-level expression in several tissues, including brain, kidney, lung, prostate, testis, spinal cord, adrenal gland, and trachea Treatment of mice in vivo with Il17e by Fort et al. (2001) resulted in induction of Th2-type cytokines, eosinophilia, increased serum immunoglobulin, and the development of histologic changes in lungs and the gastrointestinal tract. In contrast, other IL17-related cytokines induce proinflammatory cytokines and neutrophil migration. RT-PCR, ELISA, and flow cytometric analyses demonstrated that Il17e induces Th2-type cytokine expression and production by non-T, non-B accessory cells that express high levels of major histocompatibility complex class II and low levels of Cd11c (ITGAX; 151510).

[79394] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[79395] Lee, J.; Ho, W.-H.; Maruoka, M.; Corpuz, R. T.; Baldwin, D.

T.; Foster, J. S.; Goddard, A. D.; Yansura, D. G.; Vandlen, R. L.; Wood, W. L.; Gurney, A. L. : IL-17E, a novel proinflammatory ligand for the IL-17 receptor homolog IL-17Rh1. J. Biol. Chem. 276: 1660-1664, 2001. ; and

[79396] Fort, M. M.; Cheung, J.; Yen, D.; Li, J.; Zurawski, S. M.; Lo, S.; Menon, S.; Clifford, T.; Hunte, B.; Lesley, R.; Muchamuel, T.; Hurst, S. D.; Zurawski, G.; Leach, M. W.; Gorman, D. M.

[79397] Further studies establishing the function and utilities of IL17E are found in John Hopkins OMIM database record ID 605658, and in sited publications numbered 640 and 6408 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Interleukin 1 Receptor Antagonist (IL1RN, Accession NM_000577) is another VGAM2338 host target gene. IL1RN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL1RN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL1RN BINDING SITE, designated SEQ ID:6178, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79398] Another function of VGAM2338 is therefore inhibition of Interleukin 1 Receptor Antagonist (IL1RN, Accession NM_000577), a gene which inhibits the activity of il-1 by binding to its receptor. il-1ra has no il-1 like activity. Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL1RN. The function of IL1RN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM193.Muscleblind-like (Drosophila) (MBNL, Accession NM_021038) is another VGAM2338 host target gene. MBNL BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MBNL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MBNL BINDING SITE, designated SEQ ID:22026, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79399] Another function of VGAM2338 is therefore inhibition of Muscleblind-like (Drosophila) (MBNL, Accession NM_021038), a gene which binds to cug triplet repeat ex-

pansion dsrna (by similarity). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBNL. The function of MBNL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM95.Platelet-derived Growth Factor Beta Polypeptide (simian sarcoma viral (v-sis) Oncogene Homolog) (PDGFB, Accession NM_002608) is another VGAM2338 host target gene. PDGFB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDGFB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDGFB BINDING SITE, designated SEQ ID:8468, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79400] Another function of VGAM2338 is therefore inhibition of Platelet-derived Growth Factor Beta Polypeptide (simian sarcoma viral (v-sis) Oncogene Homolog) (PDGFB, Accession NM_002608), a gene which plays an important role in stimulating adjacent cells to grow and thereby heal the

wound. Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFB. The function of PDGFB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM173.Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 3 (p55, gamma) (PIK3R3, Accession XM_027982) is another VGAM2338 host target gene. PIK3R3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIK3R3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIK3R3 BINDING SITE, designated SEQ ID:30600, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79401] Another function of VGAM2338 is therefore inhibition of Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 3 (p55, gamma) (PIK3R3, Accession XM_027982). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with PIK3R3. Peanut-like 1 (Drosophila) (PNUTL1, Accession NM_002688) is another VGAM2338 host target gene. PNUTL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PNUTL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PNUTL1 BINDING SITE, designated SEQ ID:8546, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79402] Another function of VGAM2338 is therefore inhibition of Peanut-like 1 (Drosophila) (PNUTL1, Accession NM_002688). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNUTL1. Secreted Frizzled-related Protein 1 (SFRP1, Accession NM_003012) is another VGAM2338 host target gene. SFRP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFRP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRP1 BIND-

ING SITE, designated SEQ ID:8928, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79403] Another function of VGAM2338 is therefore inhibition of Secreted Frizzled-related Protein 1 (SFRP1, Accession NM_003012), a gene which is a receptor for wnt proteins that may have an anti-apoptotic function. Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRP1. The function of SFRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM250.Teratocarcinoma-derived Growth Factor 1 (TDGF1, Accession NM_003212) is another VGAM2338 host target gene. TDGF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TDGF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TDGF1 BINDING SITE, designated SEQ ID:9209, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79404] Another function of VGAM2338 is therefore inhibition of Teratocarcinoma-derived Growth Factor 1 (TDGF1, Accession NM_003212), a gene which can play a role in the determination of the epiblastic cells that subsequently give rise to the mesoderm. Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TDGF1. The function of TDGF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1322.Kell Blood Group Precursor (McLeod phenotype) (XK, Accession NM_021083) is another VGAM2338 host target gene. XK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XK BINDING SITE, designated SEQ ID:22061, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79405] Another function of VGAM2338 is therefore inhibition of Kell Blood Group Precursor (McLeod phenotype) (XK, Ac-

cession NM_021083). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XK. Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769) is another VGAM2338 host target gene. C11orf11 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C11orf11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf11 BINDING SITE, designated SEQ ID:44782, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79406] Another function of VGAM2338 is therefore inhibition of Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf11. DKFZP434E2135 (Accession NM_030804) is another VGAM2338 host target gene. DKFZP434E2135 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434E2135,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434E2135 BINDING SITE, designated SEQ ID:25116, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79407] Another function of VGAM2338 is therefore inhibition of DKFZP434E2135 (Accession NM_030804). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434E2135. EFA6R (Accession NM_015310) is another VGAM2338 host target gene. EFA6R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EFA6R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFA6R BINDING SITE, designated SEQ ID:17623, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79408] Another function of VGAM2338 is therefore inhibition of EFA6R (Accession NM_015310). Accordingly, utilities of

VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFA6R. FLJ10829 (Accession NM_018234) is another VGAM2338 host target gene. FLJ10829 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10829, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10829 BINDING SITE, designated SEQ ID:20179, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79409] Another function of VGAM2338 is therefore inhibition of FLJ10829 (Accession NM_018234). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10829. FLJ11608 (Accession NM_024557) is another VGAM2338 host target gene. FLJ11608 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11608, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11608

BINDING SITE, designated SEQ ID:23776, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79410] Another function of VGAM2338 is therefore inhibition of FLJ11608 (Accession NM_024557). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11608. FLJ20073 (Accession NM_017654) is another VGAM2338 host target gene. FLJ20073 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20073, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20073 BINDING SITE, designated SEQ ID:19164, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79411] Another function of VGAM2338 is therefore inhibition of FLJ20073 (Accession NM_017654). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20073. FLJ20274 (Accession XM_031455) is another VGAM2338 host target gene. FLJ20274 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20274, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20274 BINDING SITE, designated SEQ ID:31385, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79412] Another function of VGAM2338 is therefore inhibition of FLJ20274 (Accession XM_031455). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20274. GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568) is another VGAM2338 host target gene. GABARAPL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GABARAPL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABARAPL3 BINDING SITE, designated SEQ ID:26297, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79413] Another function of VGAM2338 is therefore inhibition of GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL3. GMPPB (Accession XM_171044) is another VGAM2338 host target gene. GMPPB BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GMPPB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GMPPB BINDING SITE, designated SEQ ID:45809, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79414] Another function of VGAM2338 is therefore inhibition of GMPPB (Accession XM_171044). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GMPPB. KIAA0143 (Accession XM_035825) is another VGAM2338 host target gene. KIAA0143 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0143, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0143 BINDING SITE, designated SEQ ID:32350, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79415] Another function of VGAM2338 is therefore inhibition of KIAA0143 (Accession XM_035825). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0143. KIAA0161 (Accession NM_014746) is another VGAM2338 host target gene. KIAA0161 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0161, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0161 BINDING SITE, designated SEQ ID:16429, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79416] Another function of VGAM2338 is therefore inhibition of KIAA0161 (Accession NM_014746). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0161. KIAA0495 (Accession XM_031397) is another VGAM2338 host target gene. KIAA0495 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0495, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0495 BINDING SITE, designated SEQ ID:31367, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79417] Another function of VGAM2338 is therefore inhibition of KIAA0495 (Accession XM_031397). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0495. KIAA0542 (Accession XM_038520) is another VGAM2338 host target gene. KIAA0542 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0542, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0542 BINDING SITE, designated SEQ ID:32858, to the

nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79418] Another function of VGAM2338 is therefore inhibition of KIAA0542 (Accession XM_038520). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0542. KIAA0774 (Accession XM_166270) is another VGAM2338 host target gene. KIAA0774 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0774, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0774 BINDING SITE, designated SEQ ID:44089, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79419] Another function of VGAM2338 is therefore inhibition of KIAA0774 (Accession XM_166270). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0774. KIAA1223 (Accession XM_048747) is another VGAM2338 host target gene. KIAA1223 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1223, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1223 BINDING SITE, designated SEQ ID:35244, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79420] Another function of VGAM2338 is therefore inhibition of KIAA1223 (Accession XM_048747). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1223. LHPP (Accession NM_022126) is another VGAM2338 host target gene. LHPP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LHPP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LHPP BINDING SITE, designated SEQ ID:22673, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79421] Another function of VGAM2338 is therefore inhibition of LHPP (Accession NM_022126). Accordingly, utilities of

VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHPP. MGC14161 (Accession NM_032892) is another VGAM2338 host target gene. MGC14161 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC14161, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC14161 BINDING SITE, designated SEQ ID:26719, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79422] Another function of VGAM2338 is therefore inhibition of MGC14161 (Accession NM_032892). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14161. NECL1 (Accession NM_021189) is another VGAM2338 host target gene. NECL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NECL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NECL1 BINDING SITE,

designated SEQ ID:22164, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79423] Another function of VGAM2338 is therefore inhibition of NECL1 (Accession NM_021189). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NECL1. Proline-rich Gla (G-carboxyglutamic acid) Polypeptide 1 (PRRG1, Accession NM_000950) is another VGAM2338 host target gene. PRRG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRRG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRRG1 BINDING SITE, designated SEQ ID:6652, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79424] Another function of VGAM2338 is therefore inhibition of Proline-rich Gla (G-carboxyglutamic acid) Polypeptide 1 (PRRG1, Accession NM_000950). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRRG1.

SEC14-like 1 (S. cerevisiae) (SEC14L1, Accession NM_003003) is another VGAM2338 host target gene. SEC14L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC14L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC14L1 BINDING SITE, designated SEQ ID:8908, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79425] Another function of VGAM2338 is therefore inhibition of SEC14-like 1 (S. cerevisiae) (SEC14L1, Accession NM_003003). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC14L1. Sideroflexin 5 (SFXN5, Accession NM_144579) is another VGAM2338 host target gene. SFXN5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFXN5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFXN5 BINDING SITE, des-

ignated SEQ ID:29387, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79426] Another function of VGAM2338 is therefore inhibition of Sideroflexin 5 (SFXN5, Accession NM_144579). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN5. Unc-5 Homolog D (C. elegans) (UNC5D, Accession NM_080872) is another VGAM2338 host target gene. UNC5D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UNC5D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UNC5D BINDING SITE, designated SEQ ID:28111, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79427] Another function of VGAM2338 is therefore inhibition of Unc-5 Homolog D (C. elegans) (UNC5D, Accession NM_080872). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC5D. LOC122553

(Accession XM_058630) is another VGAM2338 host target gene. LOC122553 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC122553, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122553 BINDING SITE, designated SEQ ID:36688, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79428] Another function of VGAM2338 is therefore inhibition of LOC122553 (Accession XM_058630). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122553. LOC126823 (Accession XM_059086) is another VGAM2338 host target gene. LOC126823 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC126823, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126823 BINDING SITE, designated SEQ ID:36864, to the nucleotide sequence of VGAM2338 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5049.

[79429] Another function of VGAM2338 is therefore inhibition of LOC126823 (Accession XM_059086). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126823. LOC132338 (Accession XM_067793) is another VGAM2338 host target gene. LOC132338 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC132338, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132338 BINDING SITE, designated SEQ ID:37368, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79430] Another function of VGAM2338 is therefore inhibition of LOC132338 (Accession XM_067793). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132338. LOC146774 (Accession XM_085584) is another VGAM2338 host target gene. LOC146774 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146774, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146774 BINDING SITE, designated SEQ ID:38233, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79431] Another function of VGAM2338 is therefore inhibition of LOC146774 (Accession XM_085584). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146774. LOC149577 (Accession XM_097675) is another VGAM2338 host target gene. LOC149577 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149577 BINDING SITE, designated SEQ ID:41021, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79432] Another function of VGAM2338 is therefore inhibition of LOC149577 (Accession XM_097675). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC149577. LOC158288 (Accession XM_098912) is another VGAM2338 host target gene. LOC158288 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158288 BINDING SITE, designated SEQ ID:41928, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79433] Another function of VGAM2338 is therefore inhibition of LOC158288 (Accession XM_098912). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158288. LOC163231 (Accession XM_092094) is another VGAM2338 host target gene. LOC163231 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC163231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163231 BINDING SITE, designated SEQ ID:40098, to

the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79434] Another function of VGAM2338 is therefore inhibition of LOC163231 (Accession XM_092094). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163231. LOC255742 (Accession XM_171617) is another VGAM2338 host target gene. LOC255742 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255742, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255742 BINDING SITE, designated SEQ ID:46054, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79435] Another function of VGAM2338 is therefore inhibition of LOC255742 (Accession XM_171617). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255742. LOC85414 (Accession NM_033102) is another VGAM2338 host target gene. LOC85414 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC85414, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC85414 BINDING SITE, designated SEQ ID:26948, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79436] Another function of VGAM2338 is therefore inhibition of LOC85414 (Accession NM_033102). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC85414. LOC90268 (Accession XM_030424) is another VGAM2338 host target gene. LOC90268 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90268, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90268 BINDING SITE, designated SEQ ID:31040, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79437] Another function of VGAM2338 is therefore inhibition of LOC90268 (Accession XM_030424). Accordingly, utilities

of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90268. LOC91801 (Accession NM_138775) is another VGAM2338 host target gene. LOC91801 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91801, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91801 BINDING SITE, designated SEQ ID:29008, to the nucleotide sequence of VGAM2338 RNA, herein designated VGAM RNA, also designated SEQ ID:5049.

[79438] Another function of VGAM2338 is therefore inhibition of LOC91801 (Accession NM_138775). Accordingly, utilities of VGAM2338 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91801. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2339 (VGAM2339) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79439] VGAM2339 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2339 was detected is described hereinabove with reference to Figs. 1-8.

[79440] VGAM2339 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2339 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79441] VGAM2339 gene encodes a VGAM2339 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2339 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2339 precursor RNA is designated SEQ ID:2325, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2325 is located at position 42978 relative to the genome of Equine Herpesvirus 2.

[79442] VGAM2339 precursor RNA folds onto itself, forming VGAM2339 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79443] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2339 folded precursor RNA into VGAM2339 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 60%) nucleotide sequence of VGAM2339 RNA is designated SEQ ID:5050, and is provided hereinbelow with reference to the sequence listing part.

[79444] VGAM2339 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2339 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2339 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[79445] VGAM2339 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2339 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2339 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2339 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2339 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79446] The complementary binding of VGAM2339 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2339 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2339 host target RNA into VGAM2339 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79447] It is appreciated that VGAM2339 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2339 host target genes. The mRNA of each one of this plurality of VGAM2339 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2339 RNA, herein designated VGAM RNA, and which when bound by VGAM2339 RNA causes inhibition of translation of respective one or more VGAM2339 host target proteins.

[79448] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2339 gene, herein designated VGAM GENE, on one or more VGAM2339 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79449] It is yet further appreciated that a function of VGAM2339 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2339 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2339 correlate with, and may be deduced from, the identity of the host target genes which VGAM2339 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79450] Nucleotide sequences of the VGAM2339 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2339 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2339 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2339 are further described hereinbelow with reference to Table 1.

[79451] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2339 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2339 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79452] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2339 gene, herein designated VGAM is inhibition of expression of VGAM2339 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2339 correlate with, and may be deduced from, the identity of the target genes which VGAM2339 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79453] Potassium Inwardly-rectifying Channel, Subfamily J, Member 15 (KCNJ15, Accession NM_002243) is a VGAM2339

host target gene. KCNJ15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNJ15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNJ15 BINDING SITE, designated SEQ ID:8030, to the nucleotide sequence of VGAM2339 RNA, herein designated VGAM RNA, also designated SEQ ID:5050.

[79454] A function of VGAM2339 is therefore inhibition of Potassium Inwardly-rectifying Channel, Subfamily J, Member 15 (KCNJ15, Accession NM_002243). Accordingly, utilities of VGAM2339 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ15. Phosphoprotein Enriched In Astrocytes 15 (PEA15, Accession NM_003768) is another VGAM2339 host target gene. PEA15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PEA15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEA15 BINDING SITE, designated SEQ ID:9846, to the nucleotide sequence of

VGAM2339 RNA, herein designated VGAM RNA, also designated SEQ ID:5050.

[79455] Another function of VGAM2339 is therefore inhibition of Phosphoprotein Enriched In Astrocytes 15 (PEA15, Accession NM_003768), a gene which is a phosphoprotein and involved in glucose uptake. Accordingly, utilities of VGAM2339 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEA15. The function of PEA15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM949.Splicing Factor, Arginine/serine-rich 2, Interacting Protein (SFRS2IP, Accession NM_004719) is another VGAM2339 host target gene. SFRS2IP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SFRS2IP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRS2IP BINDING SITE, designated SEQ ID:11084, to the nucleotide sequence of VGAM2339 RNA, herein designated VGAM RNA, also designated SEQ ID:5050.

[79456] Another function of VGAM2339 is therefore inhibition of

Splicing Factor, Arginine/serine-rich 2, Interacting Protein (SFRS2IP, Accession NM_004719), a gene which plays an essential role in pre-mRNA splicing. Accordingly, utilities of VGAM2339 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRS2IP. The function of SFRS2IP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM700.Surfeit 6 (SURF6, Accession NM_006753) is another VGAM2339 host target gene. SURF6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SURF6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SURF6 BINDING SITE, designated SEQ ID:13609, to the nucleotide sequence of VGAM2339 RNA, herein designated VGAM RNA, also designated SEQ ID:5050.

[79457] Another function of VGAM2339 is therefore inhibition of Surfeit 6 (SURF6, Accession NM_006753). Accordingly, utilities of VGAM2339 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with SURF6. Ubiquitin-conjugating Enzyme E2 Variant 1 (UBE2V1, Accession NM_021988) is another VGAM2339 host target gene. UBE2V1 BINDING SITE1 through UBE2V1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by UBE2V1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE2V1 BINDING SITE1 through UBE2V1 BINDING SITE3, designated SEQ ID:22519, SEQ ID:22766 and SEQ ID:9367 respectively, to the nucleotide sequence of VGAM2339 RNA, herein designated VGAM RNA, also designated SEQ ID:5050.

[79458] Another function of VGAM2339 is therefore inhibition of Ubiquitin-conjugating Enzyme E2 Variant 1 (UBE2V1, Accession NM_021988), a gene which may play a role in signaling for DNA repair. Accordingly, utilities of VGAM2339 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE2V1. The function of UBE2V1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM155.KIAA0217 (Accession XM_040265) is another

VGAM2339 host target gene. KIAA0217 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0217, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0217 BINDING SITE, designated SEQ ID:33275, to the nucleotide sequence of VGAM2339 RNA, herein designated VGAM RNA, also designated SEQ ID:5050.

[79459] Another function of VGAM2339 is therefore inhibition of KIAA0217 (Accession XM_040265). Accordingly, utilities of VGAM2339 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0217. MCF.2 Cell Line Derived Transforming Sequence-like (MCF2L, Accession XM_027516) is another VGAM2339 host target gene. MCF2L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MCF2L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MCF2L BINDING SITE, designated SEQ ID:30507, to the nucleotide sequence of VGAM2339 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5050.

[79460] Another function of VGAM2339 is therefore inhibition of MCF.2 Cell Line Derived Transforming Sequence-like (MCF2L, Accession XM_027516). Accordingly, utilities of VGAM2339 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCF2L. LOC116028 (Accession XM_057225) is another VGAM2339 host target gene. LOC116028 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC116028, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC116028 BINDING SITE, designated SEQ ID:36491, to the nucleotide sequence of VGAM2339 RNA, herein designated VGAM RNA, also designated SEQ ID:5050.

[79461] Another function of VGAM2339 is therefore inhibition of LOC116028 (Accession XM_057225). Accordingly, utilities of VGAM2339 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC116028. LOC149013 (Accession XM_086398) is another VGAM2339 host target gene. LOC149013 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC149013, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149013 BINDING SITE, designated SEQ ID:38631, to the nucleotide sequence of VGAM2339 RNA, herein designated VGAM RNA, also designated SEQ ID:5050.

[79462] Another function of VGAM2339 is therefore inhibition of LOC149013 (Accession XM_086398). Accordingly, utilities of VGAM2339 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149013. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2340 (VGAM2340) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79463] VGAM2340 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2340 was detected is described hereinabove with reference to Figs. 1-8.

[79464] VGAM2340 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Equine Herpesvirus 2. VGAM2340 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79465] VGAM2340 gene encodes a VGAM2340 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2340 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2340 precursor RNA is designated SEQ ID:2326, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2326 is located at position 42263 relative to the genome of Equine Herpesvirus 2.

[79466] VGAM2340 precursor RNA folds onto itself, forming VGAM2340 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79467] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2340 folded precursor RNA into VGAM2340 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2340 RNA is designated SEQ ID:5051, and is provided hereinbelow with reference to the sequence listing part.

[79468] VGAM2340 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2340 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2340 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79469] VGAM2340 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2340 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2340 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2340 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2340 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79470] The complementary binding of VGAM2340 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2340 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2340

host target RNA into VGAM2340 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79471] It is appreciated that VGAM2340 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2340 host target genes. The mRNA of each one of this plurality of VGAM2340 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2340 RNA, herein designated VGAM RNA, and which when bound by VGAM2340 RNA causes inhibition of translation of respective one or more VGAM2340 host target proteins.

[79472] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2340 gene, herein designated VGAM GENE, on one or more VGAM2340 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79473] It is yet further appreciated that a function of VGAM2340 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2340 correlate with, and may be deduced from, the identity of the host target genes which VGAM2340 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79474] Nucleotide sequences of the VGAM2340 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2340 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2340 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2340 are further

described hereinbelow with reference to Table 1.

[79475] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2340 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2340 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79476] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2340 gene, herein designated VGAM is inhibition of expression of VGAM2340 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2340 correlate with, and may be deduced from, the identity of the target genes which VGAM2340 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79477] Kallmann Syndrome 1 Sequence (KAL1, Accession NM_000216) is a VGAM2340 host target gene. KAL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KAL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KAL1 BINDING SITE, designated SEQ ID:5714, to the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, also designated SEQ ID:5051.

[79478] A function of VGAM2340 is therefore inhibition of Kallmann Syndrome 1 Sequence (KAL1, Accession NM_000216). Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KAL1. Platelet-derived Growth Factor Receptor, Beta Polypeptide (PDGFRB, Accession XM_038350) is another VGAM2340 host target gene. PDGFRB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDGFRB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDGFRB BINDING SITE, designated SEQ ID:32816, to the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, also designated SEQ ID:5051.

[79479] Another function of VGAM2340 is therefore inhibition of Platelet-derived Growth Factor Receptor, Beta Polypeptide (PDGFRB, Accession XM_038350), a gene which Platelet-derived growth factor receptor beta chain; tyrosine kinase

receptor. Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDGFRB. The function of PDGFRB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM125.PTPN13-like, Y-linked (PRY, Accession XM_013161) is another VGAM2340 host target gene. PRY BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRY, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRY BINDING SITE, designated SEQ ID:30233, to the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, also designated SEQ ID:5051.

[79480] Another function of VGAM2340 is therefore inhibition of PTPN13-like, Y-linked (PRY, Accession XM_013161), a gene which may act as a protein tyrosine phosphatase . Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRY. The function of PRY and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to VGAM2280.Wingless-type MMTV Integration Site Family, Member 8B (WNT8B, Accession XM_005702) is another VGAM2340 host target gene. WNT8B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WNT8B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT8B BINDING SITE, designated SEQ ID:29982, to the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, also designated SEQ ID:5051.

[79481] Another function of VGAM2340 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 8B (WNT8B, Accession XM_005702), a gene which is the ligand for members of the frizzled family of seven transmembrane receptors and may play an important role in the development and differentiation of certain forebrain structures. Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WNT8B. The function of WNT8B and its association with various diseases and clinical con-

ditions, has been established by previous studies, as described hereinabove with reference to VGAM636.DKFZP547L112 (Accession XM_039353) is another VGAM2340 host target gene. DKFZP547L112 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP547L112, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP547L112 BINDING SITE, designated SEQ ID:33054, to the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, also designated SEQ ID:5051.

[79482] Another function of VGAM2340 is therefore inhibition of DKFZP547L112 (Accession XM_039353). Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP547L112. FLJ20694 (Accession NM_017928) is another VGAM2340 host target gene. FLJ20694 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20694, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of FLJ20694 BINDING SITE, designated SEQ ID:19604, to the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, also designated SEQ ID:5051.

[79483] Another function of VGAM2340 is therefore inhibition of FLJ20694 (Accession NM_017928). Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20694. KIAA1169 (Accession NM_017901) is another VGAM2340 host target gene. KIAA1169 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1169, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1169 BINDING SITE, designated SEQ ID:19567, to the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, also designated SEQ ID:5051.

[79484] Another function of VGAM2340 is therefore inhibition of KIAA1169 (Accession NM_017901). Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1169. KIAA1817 (Accession XM_042978) is another

VGAM2340 host target gene. KIAA1817 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1817, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1817 BINDING SITE, designated SEQ ID:33860, to the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, also designated SEQ ID:5051.

[79485] Another function of VGAM2340 is therefore inhibition of KIAA1817 (Accession XM_042978). Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1817. Lipoma HMGIC Fusion Partner-like 2 (LHFPL2, Accession XM_046054) is another VGAM2340 host target gene. LHFPL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LHFPL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LHFPL2 BINDING SITE, designated SEQ ID:34657, to the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, also designated SEQ

ID:5051.

[79486] Another function of VGAM2340 is therefore inhibition of Lipoma HMGIC Fusion Partner-like 2 (LHFPL2, Accession XM_046054). Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHFPL2. Nuclear Receptor Subfamily 2, Group F, Member 1 (NR2F1, Accession XM_171117) is another VGAM2340 host target gene. NR2F1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NR2F1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR2F1 BINDING SITE, designated SEQ ID:45915, to the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, also designated SEQ ID:5051.

[79487] Another function of VGAM2340 is therefore inhibition of Nuclear Receptor Subfamily 2, Group F, Member 1 (NR2F1, Accession XM_171117). Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR2F1. LOC159160 (Accession XM_018413) is another

VGAM2340 host target gene. LOC159160 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC159160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159160 BINDING SITE, designated SEQ ID:30357, to the nucleotide sequence of VGAM2340 RNA, herein designated VGAM RNA, also designated SEQ ID:5051.

[79488] Another function of VGAM2340 is therefore inhibition of LOC159160 (Accession XM_018413). Accordingly, utilities of VGAM2340 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159160. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2341 (VGAM2341) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79489] VGAM2341 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2341 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[79490] VGAM2341 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2341 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79491] VGAM2341 gene encodes a VGAM2341 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2341 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2341 precursor RNA is designated SEQ ID:2327, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2327 is located at position 38415 relative to the genome of Equine Herpesvirus 2.

[79492] VGAM2341 precursor RNA folds onto itself, forming VGAM2341 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79493] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2341 folded precursor RNA into VGAM2341 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2341 RNA is designated SEQ ID:5052, and is provided hereinbelow with reference to the sequence listing part.

[79494] VGAM2341 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2341 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2341 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79495] VGAM2341 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2341 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2341 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2341 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2341 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79496] The complementary binding of VGAM2341 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2341 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2341 host target RNA into VGAM2341 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79497] It is appreciated that VGAM2341 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2341 host target genes. The mRNA of each one of this plurality of VGAM2341 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2341 RNA, herein designated VGAM RNA, and which when bound by VGAM2341 RNA causes inhibition of translation of respective one or more VGAM2341 host target proteins.

[79498] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2341 gene, herein designated VGAM GENE, on one or more VGAM2341 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79499] It is yet further appreciated that a function of VGAM2341 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2341

correlate with, and may be deduced from, the identity of the host target genes which VGAM2341 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79500] Nucleotide sequences of the VGAM2341 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2341 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2341 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2341 are further described hereinbelow with reference to Table 1.

[79501] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2341 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2341 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79502] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2341 gene, herein designated VGAM is inhibition of expression of VGAM2341 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2341 correlate with, and may be deduced

from, the identity of the target genes which VGAM2341 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79503] Adenylate Cyclase 6 (ADCY6, Accession NM_020983) is a VGAM2341 host target gene. ADCY6 BINDING SITE1 and ADCY6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ADCY6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADCY6 BINDING SITE1 and ADCY6 BINDING SITE2, designated SEQ ID:21973 and SEQ ID:17585 respectively, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79504] A function of VGAM2341 is therefore inhibition of Adenylate Cyclase 6 (ADCY6, Accession NM_020983), a gene which this a membrane-bound, ca(2+)-inhibitable adenylyl cyclase (by similarity). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADCY6. The function of ADCY6 and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to VGAM22.Contactin 3 (plasmacytoma associated) (CNTN3, Accession XM_039627) is another VGAM2341 host target gene. CNTN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNTN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNTN3 BINDING SITE, designated SEQ ID:33134, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79505] Another function of VGAM2341 is therefore inhibition of Contactin 3 (plasmacytoma associated) (CNTN3, Accession XM_039627), a gene which may play a role in the initial growth and guidance of axons. Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNTN3. The function of CNTN3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM420.Dual Adaptor of Phosphotyrosine and 3-phosphoinositides (DAPP1, Accession NM_014395) is

another VGAM2341 host target gene. DAPP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DAPP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAPP1 BINDING SITE, designated SEQ ID:15733, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79506] Another function of VGAM2341 is therefore inhibition of Dual Adaptor of Phosphotyrosine and 3-phosphoinositides (DAPP1, Accession NM_014395), a gene which regulates the ras-cyclic amp pathway. Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAPP1. The function of DAPP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM283.Integrin, Alpha 6 (ITGA6, Accession NM_000210) is another VGAM2341 host target gene. ITGA6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGA6, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA6 BINDING SITE, designated SEQ ID:5705, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79507] Another function of VGAM2341 is therefore inhibition of Integrin, Alpha 6 (ITGA6, Accession NM_000210). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA6. Phosphoenolpyruvate Carboxykinase 1 (soluble) (PCK1, Accession XM_009672) is another VGAM2341 host target gene. PCK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCK1 BINDING SITE, designated SEQ ID:30116, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79508] Another function of VGAM2341 is therefore inhibition of Phosphoenolpyruvate Carboxykinase 1 (soluble) (PCK1,

Accession XM_009672), a gene which forms phosphoenolpyruvate by decarboxylation of oxaloacetate. Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCK1. The function of PCK1 has been established by previous studies. Yu et al. (1993) used primers derived from the rat liver PEPCK sequence to amplify a portion of the human liver cDNA and to screen a YAC library of human genomic DNA. The sequences of human and rat PEPCK cDNA differed at 16% of the nucleotides compared. From the nucleotide sequence of a cDNA, Stoffel et al. (1993) determined that the PEPCK1 gene product is a protein of 622 amino acids whose sequence shows 90% identity with that of the cognate rat enzyme. Animal model experiments lend further support to the function of PCK1. Olswang et al. (2002) found that an induced mutation in the binding site for peroxisome proliferator-activated receptor-gamma (PPARG; 601487), which is called the PPAR element (PPARE), in the Pepckc gene reduced adipose tissue size and fat content in mice. The mutation abolished expression of the Pepckc gene in white adipose tissue and considerably reduced its expression in brown adipose tissue, whereas the level of cytoplasmic Pepckc

mRNA in liver and kidney remained normal. Epididymal white adipose tissue from these mice had a reduced triglyceride deposition, whereas 25% of the animals displayed lipodystrophy. There was also a greatly reduced level of lipid accumulation in brown adipose tissue. A strong correlation between the hepatic content of triglycerides and the size of the epididymal fat pad in PPARE -/- mice suggested that hepatic triglyceride synthesis predominantly utilizes free fatty acids derived from the adipose tissue. Unlike other models, PPARE -/- mice with lipodystrophy did not exhibit the lipodystrophy-associated features of diabetes and displayed only moderate hyperglycemia. These studies established the importance of the PPARE site for PEPCKC gene expression in adipose tissue and the role of PEPCKC in the regulation of glyceroneogenesis, a pathway critical for maintaining the deposition of triglycerides in adipose tissue.

[79509] It is appreciated that the abovementioned animal model for PCK1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[79510] Full details of the abovementioned studies are described in the following publications, the disclosure of which are

hereby incorporated by reference:

[79511] Olswang, Y.; Cohen, H.; Papo, O.; Cassuto, H.; Croniger, C. M.; Hakimi, P.; Tilghman, S. M.; Hanson, R. W.; Reshef, L. : A mutation in the peroxisome proliferator-activated receptor gamma-binding site in the gene for the cytosolic form of phosphoenolpyruvate carboxykinase reduces adipose tissue size and fat content in mice. Proc. Nat. Acad. Sci. 99: 625-630, 2002. ; and

[79512] Yu, H.; Thun, R.; Chandrasekharappa, S.; Trent, J. M.; Zhang, J.; Meisler, M. H. : Human PCK1 encoding phosphoenolpyruvate carboxykinase is located on chromosome 20q13.2. Genomics 15: 2.

[79513] Further studies establishing the function and utilities of PCK1 are found in John Hopkins OMIM database record ID 261680, and in sited publications numbered 9409, 9413-941 and 9414-9415 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Thymine-DNA Glycosylase (TDG, Accession NM_003211) is another VGAM2341 host target gene. TDG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TDG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of TDG BINDING SITE, designated SEQ ID:9207, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79514] Another function of VGAM2341 is therefore inhibition of Thymine-DNA Glycosylase (TDG, Accession NM_003211), a gene which excises uracil and thymine from mispairs with guanidine. Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TDG. The function of TDG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM196.Zinc Finger Protein 80 (pT17) (ZNF80, Accession NM_007136) is another VGAM2341 host target gene. ZNF80 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF80, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF80 BINDING SITE, designated SEQ ID:13984, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79515] Another function of VGAM2341 is therefore inhibition of Zinc Finger Protein 80 (pT17) (ZNF80, Accession NM_007136). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF80. Butyrophilin, Subfamily 2, Member A2 (BTN2A2, Accession NM_006995) is another VGAM2341 host target gene. BTN2A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTN2A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTN2A2 BINDING SITE, designated SEQ ID:13860, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79516] Another function of VGAM2341 is therefore inhibition of Butyrophilin, Subfamily 2, Member A2 (BTN2A2, Accession NM_006995). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN2A2. FLJ20288 (Accession NM_024668) is another VGAM2341 host target gene. FLJ20288 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded

by FLJ20288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20288 BINDING SITE, designated SEQ ID:23972, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79517] Another function of VGAM2341 is therefore inhibition of FLJ20288 (Accession NM_024668). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20288. KIAA1086 (Accession XM_047610) is another VGAM2341 host target gene. KIAA1086 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1086, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1086 BINDING SITE, designated SEQ ID:35010, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79518] Another function of VGAM2341 is therefore inhibition of KIAA1086 (Accession XM_047610). Accordingly, utilities

of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1086. KIAA1600 (Accession XM_049351) is another VGAM2341 host target gene. KIAA1600 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1600, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1600 BINDING SITE, designated SEQ ID:35396, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79519] Another function of VGAM2341 is therefore inhibition of KIAA1600 (Accession XM_049351). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1600. Phosphodiesterase 3A, CGMP-inhibited (PDE3A, Accession NM_000921) is another VGAM2341 host target gene. PDE3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of PDE3A BINDING SITE, designated SEQ ID:6633, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79520] Another function of VGAM2341 is therefore inhibition of Phosphodiesterase 3A, CGMP-inhibited (PDE3A, Accession NM_000921). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE3A. Rho-related BTB Domain Containing 1 (RHOBTB1, Accession XM_166144) is another VGAM2341 host target gene. RHOBTB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RHOBTB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RHOBTB1 BINDING SITE, designated SEQ ID:43954, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79521] Another function of VGAM2341 is therefore inhibition of Rho-related BTB Domain Containing 1 (RHOBTB1, Accession XM_166144). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with RHOBTB1. Ubiquitin Specific Protease 25 (USP25, Accession NM_013396) is another VGAM2341 host target gene. USP25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP25 BINDING SITE, designated SEQ ID:15050, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79522] Another function of VGAM2341 is therefore inhibition of Ubiquitin Specific Protease 25 (USP25, Accession NM_013396). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP25. LOC147077 (Accession XM_085699) is another VGAM2341 host target gene. LOC147077 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147077, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147077 BINDING SITE, desig-

nated SEQ ID:38291, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79523] Another function of VGAM2341 is therefore inhibition of LOC147077 (Accession XM_085699). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147077. LOC153077 (Accession XM_098307) is another VGAM2341 host target gene. LOC153077 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153077, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153077 BINDING SITE, designated SEQ ID:41572, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79524] Another function of VGAM2341 is therefore inhibition of LOC153077 (Accession XM_098307). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153077. LOC255177 (Accession XM_172941) is another VGAM2341 host target gene. LOC255177 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255177, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255177 BINDING SITE, designated SEQ ID:46204, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79525] Another function of VGAM2341 is therefore inhibition of LOC255177 (Accession XM_172941). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255177. LOC92379 (Accession XM_044712) is another VGAM2341 host target gene. LOC92379 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92379, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92379 BINDING SITE, designated SEQ ID:34269, to the nucleotide sequence of VGAM2341 RNA, herein designated VGAM RNA, also designated SEQ ID:5052.

[79526] Another function of VGAM2341 is therefore inhibition of

LOC92379 (Accession XM_044712). Accordingly, utilities of VGAM2341 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92379. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2342 (VGAM2342) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79527] VGAM2342 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2342 was detected is described hereinabove with reference to Figs. 1-8.

[79528] VGAM2342 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2342 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79529] VGAM2342 gene encodes a VGAM2342 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2342 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2342 precursor RNA is designated SEQ ID:2328, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2328 is located at position 43910 relative to the genome of Equine Herpesvirus 2.

[79530] VGAM2342 precursor RNA folds onto itself, forming VGAM2342 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79531] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2342 folded precursor RNA into VGAM2342 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM2342 RNA is designated SEQ ID:5053, and is provided hereinbelow with reference to the sequence listing part.

[79532] VGAM2342 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2342 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2342 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79533] VGAM2342 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2342 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2342 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2342 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2342 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79534] The complementary binding of VGAM2342 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2342 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2342 host target RNA into VGAM2342 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79535] It is appreciated that VGAM2342 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2342 host target genes. The mRNA of each one of this plurality of VGAM2342 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2342 RNA, herein designated VGAM RNA, and which when bound by VGAM2342 RNA causes inhibition of translation of respective one or more VGAM2342 host target proteins.

[79536] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2342 gene, herein designated VGAM GENE, on one or more VGAM2342 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79537] It is yet further appreciated that a function of VGAM2342

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2342 correlate with, and may be deduced from, the identity of the host target genes which VGAM2342 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79538] Nucleotide sequences of the VGAM2342 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2342 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2342 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2342 are further described hereinbelow with reference to Table 1.

[79539] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2342 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2342 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79540] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2342 gene, herein designated VGAM is inhibition of expression of VGAM2342 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2342 correlate with, and may be deduced from, the identity of the target genes which VGAM2342 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79541] Aldehyde Dehydrogenase 3 Family, Member A2 (ALDH3A2, Accession XM_045060) is a VGAM2342 host target gene. ALDH3A2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ALDH3A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALDH3A2 BINDING SITE, designated SEQ ID:34341, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79542] A function of VGAM2342 is therefore inhibition of Aldehyde Dehydrogenase 3 Family, Member A2 (ALDH3A2, Accession XM_045060). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with ALDH3A2. Mitogen-activated Protein Kinase Kinase Kinase 14 (MAP3K14, Accession NM_003954) is another VGAM2342 host target gene. MAP3K14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K14 BINDING SITE, designated SEQ ID:10092, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79543] Another function of VGAM2342 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 14 (MAP3K14, Accession NM_003954), a gene which is involved in the activation of nf-kappa-b and its transcriptional activity. induces the processing of nf-kappa-b 2/p100. could act in a receptor-selective manner (by similarity). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K14. The function of MAP3K14 and its association with various diseases and clinical conditions, has been established by previous stud-

ies, as described hereinabove with reference to VGAM55.Multiple Endocrine Neoplasia I (MEN1, Accession XM_167804) is another VGAM2342 host target gene. MEN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MEN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEN1 BINDING SITE, designated SEQ ID:44848, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79544] Another function of VGAM2342 is therefore inhibition of Multiple Endocrine Neoplasia I (MEN1, Accession XM_167804). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEN1. Neogenin Homolog 1 (chicken) (NEO1, Accession NM_002499) is another VGAM2342 host target gene. NEO1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NEO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NEO1 BINDING SITE,

designated SEQ ID:8315, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79545] Another function of VGAM2342 is therefore inhibition of Neogenin Homolog 1 (chicken) (NEO1, Accession NM_002499), a gene which regulates the transition of undifferentiated proliferating cells to their differentiated state. Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEO1. The function of NEO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM329.ADMP (Accession NM_145035) is another VGAM2342 host target gene. ADMP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADMP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADMP BINDING SITE, designated SEQ ID:29659, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79546] Another function of VGAM2342 is therefore inhibition of

ADMP (Accession NM_145035). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADMP. Bromodomain Containing 4 (BRD4, Accession NM_058243) is another VGAM2342 host target gene. BRD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BRD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRD4 BINDING SITE, designated SEQ ID:27776, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79547] Another function of VGAM2342 is therefore inhibition of Bromodomain Containing 4 (BRD4, Accession NM_058243). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRD4. DKFZP434B205 (Accession XM_059966) is another VGAM2342 host target gene. DKFZP434B205 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434B205, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434B205 BINDING SITE, designated SEQ ID:37126, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79548] Another function of VGAM2342 is therefore inhibition of DKFZP434B205 (Accession XM_059966). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434B205. DKFZp547O146 (Accession NM_020224) is another VGAM2342 host target gene. DKFZp547O146 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp547O146, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547O146 BINDING SITE, designated SEQ ID:21482, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79549] Another function of VGAM2342 is therefore inhibition of DKFZp547O146 (Accession NM_020224). Accordingly, utilities of VGAM2342 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZp547O146. FLJ10781 (Accession NM_018215) is another VGAM2342 host target gene. FLJ10781 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10781, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10781 BINDING SITE, designated SEQ ID:20135, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79550] Another function of VGAM2342 is therefore inhibition of FLJ10781 (Accession NM_018215). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10781. FLJ12387 (Accession NM_022822) is another VGAM2342 host target gene. FLJ12387 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12387, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12387 BINDING SITE, designated SEQ ID:23101, to the nucleotide

sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79551] Another function of VGAM2342 is therefore inhibition of FLJ12387 (Accession NM_022822). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12387. FLJ14810 (Accession NM_032843) is another VGAM2342 host target gene. FLJ14810 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14810, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14810 BINDING SITE, designated SEQ ID:26633, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79552] Another function of VGAM2342 is therefore inhibition of FLJ14810 (Accession NM_032843). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14810. FLJ22059 (Accession NM_022752) is another VGAM2342 host target gene. FLJ22059 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by FLJ22059, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22059 BINDING SITE, designated SEQ ID:22975, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79553] Another function of VGAM2342 is therefore inhibition of FLJ22059 (Accession NM_022752). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22059. FLJ23462 (Accession NM_024843) is another VGAM2342 host target gene. FLJ23462 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23462, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23462 BINDING SITE, designated SEQ ID:24265, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79554] Another function of VGAM2342 is therefore inhibition of FLJ23462 (Accession NM_024843). Accordingly, utilities of

VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23462. HZFW1 (Accession NM_025236) is another VGAM2342 host target gene. HZFW1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HZFW1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HZFW1 BINDING SITE, designated SEQ ID:24915, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79555] Another function of VGAM2342 is therefore inhibition of HZFW1 (Accession NM_025236). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HZFW1. KIAA0014 (Accession NM_014665) is another VGAM2342 host target gene. KIAA0014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0014 BINDING SITE,

designated SEQ ID:16113, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79556] Another function of VGAM2342 is therefore inhibition of KIAA0014 (Accession NM_014665). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0014. KIAA0237 (Accession NM_014747) is another VGAM2342 host target gene. KIAA0237 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0237, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0237 BINDING SITE, designated SEQ ID:16445, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79557] Another function of VGAM2342 is therefore inhibition of KIAA0237 (Accession NM_014747). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0237. KIAA0514 (Accession NM_014696) is another VGAM2342 host target gene. KIAA0514 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0514, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0514 BINDING SITE, designated SEQ ID:16206, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79558] Another function of VGAM2342 is therefore inhibition of KIAA0514 (Accession NM_014696). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0514. KIAA0672 (Accession NM_014859) is another VGAM2342 host target gene. KIAA0672 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0672, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0672 BINDING SITE, designated SEQ ID:16918, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79559] Another function of VGAM2342 is therefore inhibition of

KIAA0672 (Accession NM_014859). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0672. KIAA1196 (Accession XM_028968) is another VGAM2342 host target gene. KIAA1196 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1196 BINDING SITE, designated SEQ ID:30821, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79560] Another function of VGAM2342 is therefore inhibition of KIAA1196 (Accession XM_028968). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1196. KIAA1468 (Accession XM_166289) is another VGAM2342 host target gene. KIAA1468 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1468, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1468 BINDING SITE, designated SEQ ID:44098, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79561] Another function of VGAM2342 is therefore inhibition of KIAA1468 (Accession XM_166289). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1468. KIAA1762 (Accession XM_033370) is another VGAM2342 host target gene. KIAA1762 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1762, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1762 BINDING SITE, designated SEQ ID:31911, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79562] Another function of VGAM2342 is therefore inhibition of KIAA1762 (Accession XM_033370). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1762. Leucine-rich Repeat LGI Family, Member 3

(LGI3, Accession NM_139278) is another VGAM2342 host target gene. LGI3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LGI3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LGI3 BINDING SITE, designated SEQ ID:29277, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79563] Another function of VGAM2342 is therefore inhibition of Leucine-rich Repeat LGI Family, Member 3 (LGI3, Accession NM_139278). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LGI3. MGC13170 (Accession NM_032712) is another VGAM2342 host target gene. MGC13170 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC13170, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13170 BINDING SITE, designated SEQ ID:26434, to the nucleotide sequence of

VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79564] Another function of VGAM2342 is therefore inhibition of MGC13170 (Accession NM_032712). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13170. RI58 (Accession NM_012420) is another VGAM2342 host target gene. RI58 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RI58, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RI58 BINDING SITE, designated SEQ ID:14795, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79565] Another function of VGAM2342 is therefore inhibition of RI58 (Accession NM_012420). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RI58. SP329 (Accession NM_030793) is another VGAM2342 host target gene. SP329 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded

by SP329, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SP329 BINDING SITE, designated SEQ ID:25096, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79566] Another function of VGAM2342 is therefore inhibition of SP329 (Accession NM_030793). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SP329. UBCE7IP5 (Accession NM_014948) is another VGAM2342 host target gene. UBCE7IP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UBCE7IP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBCE7IP5 BINDING SITE, designated SEQ ID:17270, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79567] Another function of VGAM2342 is therefore inhibition of UBCE7IP5 (Accession NM_014948). Accordingly, utilities of

VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBCE7IP5. LOC123591 (Accession XM_063741) is another VGAM2342 host target gene. LOC123591 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC123591, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC123591 BINDING SITE, designated SEQ ID:37252, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79568] Another function of VGAM2342 is therefore inhibition of LOC123591 (Accession XM_063741). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC123591. LOC145371 (Accession XM_085123) is another VGAM2342 host target gene. LOC145371 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145371, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC145371 BINDING SITE, designated SEQ ID:37845, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79569] Another function of VGAM2342 is therefore inhibition of LOC145371 (Accession XM_085123). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145371. LOC149478 (Accession XM_086536) is another VGAM2342 host target gene. LOC149478 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149478, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149478 BINDING SITE, designated SEQ ID:38752, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79570] Another function of VGAM2342 is therefore inhibition of LOC149478 (Accession XM_086536). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149478. LOC152762 (Accession XM_087518) is another VGAM2342 host target gene. LOC152762 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152762, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152762 BINDING SITE, designated SEQ ID:39306, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79571] Another function of VGAM2342 is therefore inhibition of LOC152762 (Accession XM_087518). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152762. LOC153516 (Accession NM_138491) is another VGAM2342 host target gene. LOC153516 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153516 BINDING SITE, designated SEQ ID:28841, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79572] Another function of VGAM2342 is therefore inhibition of

LOC153516 (Accession NM_138491). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153516. LOC163412 (Accession XM_088868) is another VGAM2342 host target gene. LOC163412 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC163412, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163412 BINDING SITE, designated SEQ ID:39952, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79573] Another function of VGAM2342 is therefore inhibition of LOC163412 (Accession XM_088868). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163412. LOC222182 (Accession XM_168471) is another VGAM2342 host target gene. LOC222182 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222182, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC222182 BINDING SITE, designated SEQ ID:45196, to the nucleotide sequence of VGAM2342 RNA, herein designated VGAM RNA, also designated SEQ ID:5053.

[79574] Another function of VGAM2342 is therefore inhibition of LOC222182 (Accession XM_168471). Accordingly, utilities of VGAM2342 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222182. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2343 (VGAM2343) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79575] VGAM2343 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2343 was detected is described hereinabove with reference to Figs. 1-8.

[79576] VGAM2343 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2343 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[79577] VGAM2343 gene encodes a VGAM2343 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2343 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2343 precursor RNA is designated SEQ ID:2329, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2329 is located at position 43126 relative to the genome of Equine Herpesvirus 2.

[79578] VGAM2343 precursor RNA folds onto itself, forming VGAM2343 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79579] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2343 folded precursor RNA into VGAM2343 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2343 RNA is designated SEQ ID:5054, and is provided hereinbelow with reference to the sequence listing part.

[79580] VGAM2343 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2343 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2343 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79581] VGAM2343 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2343 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2343 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2343 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2343 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79582] The complementary binding of VGAM2343 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2343 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2343 host target RNA into VGAM2343 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79583] It is appreciated that VGAM2343 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2343 host target genes. The mRNA of each one of this plurality of VGAM2343 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2343 RNA, herein designated VGAM RNA, and which when bound by VGAM2343 RNA causes inhibition of translation of respective one or more VGAM2343 host target proteins.

[79584] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2343 gene, herein designated VGAM GENE, on one or more VGAM2343 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79585] It is yet further appreciated that a function of VGAM2343 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2343 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2343 correlate with, and may be deduced from, the identity of the host target genes which VGAM2343 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79586] Nucleotide sequences of the VGAM2343 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2343 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2343 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2343 are further described hereinbelow with reference to Table 1.

[79587] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2343 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2343 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79588] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2343 gene, herein designated VGAM is inhibition of expression of VGAM2343 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2343 correlate with, and may be deduced from, the identity of the target genes which VGAM2343 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79589] CDT6 (Accession NM_021146) is a VGAM2343 host target gene. CDT6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CDT6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDT6 BINDING SITE, designated SEQ ID:22119, to the nucleotide sequence of VGAM2343 RNA, herein designated VGAM RNA, also designated SEQ ID:5054.

[79590] A function of VGAM2343 is therefore inhibition of CDT6

(Accession NM_021146). Accordingly, utilities of VGAM2343 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDT6. P114-RHO-GEF (Accession NM_015318) is another VGAM2343 host target gene. P114-RHO-GEF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P114-RHO-GEF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P114-RHO-GEF BINDING SITE, designated SEQ ID:17637, to the nucleotide sequence of VGAM2343 RNA, herein designated VGAM RNA, also designated SEQ ID:5054.

[79591] Another function of VGAM2343 is therefore inhibition of P114-RHO-GEF (Accession NM_015318). Accordingly, utilities of VGAM2343 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P114-RHO-GEF. ZFD25 (Accession NM_016220) is another VGAM2343 host target gene. ZFD25 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZFD25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZFD25 BINDING SITE, designated SEQ ID:18321, to the nucleotide sequence of VGAM2343 RNA, herein designated VGAM RNA, also designated SEQ ID:5054.

[79592] Another function of VGAM2343 is therefore inhibition of ZFD25 (Accession NM_016220). Accordingly, utilities of VGAM2343 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFD25. LOC151414 (Accession XM_087197) is another VGAM2343 host target gene. LOC151414 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151414, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151414 BINDING SITE, designated SEQ ID:39107, to the nucleotide sequence of VGAM2343 RNA, herein designated VGAM RNA, also designated SEQ ID:5054.

[79593] Another function of VGAM2343 is therefore inhibition of LOC151414 (Accession XM_087197). Accordingly, utilities of VGAM2343 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC151414. LOC90550 (Accession XM_054582) is another VGAM2343 host target gene. LOC90550 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90550, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90550 BINDING SITE, designated SEQ ID:36176, to the nucleotide sequence of VGAM2343 RNA, herein designated VGAM RNA, also designated SEQ ID:5054.

[79594] Another function of VGAM2343 is therefore inhibition of LOC90550 (Accession XM_054582). Accordingly, utilities of VGAM2343 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90550. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2344 (VGAM2344) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79595] VGAM2344 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2344 was detected is described hereinabove with reference to Figs. 1-8.

[79596] VGAM2344 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2344 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79597] VGAM2344 gene encodes a VGAM2344 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2344 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2344 precursor RNA is designated SEQ ID:2330, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2330 is located at position 38540 relative to the genome of Equine Herpesvirus 2.

[79598] VGAM2344 precursor RNA folds onto itself, forming VGAM2344 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79599] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2344 folded precursor RNA into VGAM2344 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 92%) nucleotide sequence of VGAM2344 RNA is designated SEQ ID:5055, and is provided hereinbelow with reference to the sequence listing part.

[79600] VGAM2344 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2344 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2344 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79601] VGAM2344 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2344 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2344 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2344 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2344 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79602] The complementary binding of VGAM2344 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2344 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2344 host target RNA into VGAM2344 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79603] It is appreciated that VGAM2344 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2344 host target genes. The mRNA of each one of this plurality of VGAM2344 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2344 RNA, herein designated VGAM RNA, and which when bound by VGAM2344 RNA causes inhibition of translation of respective one or more VGAM2344 host target proteins.

[79604] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2344 gene, herein designated VGAM GENE, on one or more VGAM2344 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79605] It is yet further appreciated that a function of VGAM2344 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2344 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2344 correlate with, and may be deduced from, the identity of the host target genes which VGAM2344 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79606] Nucleotide sequences of the VGAM2344 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2344 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2344 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2344 are further described hereinbelow with reference to Table 1.

[79607] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2344 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2344 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79608] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2344 gene, herein designated VGAM is inhibition of expression of VGAM2344 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2344 correlate with, and may be deduced from, the identity of the target genes which VGAM2344 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79609] Dual Adaptor of Phosphotyrosine and 3-phosphoinositides (DAPP1, Accession NM_014395) is a VGAM2344 host target gene. DAPP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by DAPP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAPP1 BINDING SITE, designated SEQ ID:15730, to the nucleotide sequence of VGAM2344 RNA, herein designated VGAM RNA, also designated SEQ ID:5055.

[79610] A function of VGAM2344 is therefore inhibition of Dual Adaptor of Phosphotyrosine and 3-phosphoinositides (DAPP1, Accession NM_014395), a gene which regulates the ras-cyclic amp pathway. Accordingly, utilities of VGAM2344 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAPP1. The function of DAPP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM283.FLJ23189 (Accession NM_025057) is another VGAM2344 host target gene. FLJ23189 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23189, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23189

BINDING SITE, designated SEQ ID:24657, to the nucleotide sequence of VGAM2344 RNA, herein designated VGAM RNA, also designated SEQ ID:5055.

[79611] Another function of VGAM2344 is therefore inhibition of FLJ23189 (Accession NM_025057). Accordingly, utilities of VGAM2344 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23189. KIAA0063 (Accession NM_014876) is another VGAM2344 host target gene. KIAA0063 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0063, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0063 BINDING SITE, designated SEQ ID:17017, to the nucleotide sequence of VGAM2344 RNA, herein designated VGAM RNA, also designated SEQ ID:5055.

[79612] Another function of VGAM2344 is therefore inhibition of KIAA0063 (Accession NM_014876). Accordingly, utilities of VGAM2344 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0063. KIAA0802 (Accession XM_031357) is another VGAM2344 host target gene. KIAA0802 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0802, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0802 BINDING SITE, designated SEQ ID:31351, to the nucleotide sequence of VGAM2344 RNA, herein designated VGAM RNA, also designated SEQ ID:5055.

[79613] Another function of VGAM2344 is therefore inhibition of KIAA0802 (Accession XM_031357). Accordingly, utilities of VGAM2344 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0802. KIAA1560 (Accession XM_034422) is another VGAM2344 host target gene. KIAA1560 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1560, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1560 BINDING SITE, designated SEQ ID:32101, to the nucleotide sequence of VGAM2344 RNA, herein designated VGAM RNA, also designated SEQ ID:5055.

[79614] Another function of VGAM2344 is therefore inhibition of

KIAA1560 (Accession XM_034422). Accordingly, utilities of VGAM2344 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1560. Solute Carrier Family 25 (mitochondrial oxodicarboxylate carrier), Member 21 (SLC25A21, Accession NM_030631) is another VGAM2344 host target gene. SLC25A21 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC25A21, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC25A21 BINDING SITE, designated SEQ ID:24967, to the nucleotide sequence of VGAM2344 RNA, herein designated VGAM RNA, also designated SEQ ID:5055.

[79615] Another function of VGAM2344 is therefore inhibition of Solute Carrier Family 25 (mitochondrial oxodicarboxylate carrier), Member 21 (SLC25A21, Accession NM_030631). Accordingly, utilities of VGAM2344 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC25A21. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here

as Viral Genomic Address Messenger 2345 (VGAM2345) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79616] VGAM2345 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2345 was detected is described hereinabove with reference to Figs. 1-8.

[79617] VGAM2345 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2345 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79618] VGAM2345 gene encodes a VGAM2345 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2345 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2345 precursor RNA is designated SEQ ID:2331, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2331 is located at position 41319 relative to the genome of Equine Herpesvirus 2.

[79619] VGAM2345 precursor RNA folds onto itself, forming VGAM2345 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79620] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2345 folded precursor RNA into VGAM2345 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2345 RNA is designated SEQ ID:5056, and is provided hereinbelow with reference to the sequence listing part.

[79621] VGAM2345 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2345 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2345 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79622] VGAM2345 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2345 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2345 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2345 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2345 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79623] The complementary binding of VGAM2345 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2345 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2345 host target RNA into VGAM2345 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79624] It is appreciated that VGAM2345 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2345 host target genes. The mRNA of each one of this plurality of VGAM2345 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2345 RNA, herein designated VGAM RNA, and which when bound by VGAM2345 RNA causes inhibition of translation of respective one or more VGAM2345 host target proteins.

[79625] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2345 gene, herein designated VGAM GENE, on one or more VGAM2345 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79626] It is yet further appreciated that a function of VGAM2345 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2345 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2345 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79627] Nucleotide sequences of the VGAM2345 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2345 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2345 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2345 are further described hereinbelow with reference to Table 1.

[79628] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2345 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2345 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79629] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2345 gene, herein designated VGAM is inhibition of expression of VGAM2345 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2345 correlate with, and may be deduced from, the identity of the target genes which VGAM2345

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79630] Ets Variant Gene 3 (ETV3, Accession NM_005240) is a VGAM2345 host target gene. ETV3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ETV3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ETV3 BINDING SITE, designated SEQ ID:11750, to the nucleotide sequence of VGAM2345 RNA, herein designated VGAM RNA, also designated SEQ ID:5056.

[79631] A function of VGAM2345 is therefore inhibition of Ets Variant Gene 3 (ETV3, Accession NM_005240), a gene which Member of the ETS oncoprotein family. Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ETV3. The function of ETV3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM791.Nuclear Receptor Subfamily 5, Group A, Member 2 (NR5A2, Accession NM_003822) is another VGAM2345 host target gene. NR5A2 BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NR5A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR5A2 BINDING SITE, designated SEQ ID:9912, to the nucleotide sequence of VGAM2345 RNA, herein designated VGAM RNA, also designated SEQ ID:5056.

[79632] Another function of VGAM2345 is therefore inhibition of Nuclear Receptor Subfamily 5, Group A, Member 2 (NR5A2, Accession NM_003822), a gene which is a member of nuclear receptor superfamily of trancriptional activators and activates the hepatitis B virus (HBV) promoter. Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR5A2. The function of NR5A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM375.Uncoupling Protein 3 (mitochondrial, proton carrier) (UCP3, Accession NM_003356) is another VGAM2345 host target gene. UCP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by UCP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UCP3 BINDING SITE, designated SEQ ID:9383, to the nucleotide sequence of VGAM2345 RNA, herein designated VGAM RNA, also designated SEQ ID:5056.

[79633] Another function of VGAM2345 is therefore inhibition of Uncoupling Protein 3 (mitochondrial, proton carrier) (UCP3, Accession NM_003356), a gene which is a mitochondrial transporter protein that creates proton leaks across the inner mitochondrial membrane, thus uncoupling oxidative phosphorylation. Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UCP3. The function of UCP3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1317.DKFZp762K2015 (Accession XM_051791) is another VGAM2345 host target gene. DKFZp762K2015 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp762K2015, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp762K2015 BINDING SITE, designated SEQ ID:35884, to the nucleotide sequence of VGAM2345 RNA, herein designated VGAM RNA, also designated SEQ ID:5056.

[79634] Another function of VGAM2345 is therefore inhibition of DKFZp762K2015 (Accession XM_051791). Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762K2015. FLJ13340 (Accession NM_057175) is another VGAM2345 host target gene. FLJ13340 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13340, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13340 BINDING SITE, designated SEQ ID:27703, to the nucleotide sequence of VGAM2345 RNA, herein designated VGAM RNA, also designated SEQ ID:5056.

[79635] Another function of VGAM2345 is therefore inhibition of FLJ13340 (Accession NM_057175). Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ13340. HTEX4 (Accession XM_166378) is another VGAM2345 host target gene. HTEX4 BINDING SITE1 through HTEX4 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HTEX4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HTEX4 BINDING SITE1 through HTEX4 BINDING SITE3, designated SEQ ID:44215, SEQ ID:46651 and SEQ ID:46720 respectively, to the nucleotide sequence of VGAM2345 RNA, herein designated VGAM RNA, also designated SEQ ID:5056.

[79636] Another function of VGAM2345 is therefore inhibition of HTEX4 (Accession XM_166378). Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTEX4. TBDN100 (Accession NM_025085) is another VGAM2345 host target gene. TBDN100 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBDN100, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of TBDN100 BINDING SITE, designated SEQ ID:24692, to the nucleotide sequence of VGAM2345 RNA, herein designated VGAM RNA, also designated SEQ ID:5056.

[79637] Another function of VGAM2345 is therefore inhibition of TBDN100 (Accession NM_025085). Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBDN100. TU3A (Accession NM_007177) is another VGAM2345 host target gene. TU3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TU3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TU3A BINDING SITE, designated SEQ ID:14031, to the nucleotide sequence of VGAM2345 RNA, herein designated VGAM RNA, also designated SEQ ID:5056.

[79638] Another function of VGAM2345 is therefore inhibition of TU3A (Accession NM_007177). Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TU3A. ZNF-U69274 (Accession NM_014415) is another

VGAM2345 host target gene. ZNF-U69274 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF-U69274, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF-U69274 BINDING SITE, designated SEQ ID:15761, to the nucleotide sequence of VGAM2345 RNA, herein designated VGAM RNA, also designated SEQ ID:5056.

[79639] Another function of VGAM2345 is therefore inhibition of ZNF-U69274 (Accession NM_014415). Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF-U69274. LOC201627 (Accession XM_114353) is another VGAM2345 host target gene. LOC201627 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201627, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201627 BINDING SITE, designated SEQ ID:42893, to the nucleotide sequence of VGAM2345 RNA, herein designated VGAM RNA, also designated SEQ ID:5056.

[79640] Another function of VGAM2345 is therefore inhibition of LOC201627 (Accession XM_114353). Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201627. LOC255777 (Accession XM_171342) is another VGAM2345 host target gene. LOC255777 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255777, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255777 BINDING SITE, designated SEQ ID:46041, to the nucleotide sequence of VGAM2345 RNA, herein designated VGAM RNA, also designated SEQ ID:5056.

[79641] Another function of VGAM2345 is therefore inhibition of LOC255777 (Accession XM_171342). Accordingly, utilities of VGAM2345 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255777. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2346 (VGAM2346) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[79642] VGAM2346 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2346 was detected is described hereinabove with reference to Figs. 1-8.

[79643] VGAM2346 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2346 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79644] VGAM2346 gene encodes a VGAM2346 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2346 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2346 precursor RNA is designated SEQ ID:2332, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2332 is located at position 38013 relative to the genome of Equine Herpesvirus 2.

[79645] VGAM2346 precursor RNA folds onto itself, forming VGAM2346 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79646] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2346 folded precursor RNA into VGAM2346 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2346 RNA is designated SEQ ID:5057, and is provided hereinbelow with reference to the sequence listing part.

[79647] VGAM2346 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2346 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2346 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79648] VGAM2346 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2346 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2346 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2346 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2346 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79649] The complementary binding of VGAM2346 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2346 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2346 host target RNA into VGAM2346 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79650] It is appreciated that VGAM2346 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2346 host target genes. The mRNA of each one of this plurality of VGAM2346 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2346 RNA, herein designated VGAM RNA, and which when bound by VGAM2346 RNA causes inhibition of translation of respective one or more VGAM2346 host target proteins.

[79651] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2346 gene, herein designated VGAM GENE, on one or more VGAM2346 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79652] It is yet further appreciated that a function of VGAM2346 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2346 correlate with, and may be deduced from, the identity of the host target genes which VGAM2346 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[79653] Nucleotide sequences of the VGAM2346 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2346 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2346 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2346 are further described hereinbelow with reference to Table 1.

[79654] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2346 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2346 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79655] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2346 gene, herein designated VGAM is inhibition of expression of VGAM2346 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2346 correlate with, and may be deduced from, the identity of the target genes which VGAM2346 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79656] Aquaporin 6, Kidney Specific (AQP6, Accession NM_053286) is a VGAM2346 host target gene. AQP6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AQP6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE, designated SEQ ID:27616, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79657] A function of VGAM2346 is therefore inhibition of Aquaporin 6, Kidney Specific (AQP6, Accession NM_053286), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid-base metabolism. Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6. The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM340.Rho GTPase Activating Protein 6 (ARHGAP6, Accession NM_001174) is another VGAM2346 host target gene. ARHGAP6 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by ARHGAP6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGAP6 BINDING SITE, designated SEQ ID:6846, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79658] Another function of VGAM2346 is therefore inhibition of Rho GTPase Activating Protein 6 (ARHGAP6, Accession NM_001174), a gene which activates the rho-type GTPases by converting them to an inactive GTP-bound state. Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP6. The function of ARHGAP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1, Accession NM_001276) is another VGAM2346 host target gene. CHI3L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHI3L1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHI3L1 BINDING SITE, designated SEQ ID:6942, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79659] Another function of VGAM2346 is therefore inhibition of Chitinase 3-like 1 (cartilage glycoprotein-39) (CHI3L1, Accession NM_001276), a gene which participates in the capacity of cells to respond to and cope with changes. Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHI3L1. The function of CHI3L1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1727.Collagen, Type VI, Alpha 3 (COL6A3, Accession NM_057167) is another VGAM2346 host target gene. COL6A3 BINDING SITE1 and COL6A3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by COL6A3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of COL6A3 BINDING SITE1 and COL6A3 BINDING SITE2, designated SEQ ID:27671 and SEQ ID:10587 respectively, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79660] Another function of VGAM2346 is therefore inhibition of Collagen, Type VI, Alpha 3 (COL6A3, Accession NM_057167). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A3. DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 20, 103kDa (DDX20, Accession NM_007204) is another VGAM2346 host target gene. DDX20 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DDX20, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDX20 BINDING SITE, designated SEQ ID:14067, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79661] Another function of VGAM2346 is therefore inhibition of DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 20,

103kDa (DDX20, Accession NM_007204), a gene which interacts with SMN and is required for pre-mRNA splicing in the nucleus. Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX20. The function of DDX20 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1929.Dishevelled, Dsh Homolog 1 (Drosophila) (DVL1, Accession XM_001589) is another VGAM2346 host target gene. DVL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DVL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DVL1 BINDING SITE, designated SEQ ID:29843, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79662] Another function of VGAM2346 is therefore inhibition of Dishevelled, Dsh Homolog 1 (Drosophila) (DVL1, Accession XM_001589), a gene which may play a role in the signal transduction pathway . Accordingly, utilities of

VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DVL1. The function of DVL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM232.Gamma-glutamyltransferase 2 (GGT2, Accession XM_057166) is another VGAM2346 host target gene. GGT2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GGT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GGT2 BINDING SITE, designated SEQ ID:36490, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79663] Another function of VGAM2346 is therefore inhibition of Gamma-glutamyltransferase 2 (GGT2, Accession XM_057166). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGT2. Mannosyl (alpha-1,3-)-glycoprotein Beta-1,2-N-acetylglucosaminyltransferase (MGAT1, Accession NM_002406) is another VGAM2346 host target gene.

MGAT1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGAT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGAT1 BINDING SITE, designated SEQ ID:8227, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79664] Another function of VGAM2346 is therefore inhibition of Mannosyl (alpha-1,3-)-glycoprotein Beta-1,2-N-acetylglucosaminyltransferase (MGAT1, Accession NM_002406), a gene which exists as a single protein-encoding exon. Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGAT1. The function of MGAT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM165.Nuclear Receptor Co-repressor 2 (NCOR2, Accession NM_006312) is another VGAM2346 host target gene. NCOR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

NCOR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOR2 BINDING SITE, designated SEQ ID:13004, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79665] Another function of VGAM2346 is therefore inhibition of Nuclear Receptor Co-repressor 2 (NCOR2, Accession NM_006312), a gene which mediates the transcriptional repression activity of some nuclear receptors by promoting chromatin condensation, thus preventing access of the basal transcription. Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOR2. The function of NCOR2 has been established by previous studies. Fischle et al. (2002) showed that the catalytic domain of HDAC4 (OMIM Ref. No. 605314) interacts with HDAC3 (OMIM Ref. No. 605166) via the transcriptional corepressor NCOR2. All experimental conditions leading to the suppression of HDAC4 binding to NCOR2 and to HDAC3 resulted in loss of enzymatic activity associated with HDAC4. These observations indicated that class II HDACs regulate tran-

scription by bridging the enzymatically active NCOR2-HDAC3 complex and select transcription factors.

[79666] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[79667] Fischle, W.; Dequiedt, F.; Hendzel, M. J.; Guenther, M. G.; Lazar, M. A.; Voelter, W.; Verdin, E. : Enzymatic activity associated with class II HDACs is dependent on a multiprotein complex containing HDAC3 and SMRT/N-CoR. Molec. Cell 9: 45-57, 2002. ; and

[79668] Horlein, A. J.; Naar, A. M.; Heinzel, T.; Torchia, J.; Gloss, B.; Kurokawa, R.; Ryan, A.; Kamel, Y.; Soderstrom, M.; Glass, C. K.; Rosenfeld, M. G. : Ligand-independent repression by t.

[79669] Further studies establishing the function and utilities of NCOR2 are found in John Hopkins OMIM database record ID 600848, and in sited publications numbered 9945-9950 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Phosphomannomutase 2 (PMM2, Accession XM_050755) is another VGAM2346 host target gene. PMM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PMM2,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMM2 BINDING SITE, designated SEQ ID:35681, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79670] Another function of VGAM2346 is therefore inhibition of Phosphomannomutase 2 (PMM2, Accession XM_050755). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMM2. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 8 (PPP1R8, Accession NM_138558) is another VGAM2346 host target gene. PPP1R8 BINDING SITE1 and PPP1R8 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PPP1R8, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R8 BINDING SITE1 and PPP1R8 BINDING SITE2, designated SEQ ID:28854 and SEQ ID:8568 respectively, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM

RNA, also designated SEQ ID:5057.

[79671] Another function of VGAM2346 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 8 (PPP1R8, Accession NM_138558), a gene which is an inhibitor subunit of the major nuclear protein phosphatase-1 (pp-1). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R8. The function of PPP1R8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM101.Chromosome 20 Open Reading Frame 175 (C20orf175, Accession NM_080829) is another VGAM2346 host target gene. C20orf175 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C20orf175, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf175 BINDING SITE, designated SEQ ID:28094, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79672] Another function of VGAM2346 is therefore inhibition of

Chromosome 20 Open Reading Frame 175 (C20orf175, Accession NM_080829). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf175. CUB and Sushi Multiple Domains 1 (CSMD1, Accession NM_033225) is another VGAM2346 host target gene. CSMD1 BINDING SITE1 and CSMD1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CSMD1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSMD1 BINDING SITE1 and CSMD1 BINDING SITE2, designated SEQ ID:27069 and SEQ ID:36187 respectively, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79673] Another function of VGAM2346 is therefore inhibition of CUB and Sushi Multiple Domains 1 (CSMD1, Accession NM_033225). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSMD1. DKFZP564B147 (Accession XM_088745) is another VGAM2346 host target gene. DKFZP564B147 BINDING SITE is HOST TARGET bind-

ing site found in the 5` untranslated region of mRNA encoded by DKFZP564B147, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564B147 BINDING SITE, designated SEQ ID:39935, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79674] Another function of VGAM2346 is therefore inhibition of DKFZP564B147 (Accession XM_088745). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564B147. Dedicator of Cyto-kinesis 3 (DOCK3, Accession XM_039259) is another VGAM2346 host target gene. DOCK3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DOCK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DOCK3 BINDING SITE, designated SEQ ID:33038, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79675] Another function of VGAM2346 is therefore inhibition of Dedicator of Cyto-kinesis 3 (DOCK3, Accession XM_039259). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DOCK3. FLJ13153 (Accession NM_024786) is another VGAM2346 host target gene. FLJ13153 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13153, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13153 BINDING SITE, designated SEQ ID:24166, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79676] Another function of VGAM2346 is therefore inhibition of FLJ13153 (Accession NM_024786). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13153. FLJ14621 (Accession NM_032811) is another VGAM2346 host target gene. FLJ14621 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ14621, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14621 BINDING SITE, designated SEQ ID:26580, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79677] Another function of VGAM2346 is therefore inhibition of FLJ14621 (Accession NM_032811). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14621. FLJ20752 (Accession NM_019048) is another VGAM2346 host target gene. FLJ20752 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20752, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20752 BINDING SITE, designated SEQ ID:21129, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79678] Another function of VGAM2346 is therefore inhibition of FLJ20752 (Accession NM_019048). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ20752. FLJ21709 (Accession XM_085480) is another VGAM2346 host target gene. FLJ21709 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21709, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21709 BINDING SITE, designated SEQ ID:38172, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79679] Another function of VGAM2346 is therefore inhibition of FLJ21709 (Accession XM_085480). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21709. FLJ22477 (Accession NM_024735) is another VGAM2346 host target gene. FLJ22477 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22477, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22477 BINDING SITE, designated SEQ ID:24075, to the nucleotide

sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79680] Another function of VGAM2346 is therefore inhibition of FLJ22477 (Accession NM_024735). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22477. FLJ32865 (Accession NM_144613) is another VGAM2346 host target gene. FLJ32865 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ32865, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32865 BINDING SITE, designated SEQ ID:29429, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79681] Another function of VGAM2346 is therefore inhibition of FLJ32865 (Accession NM_144613). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32865. HGC6.1.1 (Accession NM_014354) is another VGAM2346 host target gene. HGC6.1.1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by HGC6.1.1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HGC6.1.1 BINDING SITE, designated SEQ ID:15685, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79682] Another function of VGAM2346 is therefore inhibition of HGC6.1.1 (Accession NM_014354). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HGC6.1.1. KIAA0010 (Accession NM_014671) is another VGAM2346 host target gene. KIAA0010 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0010, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0010 BINDING SITE, designated SEQ ID:16131, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79683] Another function of VGAM2346 is therefore inhibition of KIAA0010 (Accession NM_014671). Accordingly, utilities

of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0010. KIAA1881 (Accession XM_170901) is another VGAM2346 host target gene. KIAA1881 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1881, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1881 BINDING SITE, designated SEQ ID:45657, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79684] Another function of VGAM2346 is therefore inhibition of KIAA1881 (Accession XM_170901). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1881. MGC20486 (Accession NM_052844) is another VGAM2346 host target gene. MGC20486 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC20486, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

MGC20486 BINDING SITE, designated SEQ ID:27422, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79685] Another function of VGAM2346 is therefore inhibition of MGC20486 (Accession NM_052844). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC20486. PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335) is another VGAM2346 host target gene. PRPF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRPF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRPF8 BINDING SITE, designated SEQ ID:30685, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79686] Another function of VGAM2346 is therefore inhibition of PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRPF8.

ZD52F10 (Accession NM_033317) is another VGAM2346 host target gene. ZD52F10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZD52F10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZD52F10 BINDING SITE, designated SEQ ID:27155, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79687] Another function of VGAM2346 is therefore inhibition of ZD52F10 (Accession NM_033317). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZD52F10. LOC150538 (Accession XM_086945) is another VGAM2346 host target gene. LOC150538 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150538, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150538 BINDING SITE, designated SEQ ID:38992, to the nucleotide sequence of VGAM2346 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5057.

[79688] Another function of VGAM2346 is therefore inhibition of LOC150538 (Accession XM_086945). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150538. LOC157740 (Accession XM_088375) is another VGAM2346 host target gene. LOC157740 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157740, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157740 BINDING SITE, designated SEQ ID:39648, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79689] Another function of VGAM2346 is therefore inhibition of LOC157740 (Accession XM_088375). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157740. LOC158117 (Accession XM_088483) is another VGAM2346 host target gene. LOC158117 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158117, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158117 BINDING SITE, designated SEQ ID:39729, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79690] Another function of VGAM2346 is therefore inhibition of LOC158117 (Accession XM_088483). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158117. LOC158972 (Accession XM_099009) is another VGAM2346 host target gene. LOC158972 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158972, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158972 BINDING SITE, designated SEQ ID:42043, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79691] Another function of VGAM2346 is therefore inhibition of LOC158972 (Accession XM_099009). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC158972. LOC203275 (Accession XM_114667) is another VGAM2346 host target gene. LOC203275 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203275, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203275 BINDING SITE, designated SEQ ID:43027, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79692] Another function of VGAM2346 is therefore inhibition of LOC203275 (Accession XM_114667). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203275. LOC219513 (Accession XM_169166) is another VGAM2346 host target gene. LOC219513 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219513, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219513 BINDING SITE, designated SEQ ID:45293, to

the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79693] Another function of VGAM2346 is therefore inhibition of LOC219513 (Accession XM_169166). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219513. LOC221271 (Accession XM_166307) is another VGAM2346 host target gene. LOC221271 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221271 BINDING SITE, designated SEQ ID:44124, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79694] Another function of VGAM2346 is therefore inhibition of LOC221271 (Accession XM_166307). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221271. LOC256812 (Accession XM_174147) is another VGAM2346 host target gene. LOC256812 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC256812, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256812 BINDING SITE, designated SEQ ID:46579, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79695] Another function of VGAM2346 is therefore inhibition of LOC256812 (Accession XM_174147). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256812. LOC257422 (Accession XM_172923) is another VGAM2346 host target gene. LOC257422 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257422, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257422 BINDING SITE, designated SEQ ID:46190, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79696] Another function of VGAM2346 is therefore inhibition of LOC257422 (Accession XM_172923). Accordingly, utilities

of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257422. LOC57228 (Accession NM_020467) is another VGAM2346 host target gene. LOC57228 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC57228, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57228 BINDING SITE, designated SEQ ID:21706, to the nucleotide sequence of VGAM2346 RNA, herein designated VGAM RNA, also designated SEQ ID:5057.

[79697] Another function of VGAM2346 is therefore inhibition of LOC57228 (Accession NM_020467). Accordingly, utilities of VGAM2346 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57228. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2347 (VGAM2347) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79698] VGAM2347 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2347 was detected is described hereinabove with reference to Figs. 1-8.

[79699] VGAM2347 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2347 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79700] VGAM2347 gene encodes a VGAM2347 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2347 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2347 precursor RNA is designated SEQ ID:2333, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2333 is located at position 44095 relative to the genome of Equine Herpesvirus 2.

[79701] VGAM2347 precursor RNA folds onto itself, forming VGAM2347 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79702] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2347 folded precursor RNA into VGAM2347 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM2347 RNA is designated SEQ ID:5058, and is provided hereinbelow with reference to the sequence listing part.

[79703] VGAM2347 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2347 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2347 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[79704] VGAM2347 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2347 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2347 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2347 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2347 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79705] The complementary binding of VGAM2347 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2347 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2347 host target RNA into VGAM2347 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79706] It is appreciated that VGAM2347 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2347 host target genes. The mRNA of each one of this plurality of VGAM2347 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2347 RNA, herein designated VGAM RNA, and which when bound by VGAM2347 RNA causes inhibition of translation of respective one or more VGAM2347 host target proteins.

[79707] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2347 gene, herein designated VGAM GENE, on one or more VGAM2347 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79708] It is yet further appreciated that a function of VGAM2347 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2347 correlate with, and may be deduced from, the identity of the host target genes which VGAM2347 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79709] Nucleotide sequences of the VGAM2347 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2347 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2347 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2347 are further described hereinbelow with reference to Table 1.

[79710] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2347 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2347 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79711] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2347 gene, herein designated VGAM is inhibition of expression of VGAM2347 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2347 correlate with, and may be deduced from, the identity of the target genes which VGAM2347 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79712] Casein Kinase 1, Alpha 1 (CSNK1A1, Accession NM_001892) is a VGAM2347 host target gene. CSNK1A1

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSNK1A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSNK1A1 BINDING SITE, designated SEQ ID:7620, to the nucleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, also designated SEQ ID:5058.

[79713] A function of VGAM2347 is therefore inhibition of Casein Kinase 1, Alpha 1 (CSNK1A1, Accession NM_001892). Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK1A1. MAP-kinase Activating Death Domain (MADD, Accession NM_003682) is another VGAM2347 host target gene. MADD BINDING SITE1 through MADD BINDING SITE6 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MADD, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MADD BINDING SITE1 through MADD BINDING SITE6, designated SEQ ID:9788, SEQ ID:28237, SEQ

ID:28243, SEQ ID:28248, SEQ ID:28253 and SEQ ID:28258 respectively, to the nucleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, also designated SEQ ID:5058.

[79714] Another function of VGAM2347 is therefore inhibition of MAP-kinase Activating Death Domain (MADD, Accession NM_003682), a gene which may regulate two different pathways for neural activities.interacts with the type-1 tumor necrosis factor receptor (TNFR1); death domain-containing protein. Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADD. The function of MADD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM430.CMRF-35H (Accession XM_046925) is another VGAM2347 host target gene. CMRF-35H BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CMRF-35H, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CMRF-35H BINDING SITE, designated SEQ ID:34861, to the nu-

cleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, also designated SEQ ID:5058.

[79715] Another function of VGAM2347 is therefore inhibition of CMRF-35H (Accession XM_046925). Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CMRF-35H. CCR4-NOT Transcription Complex, Subunit 3 (CNOT3, Accession NM_014516) is another VGAM2347 host target gene. CNOT3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CNOT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNOT3 BINDING SITE, designated SEQ ID:15843, to the nucleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, also designated SEQ ID:5058.

[79716] Another function of VGAM2347 is therefore inhibition of CCR4-NOT Transcription Complex, Subunit 3 (CNOT3, Accession NM_014516). Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNOT3. DKFZP564D172 (Accession NM_032042) is another

VGAM2347 host target gene. DKFZP564D172 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564D172, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564D172 BINDING SITE, designated SEQ ID:25753, to the nucleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, also designated SEQ ID:5058.

[79717] Another function of VGAM2347 is therefore inhibition of DKFZP564D172 (Accession NM_032042). Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564D172. FLJ14327 (Accession NM_024912) is another VGAM2347 host target gene. FLJ14327 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14327, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14327 BINDING SITE, designated SEQ ID:24430, to the nucleotide sequence of VGAM2347 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5058.

[79718] Another function of VGAM2347 is therefore inhibition of FLJ14327 (Accession NM_024912). Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14327. FLJ22233 (Accession NM_024959) is another VGAM2347 host target gene. FLJ22233 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22233, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22233 BINDING SITE, designated SEQ ID:24514, to the nucleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, also designated SEQ ID:5058.

[79719] Another function of VGAM2347 is therefore inhibition of FLJ22233 (Accession NM_024959). Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22233. NEU4 (Accession NM_080741) is another VGAM2347 host target gene. NEU4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NEU4, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NEU4 BINDING SITE, designated SEQ ID:28028, to the nucleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, also designated SEQ ID:5058.

[79720] Another function of VGAM2347 is therefore inhibition of NEU4 (Accession NM_080741). Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEU4. LOC112868 (Accession XM_053402) is another VGAM2347 host target gene. LOC112868 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC112868, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112868 BINDING SITE, designated SEQ ID:36079, to the nucleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, also designated SEQ ID:5058.

[79721] Another function of VGAM2347 is therefore inhibition of LOC112868 (Accession XM_053402). Accordingly, utilities of VGAM2347 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC112868. LOC151826 (Accession XM_087312) is another VGAM2347 host target gene. LOC151826 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151826, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151826 BINDING SITE, designated SEQ ID:39165, to the nucleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, also designated SEQ ID:5058.

[79722] Another function of VGAM2347 is therefore inhibition of LOC151826 (Accession XM_087312). Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151826. LOC152313 (Accession XM_098190) is another VGAM2347 host target gene. LOC152313 BINDING SITE1 and LOC152313 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC152313, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152313 BINDING SITE1

and LOC152313 BINDING SITE2, designated SEQ ID:41478 and SEQ ID:41479 respectively, to the nucleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, also designated SEQ ID:5058.

[79723] Another function of VGAM2347 is therefore inhibition of LOC152313 (Accession XM_098190). Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152313. LOC92568 (Accession XM_045852) is another VGAM2347 host target gene. LOC92568 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92568, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92568 BINDING SITE, designated SEQ ID:34580, to the nucleotide sequence of VGAM2347 RNA, herein designated VGAM RNA, also designated SEQ ID:5058.

[79724] Another function of VGAM2347 is therefore inhibition of LOC92568 (Accession XM_045852). Accordingly, utilities of VGAM2347 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92568. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2348 (VGAM2348) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79725] VGAM2348 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2348 was detected is described hereinabove with reference to Figs. 1-8.

[79726] VGAM2348 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2348 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79727] VGAM2348 gene encodes a VGAM2348 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2348 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2348 precursor RNA is designated SEQ ID:2334, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2334 is located at position 16485 relative to the genome of Equine Herpesvirus 2.

[79728] VGAM2348 precursor RNA folds onto itself, forming VGAM2348 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79729] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2348 folded precursor RNA into VGAM2348 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2348 RNA is designated SEQ ID:5059, and is provided hereinbelow with reference to the sequence listing part.

[79730] VGAM2348 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2348 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2348 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79731] VGAM2348 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2348 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2348 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2348 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2348 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79732] The complementary binding of VGAM2348 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2348 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2348 host target RNA into VGAM2348 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79733] It is appreciated that VGAM2348 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2348 host target genes. The mRNA of each one of this plurality of VGAM2348 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2348 RNA, herein designated VGAM RNA, and which when bound by VGAM2348 RNA causes inhibition of translation of respective one or more

VGAM2348 host target proteins.

[79734] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2348 gene, herein designated VGAM GENE, on one or more VGAM2348 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79735] It is yet further appreciated that a function of VGAM2348 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2348 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Spe-

cific functions, and accordingly utilities, of VGAM2348 correlate with, and may be deduced from, the identity of the host target genes which VGAM2348 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79736] Nucleotide sequences of the VGAM2348 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2348 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2348 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2348 are further described hereinbelow with reference to Table 1.

[79737] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2348 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2348 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79738] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2348 gene, herein designated VGAM is inhibition of expression of VGAM2348 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2348 correlate with, and may be deduced from, the identity of the target genes which VGAM2348 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79739] Isocitrate Dehydrogenase 1 (NADP+), Soluble (IDH1, Accession XM_028869) is a VGAM2348 host target gene. IDH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IDH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IDH1 BINDING SITE, designated SEQ ID:30800, to the nucleotide sequence of VGAM2348 RNA, herein designated VGAM RNA, also designated SEQ ID:5059.

[79740] A function of VGAM2348 is therefore inhibition of Isocitrate Dehydrogenase 1 (NADP+), Soluble (IDH1, Accession XM_028869), a gene which decarboxylates isocitrate into alpha-ketoglutarate. Accordingly, utilities of VGAM2348 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IDH1. The function of IDH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM1928.FLJ20060 (Accession NM_017645) is another VGAM2348 host target gene. FLJ20060 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20060, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20060 BINDING SITE, designated SEQ ID:19150, to the nucleotide sequence of VGAM2348 RNA, herein designated VGAM RNA, also designated SEQ ID:5059.

[79741] Another function of VGAM2348 is therefore inhibition of FLJ20060 (Accession NM_017645). Accordingly, utilities of VGAM2348 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20060. Growth Hormone Inducible Transmembrane Protein (GHITM, Accession NM_014394) is another VGAM2348 host target gene. GHITM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GHITM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GHITM BINDING SITE, designated SEQ ID:15727, to the nucleotide sequence of

VGAM2348 RNA, herein designated VGAM RNA, also designated SEQ ID:5059.

[79742] Another function of VGAM2348 is therefore inhibition of Growth Hormone Inducible Transmembrane Protein (GHITM, Accession NM_014394). Accordingly, utilities of VGAM2348 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GHITM. Guanine Nucleotide Binding Protein (G protein), Gamma 4 (GNG4, Accession NM_004485) is another VGAM2348 host target gene. GNG4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNG4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNG4 BINDING SITE, designated SEQ ID:10812, to the nucleotide sequence of VGAM2348 RNA, herein designated VGAM RNA, also designated SEQ ID:5059.

[79743] Another function of VGAM2348 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Gamma 4 (GNG4, Accession NM_004485). Accordingly, utilities of VGAM2348 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNG4.

KIAA1228 (Accession XM_036408) is another VGAM2348 host target gene. KIAA1228 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1228, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1228 BINDING SITE, designated SEQ ID:32447, to the nucleotide sequence of VGAM2348 RNA, herein designated VGAM RNA, also designated SEQ ID:5059.

[79744] Another function of VGAM2348 is therefore inhibition of KIAA1228 (Accession XM_036408). Accordingly, utilities of VGAM2348 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1228. KIAA1361 (Accession XM_030845) is another VGAM2348 host target gene. KIAA1361 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1361, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1361 BINDING SITE, designated SEQ ID:31166, to the nucleotide sequence of VGAM2348 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5059.

[79745] Another function of VGAM2348 is therefore inhibition of KIAA1361 (Accession XM_030845). Accordingly, utilities of VGAM2348 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1361. LOC222001 (Accession XM_167489) is another VGAM2348 host target gene. LOC222001 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222001, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222001 BINDING SITE, designated SEQ ID:44641, to the nucleotide sequence of VGAM2348 RNA, herein designated VGAM RNA, also designated SEQ ID:5059.

[79746] Another function of VGAM2348 is therefore inhibition of LOC222001 (Accession XM_167489). Accordingly, utilities of VGAM2348 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222001. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2349 (VGAM2349) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79747] VGAM2349 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2349 was detected is described hereinabove with reference to Figs. 1-8.

[79748] VGAM2349 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2349 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79749] VGAM2349 gene encodes a VGAM2349 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2349 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2349 precursor RNA is designated SEQ ID:2335, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2335 is located at position 19286 relative to the genome of Equine Herpesvirus 2.

[79750] VGAM2349 precursor RNA folds onto itself, forming

VGAM2349 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79751] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2349 folded precursor RNA into VGAM2349 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2349 RNA is designated SEQ ID:5060, and is provided hereinbelow with reference to the sequence listing part.

[79752] VGAM2349 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2349 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2349 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79753] VGAM2349 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2349 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2349 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2349 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2349 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79754] The complementary binding of VGAM2349 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2349 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2349 host target RNA into VGAM2349 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79755] It is appreciated that VGAM2349 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2349 host target genes. The mRNA of each one of this plurality of VGAM2349 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2349 RNA, herein designated VGAM RNA, and which when bound by VGAM2349 RNA causes inhibition of translation of respective one or more VGAM2349 host target proteins.

[79756] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2349 gene, herein designated VGAM GENE, on one or more VGAM2349 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79757] It is yet further appreciated that a function of VGAM2349 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2349 correlate with, and may be deduced from, the identity of the host target genes which VGAM2349 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[79758] Nucleotide sequences of the VGAM2349 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2349 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2349 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2349 are further described hereinbelow with reference to Table 1.

[79759] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2349 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2349 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79760] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2349 gene, herein designated VGAM is inhibition of expression of VGAM2349 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2349 correlate with, and may be deduced from, the identity of the target genes which VGAM2349 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[79761] ATP-binding Cassette, Sub-family D (ALD), Member 1 (ABCD1, Accession NM_000033) is a VGAM2349 host target gene. ABCD1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ABCD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCD1 BINDING SITE, designated SEQ ID:5471, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79762] A function of VGAM2349 is therefore inhibition of ATP-binding Cassette, Sub-family D (ALD), Member 1 (ABCD1, Accession NM_000033). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCD1. Ankyrin 1, Erythrocytic (ANK1, Accession XM_016774) is another VGAM2349 host target gene. ANK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ANK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of ANK1 BINDING SITE, designated SEQ ID:30286, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79763] Another function of VGAM2349 is therefore inhibition of Ankyrin 1, Erythrocytic (ANK1, Accession XM_016774). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANK1. AXL Receptor Tyrosine Kinase (AXL, Accession NM_021913) is another VGAM2349 host target gene. AXL BINDING SITE1 and AXL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AXL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE1 and AXL BINDING SITE2, designated SEQ ID:22444 and SEQ ID:7423 respectively, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79764] Another function of VGAM2349 is therefore inhibition of AXL Receptor Tyrosine Kinase (AXL, Accession NM_021913). Accordingly, utilities of VGAM2349 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL. Collagen, Type XI, Alpha 2 (COL11A2, Accession NM_080681) is another VGAM2349 host target gene. COL11A2 BINDING SITE1 and COL11A2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by COL11A2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL11A2 BINDING SITE1 and COL11A2 BINDING SITE2, designated SEQ ID:27981 and SEQ ID:35917 respectively, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79765] Another function of VGAM2349 is therefore inhibition of Collagen, Type XI, Alpha 2 (COL11A2, Accession NM_080681). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL11A2. Discs, Large (Drosophila) Homolog 5 (DLG5, Accession XM_096398) is another VGAM2349 host target gene. DLG5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DLG5, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLG5 BINDING SITE, designated SEQ ID:40338, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79766] Another function of VGAM2349 is therefore inhibition of Discs, Large (Drosophila) Homolog 5 (DLG5, Accession XM_096398), a gene which may transmit extracellular signals to inhibit cell proliferation. Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLG5. The function of DLG5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM444.Fibroblast Growth Factor Receptor-like 1 (FGFRL1, Accession NM_021923) is another VGAM2349 host target gene. FGFRL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGFRL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGFRL1 BINDING SITE, des-

ignated SEQ ID:22450, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79767] Another function of VGAM2349 is therefore inhibition of Fibroblast Growth Factor Receptor-like 1 (FGFRL1, Accession NM_021923). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGFRL1. General Transcription Factor II, I (GTF2I, Accession NM_032999) is another VGAM2349 host target gene. GTF2I BINDING SITE1 and GTF2I BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GTF2I, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTF2I BINDING SITE1 and GTF2I BINDING SITE2, designated SEQ ID:26886 and SEQ ID:26890 respectively, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79768] Another function of VGAM2349 is therefore inhibition of General Transcription Factor II, I (GTF2I, Accession NM_032999), a gene which interacts with the basal tran-

scription machinery by coordinating the formation of a multiprotein complex at the c-fos promoter, and linking specific signal responsive activator complexes. Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2I. The function of GTF2I and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM115.Homeo Box D3 (HOXD3, Accession NM_006898) is another VGAM2349 host target gene. HOXD3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HOXD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOXD3 BINDING SITE, designated SEQ ID:13773, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79769] Another function of VGAM2349 is therefore inhibition of Homeo Box D3 (HOXD3, Accession NM_006898), a gene which plays a role in the differentiation process of hematopoietic cells. Accordingly, utilities of VGAM2349

include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXD3. The function of HOXD3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1384.Kinesin Family Member 3C (KIF3C, Accession NM_002254) is another VGAM2349 host target gene. KIF3C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIF3C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIF3C BINDING SITE, designated SEQ ID:8059, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79770] Another function of VGAM2349 is therefore inhibition of Kinesin Family Member 3C (KIF3C, Accession NM_002254). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIF3C. Myeloid/lymphoid Or Mixed-lineage Leukemia (trithorax homolog, Drosophila); Translocated To, 7 (MLLT7, Accession NM_005938) is another VGAM2349 host target gene.

MLLT7 BINDING SITE1 and MLLT7 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MLLT7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MLLT7 BINDING SITE1 and MLLT7 BINDING SITE2, designated SEQ ID:12576 and SEQ ID:12577 respectively, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79771] Another function of VGAM2349 is therefore inhibition of Myeloid/lymphoid Or Mixed-lineage Leukemia (trithorax homolog, Drosophila); Translocated To, 7 (MLLT7, Accession NM_005938), a gene which is a Member of the forkhead family. Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLLT7. The function of MLLT7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM175.Mevalonate Kinase (mevalonic aciduria) (MVK, Accession XM_027151) is another VGAM2349 host target gene. MVK BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by MVK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MVK BINDING SITE, designated SEQ ID:30426, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79772] Another function of VGAM2349 is therefore inhibition of Mevalonate Kinase (mevalonic aciduria) (MVK, Accession XM_027151). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MVK. Myosin Light Chain Kinase 2, Skeletal Muscle (MYLK2, Accession NM_033118) is another VGAM2349 host target gene. MYLK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYLK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYLK2 BINDING SITE, designated SEQ ID:26965, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79773] Another function of VGAM2349 is therefore inhibition of

Myosin Light Chain Kinase 2, Skeletal Muscle (MYLK2, Accession NM_033118). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYLK2. Myosin XVA (MYO15A, Accession NM_016239) is another VGAM2349 host target gene. MYO15A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYO15A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYO15A BINDING SITE, designated SEQ ID:18354, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79774] Another function of VGAM2349 is therefore inhibition of Myosin XVA (MYO15A, Accession NM_016239), a gene which acts as actin-based motors. Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYO15A. The function of MYO15A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM985.Neuro-oncological Ventral

Antigen 1 (NOVA1, Accession NM_006489) is another VGAM2349 host target gene. NOVA1 BINDING SITE1 and NOVA1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NOVA1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NOVA1 BINDING SITE1 and NOVA1 BINDING SITE2, designated SEQ ID:13216 and SEQ ID:8347 respectively, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79775] Another function of VGAM2349 is therefore inhibition of Neuro-oncological Ventral Antigen 1 (NOVA1, Accession NM_006489), a gene which may regulate rna splicing or metabolism in a specific subset of developing neurons. Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOVA1. The function of NOVA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM521.PCTAIRE Protein Kinase 1 (PCTK1, Accession NM_033018) is an-

other VGAM2349 host target gene. PCTK1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PCTK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCTK1 BINDING SITE, designated SEQ ID:26910, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79776] Another function of VGAM2349 is therefore inhibition of PCTAIRE Protein Kinase 1 (PCTK1, Accession NM_033018), a gene which may play a role in signal transduction cascades in terminally differentiated cells. Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCTK1. The function of PCTK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM75.Polymeric Immunoglobulin Receptor (PIGR, Accession XM_052013) is another VGAM2349 host target gene. PIGR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIGR, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIGR BINDING SITE, designated SEQ ID:35939, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79777] Another function of VGAM2349 is therefore inhibition of Polymeric Immunoglobulin Receptor (PIGR, Accession XM_052013). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGR. Ret Proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease) (RET, Accession NM_020630) is another VGAM2349 host target gene. RET BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RET, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RET BINDING SITE, designated SEQ ID:21784, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79778] Another function of VGAM2349 is therefore inhibition of

Ret Proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease) (RET, Accession NM_020630), a gene which transduces signals for cell growth and differentiation. Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RET. The function of RET and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Ret Finger Protein (RFP, Accession NM_006510) is another VGAM2349 host target gene. RFP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RFP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RFP BINDING SITE, designated SEQ ID:13259, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79779] Another function of VGAM2349 is therefore inhibition of Ret Finger Protein (RFP, Accession NM_006510), a gene which involvels in transcriptional regulation and may act in male germ cell development . Accordingly, utilities of

VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFP. The function of RFP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM302.Seizure Related 6 Homolog (mouse)-like (SEZ6L, Accession NM_021115) is another VGAM2349 host target gene. SEZ6L BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SEZ6L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEZ6L BINDING SITE, designated SEQ ID:22093, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79780] Another function of VGAM2349 is therefore inhibition of Seizure Related 6 Homolog (mouse)-like (SEZ6L, Accession NM_021115). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEZ6L. Small Glutamine-rich Tetratricopeptide Repeat (TPR)-containing (SGT, Accession NM_003021) is another VGAM2349 host

target gene. SGT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SGT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SGT BINDING SITE, designated SEQ ID:8941, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79781] Another function of VGAM2349 is therefore inhibition of Small Glutamine-rich Tetratricopeptide Repeat (TPR)-containing (SGT, Accession NM_003021). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SGT. Testis Enhanced Gene Transcript (BAX inhibitor 1) (TEGT, Accession XM_035490) is another VGAM2349 host target gene. TEGT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEGT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEGT BINDING SITE, designated SEQ ID:32273, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5060.

[79782] Another function of VGAM2349 is therefore inhibition of Testis Enhanced Gene Transcript (BAX inhibitor 1) (TEGT, Accession XM_035490), a gene which is a suppressor of apoptosis. Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEGT. The function of TEGT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2276.Tensin (TNS, Accession NM_022648) is another VGAM2349 host target gene. TNS BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TNS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNS BINDING SITE, designated SEQ ID:22902, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79783] Another function of VGAM2349 is therefore inhibition of Tensin (TNS, Accession NM_022648). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with TNS. Topoisomerase (DNA) III Beta (TOP3B, Accession NM_003935) is another VGAM2349 host target gene. TOP3B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TOP3B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOP3B BINDING SITE, designated SEQ ID:10037, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79784] Another function of VGAM2349 is therefore inhibition of Topoisomerase (DNA) III Beta (TOP3B, Accession NM_003935). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOP3B. Activating Transcription Factor 3 (ATF3, Accession NM_004024) is another VGAM2349 host target gene. ATF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of ATF3 BINDING SITE, designated SEQ ID:10244, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79785] Another function of VGAM2349 is therefore inhibition of Activating Transcription Factor 3 (ATF3, Accession NM_004024). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATF3. Chromosome 20 Open Reading Frame 178 (C20orf178, Accession XM_059282) is another VGAM2349 host target gene. C20orf178 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf178 BINDING SITE, designated SEQ ID:36935, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79786] Another function of VGAM2349 is therefore inhibition of Chromosome 20 Open Reading Frame 178 (C20orf178, Accession XM_059282). Accordingly, utilities of

VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf178. Casein Kinase 1, Gamma 1 (CSNK1G1, Accession NM_022048) is another VGAM2349 host target gene. CSNK1G1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSNK1G1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CSNK1G1 BINDING SITE, designated SEQ ID:22569, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79787] Another function of VGAM2349 is therefore inhibition of Casein Kinase 1, Gamma 1 (CSNK1G1, Accession NM_022048). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSNK1G1. CSR1 (Accession NM_016240) is another VGAM2349 host target gene. CSR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CSR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of CSR1 BINDING SITE, designated SEQ ID:18359, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79788] Another function of VGAM2349 is therefore inhibition of CSR1 (Accession NM_016240). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CSR1. Diacylglycerol Kinase, Delta 130kDa (DGKD, Accession XM_002384) is another VGAM2349 host target gene. DGKD BINDING SITE1 and DGKD BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DGKD, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGKD BINDING SITE1 and DGKD BINDING SITE2, designated SEQ ID:29885 and SEQ ID:29886 respectively, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79789] Another function of VGAM2349 is therefore inhibition of Diacylglycerol Kinase, Delta 130kDa (DGKD, Accession XM_002384). Accordingly, utilities of VGAM2349 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with DGKD. DKFZP564O0423 (Accession XM_166254) is another VGAM2349 host target gene. DKFZP564O0423 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O0423, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564O0423 BINDING SITE, designated SEQ ID:44067, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79790] Another function of VGAM2349 is therefore inhibition of DKFZP564O0423 (Accession XM_166254). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564O0423. DKFZP761D0211 (Accession NM_032039) is another VGAM2349 host target gene. DKFZP761D0211 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP761D0211, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the

nucleotide sequences of DKFZP761D0211 BINDING SITE, designated SEQ ID:25736, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79791] Another function of VGAM2349 is therefore inhibition of DKFZP761D0211 (Accession NM_032039). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761D0211. FLJ10597 (Accession NM_018150) is another VGAM2349 host target gene. FLJ10597 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10597, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10597 BINDING SITE, designated SEQ ID:19953, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79792] Another function of VGAM2349 is therefore inhibition of FLJ10597 (Accession NM_018150). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10597. FLJ10661 (Accession NM_018172) is another

VGAM2349 host target gene. FLJ10661 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10661, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10661 BINDING SITE, designated SEQ ID:19997, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79793] Another function of VGAM2349 is therefore inhibition of FLJ10661 (Accession NM_018172). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10661. FLJ21276 (Accession NM_024633) is another VGAM2349 host target gene. FLJ21276 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21276, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21276 BINDING SITE, designated SEQ ID:23902, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79794] Another function of VGAM2349 is therefore inhibition of FLJ21276 (Accession NM_024633). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21276. Golgi Associated, Gamma Adaptin Ear Containing, ARF Binding Protein 2 (GGA2, Accession NM_138640) is another VGAM2349 host target gene. GGA2 BINDING SITE1 and GGA2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GGA2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GGA2 BINDING SITE1 and GGA2 BINDING SITE2, designated SEQ ID:28921 and SEQ ID:17400 respectively, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79795] Another function of VGAM2349 is therefore inhibition of Golgi Associated, Gamma Adaptin Ear Containing, ARF Binding Protein 2 (GGA2, Accession NM_138640). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGA2. H326 (Accession NM_015726) is another

VGAM2349 host target gene. H326 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by H326, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H326 BINDING SITE, designated SEQ ID:17939, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79796] Another function of VGAM2349 is therefore inhibition of H326 (Accession NM_015726). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H326. KIAA0153 (Accession NM_015140) is another VGAM2349 host target gene. KIAA0153 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0153, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0153 BINDING SITE, designated SEQ ID:17498, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79797] Another function of VGAM2349 is therefore inhibition of KIAA0153 (Accession NM_015140). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0153. KIAA0527 (Accession XM_171054) is another VGAM2349 host target gene. KIAA0527 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0527, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0527 BINDING SITE, designated SEQ ID:45843, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79798] Another function of VGAM2349 is therefore inhibition of KIAA0527 (Accession XM_171054). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0527. KIAA0819 (Accession XM_032996) is another VGAM2349 host target gene. KIAA0819 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0819, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0819 BINDING SITE, designated SEQ ID:31808, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79799] Another function of VGAM2349 is therefore inhibition of KIAA0819 (Accession XM_032996). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0819. KIAA1110 (Accession XM_029973) is another VGAM2349 host target gene. KIAA1110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1110 BINDING SITE, designated SEQ ID:30985, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79800] Another function of VGAM2349 is therefore inhibition of KIAA1110 (Accession XM_029973). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1110. KIAA1228 (Accession XM_036408) is another VGAM2349 host target gene. KIAA1228 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1228, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1228 BINDING SITE, designated SEQ ID:32445, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79801] Another function of VGAM2349 is therefore inhibition of KIAA1228 (Accession XM_036408). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1228. KIAA1538 (Accession XM_049474) is another VGAM2349 host target gene. KIAA1538 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1538, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1538 BINDING SITE, designated SEQ ID:35430, to the nucleotide sequence of VGAM2349 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5060.

[79802] Another function of VGAM2349 is therefore inhibition of KIAA1538 (Accession XM_049474). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1538. KIAA1559 (Accession XM_054472) is another VGAM2349 host target gene. KIAA1559 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1559, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1559 BINDING SITE, designated SEQ ID:36163, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79803] Another function of VGAM2349 is therefore inhibition of KIAA1559 (Accession XM_054472). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1559. KIAA1751 (Accession XM_049768) is another VGAM2349 host target gene. KIAA1751 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1751, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1751 BINDING SITE, designated SEQ ID:35497, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79804] Another function of VGAM2349 is therefore inhibition of KIAA1751 (Accession XM_049768). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1751. KIAA1755 (Accession XM_028810) is another VGAM2349 host target gene. KIAA1755 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1755, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1755 BINDING SITE, designated SEQ ID:30751, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79805] Another function of VGAM2349 is therefore inhibition of KIAA1755 (Accession XM_028810). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1755. KIAA1784 (Accession XM_036660) is another VGAM2349 host target gene. KIAA1784 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1784, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1784 BINDING SITE, designated SEQ ID:32485, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79806] Another function of VGAM2349 is therefore inhibition of KIAA1784 (Accession XM_036660). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1784. KIAA1870 (Accession NM_032888) is another VGAM2349 host target gene. KIAA1870 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1870, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1870 BINDING SITE, designated SEQ ID:26710, to the

nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79807] Another function of VGAM2349 is therefore inhibition of KIAA1870 (Accession NM_032888). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1870. KIAA1957 (Accession XM_065166) is another VGAM2349 host target gene. KIAA1957 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1957, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1957 BINDING SITE, designated SEQ ID:37277, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79808] Another function of VGAM2349 is therefore inhibition of KIAA1957 (Accession XM_065166). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1957. MGC16279 (Accession NM_032916) is another VGAM2349 host target gene. MGC16279 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by MGC16279, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16279 BINDING SITE, designated SEQ ID:26732, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79809] Another function of VGAM2349 is therefore inhibition of MGC16279 (Accession NM_032916). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16279. MGC33182 (Accession XM_062903) is another VGAM2349 host target gene. MGC33182 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC33182, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC33182 BINDING SITE, designated SEQ ID:37233, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79810] Another function of VGAM2349 is therefore inhibition of MGC33182 (Accession XM_062903). Accordingly, utilities

of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC33182. MGC4415 (Accession NM_031484) is another VGAM2349 host target gene. MGC4415 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4415, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4415 BINDING SITE, designated SEQ ID:25568, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79811] Another function of VGAM2349 is therefore inhibition of MGC4415 (Accession NM_031484). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4415. MGC4677 (Accession NM_052871) is another VGAM2349 host target gene. MGC4677 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC4677, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4677

BINDING SITE, designated SEQ ID:27452, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79812] Another function of VGAM2349 is therefore inhibition of MGC4677 (Accession NM_052871). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4677. Myelin Transcription Factor 1-like (MYT1L, Accession XM_039762) is another VGAM2349 host target gene. MYT1L BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MYT1L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYT1L BINDING SITE, designated SEQ ID:33185, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79813] Another function of VGAM2349 is therefore inhibition of Myelin Transcription Factor 1-like (MYT1L, Accession XM_039762). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYT1L. Phosphatidylinosi-

tol-4-phosphate 5-kinase, Type II, Beta (PIP5K2B, Accession NM_003559) is another VGAM2349 host target gene. PIP5K2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIP5K2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIP5K2B BINDING SITE, designated SEQ ID:9613, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79814] Another function of VGAM2349 is therefore inhibition of Phosphatidylinositol-4-phosphate 5-kinase, Type II, Beta (PIP5K2B, Accession NM_003559). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIP5K2B. Phospholipase A2, Group VI (cytosolic, calcium-independent) (PLA2G6, Accession XM_039248) is another VGAM2349 host target gene. PLA2G6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLA2G6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PLA2G6 BINDING SITE, designated SEQ ID:33031, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79815] Another function of VGAM2349 is therefore inhibition of Phospholipase A2, Group VI (cytosolic, calcium-independent) (PLA2G6, Accession XM_039248). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLA2G6. Sodium Channel, Voltage-gated, Type XII, Alpha Polypeptide (SCN12A, Accession NM_014139) is another VGAM2349 host target gene. SCN12A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCN12A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCN12A BINDING SITE, designated SEQ ID:15411, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79816] Another function of VGAM2349 is therefore inhibition of Sodium Channel, Voltage-gated, Type XII, Alpha Polypeptide (SCN12A, Accession NM_014139). Accordingly, utili-

ties of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN12A. Stathmin-like 3 (STMN3, Accession NM_015894) is another VGAM2349 host target gene. STMN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STMN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STMN3 BINDING SITE, designated SEQ ID:18038, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79817] Another function of VGAM2349 is therefore inhibition of Stathmin-like 3 (STMN3, Accession NM_015894). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STMN3. TUSP (Accession NM_020245) is another VGAM2349 host target gene. TUSP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TUSP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of TUSP BINDING SITE, designated SEQ ID:21525, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79818] Another function of VGAM2349 is therefore inhibition of TUSP (Accession NM_020245). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUSP. VI (Accession NM_013443) is another VGAM2349 host target gene. VI BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VI BINDING SITE, designated SEQ ID:15107, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79819] Another function of VGAM2349 is therefore inhibition of VI (Accession NM_013443). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VI. VIT1 (Accession NM_018693) is another VGAM2349 host target gene. VIT1 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by VIT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VIT1 BINDING SITE, designated SEQ ID:20765, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79820] Another function of VGAM2349 is therefore inhibition of VIT1 (Accession NM_018693). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIT1. VTI2 (Accession NM_006370) is another VGAM2349 host target gene. VTI2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by VTI2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VTI2 BINDING SITE, designated SEQ ID:13057, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79821] Another function of VGAM2349 is therefore inhibition of VTI2 (Accession NM_006370). Accordingly, utilities of

VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VTI2. Zinc Finger Protein 95 Homolog (mouse) (ZFP95, Accession NM_014569) is another VGAM2349 host target gene. ZFP95 BINDING SITE1 and ZFP95 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ZFP95, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZFP95 BINDING SITE1 and ZFP95 BINDING SITE2, designated SEQ ID:15919 and SEQ ID:29709 respectively, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79822] Another function of VGAM2349 is therefore inhibition of Zinc Finger Protein 95 Homolog (mouse) (ZFP95, Accession NM_014569). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP95. LOC115073 (Accession XM_055193) is another VGAM2349 host target gene. LOC115073 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC115073, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115073 BINDING SITE, designated SEQ ID:36239, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79823] Another function of VGAM2349 is therefore inhibition of LOC115073 (Accession XM_055193). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115073. LOC121274 (Accession XM_058547) is another VGAM2349 host target gene. LOC121274 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC121274, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC121274 BINDING SITE, designated SEQ ID:36656, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79824] Another function of VGAM2349 is therefore inhibition of LOC121274 (Accession XM_058547). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC121274. LOC135763 (Accession NM_138572) is another VGAM2349 host target gene. LOC135763 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC135763, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC135763 BINDING SITE, designated SEQ ID:28881, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79825] Another function of VGAM2349 is therefore inhibition of LOC135763 (Accession NM_138572). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135763. LOC144231 (Accession XM_096561) is another VGAM2349 host target gene. LOC144231 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144231, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144231 BINDING SITE, designated SEQ ID:40393, to

the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79826] Another function of VGAM2349 is therefore inhibition of LOC144231 (Accession XM_096561). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144231. LOC144465 (Accession XM_084874) is another VGAM2349 host target gene. LOC144465 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144465, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144465 BINDING SITE, designated SEQ ID:37751, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79827] Another function of VGAM2349 is therefore inhibition of LOC144465 (Accession XM_084874). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144465. LOC145945 (Accession XM_096908) is another VGAM2349 host target gene. LOC145945 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC145945, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145945 BINDING SITE, designated SEQ ID:40632, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79828] Another function of VGAM2349 is therefore inhibition of LOC145945 (Accession XM_096908). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145945. LOC148760 (Accession XM_097514) is another VGAM2349 host target gene. LOC148760 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148760, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148760 BINDING SITE, designated SEQ ID:40896, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79829] Another function of VGAM2349 is therefore inhibition of LOC148760 (Accession XM_097514). Accordingly, utilities

of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148760. LOC149194 (Accession XM_086458) is another VGAM2349 host target gene. LOC149194 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149194, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149194 BINDING SITE, designated SEQ ID:38670, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79830] Another function of VGAM2349 is therefore inhibition of LOC149194 (Accession XM_086458). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149194. LOC151162 (Accession XM_098012) is another VGAM2349 host target gene. LOC151162 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC151162 BINDING SITE, designated SEQ ID:41305, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79831] Another function of VGAM2349 is therefore inhibition of LOC151162 (Accession XM_098012). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151162. LOC154449 (Accession XM_087928) is another VGAM2349 host target gene. LOC154449 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154449, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154449 BINDING SITE, designated SEQ ID:39475, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79832] Another function of VGAM2349 is therefore inhibition of LOC154449 (Accession XM_087928). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154449. LOC157450 (Accession XM_048209) is another VGAM2349 host target gene. LOC157450 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157450, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157450 BINDING SITE, designated SEQ ID:35147, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79833] Another function of VGAM2349 is therefore inhibition of LOC157450 (Accession XM_048209). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157450. LOC157860 (Accession XM_098832) is another VGAM2349 host target gene. LOC157860 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157860, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157860 BINDING SITE, designated SEQ ID:41859, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79834] Another function of VGAM2349 is therefore inhibition of

LOC157860 (Accession XM_098832). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157860. LOC158490 (Accession XM_088585) is another VGAM2349 host target gene. LOC158490 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158490, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158490 BINDING SITE, designated SEQ ID:39851, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79835] Another function of VGAM2349 is therefore inhibition of LOC158490 (Accession XM_088585). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158490. LOC158819 (Accession XM_098995) is another VGAM2349 host target gene. LOC158819 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158819, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC158819 BINDING SITE, designated SEQ ID:42025, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79836] Another function of VGAM2349 is therefore inhibition of LOC158819 (Accession XM_098995). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158819. LOC168489 (Accession XM_095134) is another VGAM2349 host target gene. LOC168489 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC168489, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC168489 BINDING SITE, designated SEQ ID:40250, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79837] Another function of VGAM2349 is therefore inhibition of LOC168489 (Accession XM_095134). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168489. LOC203377 (Accession XM_117540) is an-

other VGAM2349 host target gene. LOC203377 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203377, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203377 BINDING SITE, designated SEQ ID:43540, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79838] Another function of VGAM2349 is therefore inhibition of LOC203377 (Accession XM_117540). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203377. LOC221692 (Accession XM_166420) is another VGAM2349 host target gene. LOC221692 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221692, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221692 BINDING SITE, designated SEQ ID:44298, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79839] Another function of VGAM2349 is therefore inhibition of LOC221692 (Accession XM_166420). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221692. LOC221715 (Accession XM_168092) is another VGAM2349 host target gene. LOC221715 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221715, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221715 BINDING SITE, designated SEQ ID:45017, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79840] Another function of VGAM2349 is therefore inhibition of LOC221715 (Accession XM_168092). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221715. LOC254205 (Accession XM_172962) is another VGAM2349 host target gene. LOC254205 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254205, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254205 BINDING SITE, designated SEQ ID:46218, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79841] Another function of VGAM2349 is therefore inhibition of LOC254205 (Accession XM_172962). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254205. LOC255101 (Accession XM_173080) is another VGAM2349 host target gene. LOC255101 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255101, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255101 BINDING SITE, designated SEQ ID:46339, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79842] Another function of VGAM2349 is therefore inhibition of LOC255101 (Accession XM_173080). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC255101. LOC256337 (Accession XM_170643) is another VGAM2349 host target gene. LOC256337 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256337, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256337 BINDING SITE, designated SEQ ID:45421, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79843] Another function of VGAM2349 is therefore inhibition of LOC256337 (Accession XM_170643). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256337. LOC90309 (Accession XM_030830) is another VGAM2349 host target gene. LOC90309 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90309, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90309 BINDING SITE, designated SEQ ID:31151, to the nucleotide sequence of VGAM2349 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5060.

[79844] Another function of VGAM2349 is therefore inhibition of LOC90309 (Accession XM_030830). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90309. LOC91960 (Accession XM_041872) is another VGAM2349 host target gene. LOC91960 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91960, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91960 BINDING SITE, designated SEQ ID:33612, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79845] Another function of VGAM2349 is therefore inhibition of LOC91960 (Accession XM_041872). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91960. LOC92340 (Accession XM_044426) is another VGAM2349 host target gene. LOC92340 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92340, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92340 BINDING SITE, designated SEQ ID:34198, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79846] Another function of VGAM2349 is therefore inhibition of LOC92340 (Accession XM_044426). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92340. LOC92822 (Accession XM_047520) is another VGAM2349 host target gene. LOC92822 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92822, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92822 BINDING SITE, designated SEQ ID:34985, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79847] Another function of VGAM2349 is therefore inhibition of LOC92822 (Accession XM_047520). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC92822. LOC93320 (Accession XM_050534) is another VGAM2349 host target gene. LOC93320 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93320, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93320 BINDING SITE, designated SEQ ID:35656, to the nucleotide sequence of VGAM2349 RNA, herein designated VGAM RNA, also designated SEQ ID:5060.

[79848] Another function of VGAM2349 is therefore inhibition of LOC93320 (Accession XM_050534). Accordingly, utilities of VGAM2349 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93320. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2350 (VGAM2350) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79849] VGAM2350 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2350 was detected is described hereinabove with reference to Figs. 1-8.

[79850] VGAM2350 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2350 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79851] VGAM2350 gene encodes a VGAM2350 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2350 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2350 precursor RNA is designated SEQ ID:2336, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2336 is located at position 13649 relative to the genome of Equine Herpesvirus 2.

[79852] VGAM2350 precursor RNA folds onto itself, forming VGAM2350 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79853] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2350 folded precursor RNA into VGAM2350 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2350 RNA is designated SEQ ID:5061, and is provided hereinbelow with reference to the sequence listing part.

[79854] VGAM2350 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2350 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2350 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79855] VGAM2350 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2350 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2350 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2350 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2350 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79856] The complementary binding of VGAM2350 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2350 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2350 host target RNA into VGAM2350 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79857] It is appreciated that VGAM2350 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2350 host target genes. The mRNA of each one of this plurality of VGAM2350 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2350 RNA, herein designated VGAM RNA, and which when bound by VGAM2350 RNA causes inhibition of translation of respective one or more VGAM2350 host target proteins.

[79858] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2350 gene, herein designated VGAM GENE, on one or more VGAM2350 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79859] It is yet further appreciated that a function of VGAM2350 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2350 correlate with, and may be deduced from, the identity of the host target genes which VGAM2350 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79860] Nucleotide sequences of the VGAM2350 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2350 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2350 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2350 are further described hereinbelow with reference to Table 1.

[79861] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2350 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2350 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79862] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2350 gene, herein designated VGAM is inhibition of expression of VGAM2350 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2350 correlate with, and may be deduced from, the identity of the target genes which VGAM2350 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79863] A Disintegrin and Metalloproteinase Domain 8 (ADAM8, Accession NM_001109) is a VGAM2350 host target gene. ADAM8 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by ADAM8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAM8 BINDING SITE, designated SEQ ID:6766, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79864] A function of VGAM2350 is therefore inhibition of A Disintegrin and Metalloproteinase Domain 8 (ADAM8, Accession NM_001109). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAM8. Bone Morphogenetic Protein 1 (BMP1, Accession NM_006131) is another VGAM2350 host target gene. BMP1 BINDING SITE1 and BMP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by BMP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BMP1 BINDING SITE1 and BMP1 BINDING SITE2, designated SEQ ID:12771 and SEQ ID:12774 respectively, to the nucleotide sequence of VGAM2350 RNA, herein

designated VGAM RNA, also designated SEQ ID:5061.

[79865] Another function of VGAM2350 is therefore inhibition of Bone Morphogenetic Protein 1 (BMP1, Accession NM_006131), a gene which cleaves procollagens leading to formation of extracellular matrix. Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BMP1. The function of BMP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM247.Integrin, Alpha L (antigen CD11A (p180), Lymphocyte Function-associated Antigen 1; Alpha Polypeptide) (ITGAL, Accession NM_002209) is another VGAM2350 host target gene. ITGAL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGAL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGAL BINDING SITE, designated SEQ ID:7970, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79866] Another function of VGAM2350 is therefore inhibition of

Integrin, Alpha L (antigen CD11A (p180), Lymphocyte Function-associated Antigen 1; Alpha Polypeptide) (ITGAL, Accession NM_002209), a gene which s a receptor for icam1, icam2, icam3 and icam4. it is involved in a variety of immune phenomena including leukocyte-endothelial cell interaction, cytotoxic t-cell mediated killing, and antibody dependent killing by granulocytes and monocytes. Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAL. The function of ITGAL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Laminin, Gamma 1 (formerly LAMB2) (LAMC1, Accession NM_002293) is another VGAM2350 host target gene. LAMC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LAMC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LAMC1 BINDING SITE, designated SEQ ID:8076, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79867] Another function of VGAM2350 is therefore inhibition of Laminin, Gamma 1 (formerly LAMB2) (LAMC1, Accession NM_002293), a gene which may mediate the attachment, migration, and organization of cells into tissues. Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LAMC1. The function of LAMC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM812.P3 (Accession NM_019848) is another VGAM2350 host target gene. P3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by P3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P3 BINDING SITE, designated SEQ ID:21255, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79868] Another function of VGAM2350 is therefore inhibition of P3 (Accession NM_019848). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P3.

Presenilin 2 (Alzheimer disease 4) (PSEN2, Accession NM_000447) is another VGAM2350 host target gene. PSEN2 BINDING SITE1 and PSEN2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PSEN2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSEN2 BINDING SITE1 and PSEN2 BINDING SITE2, designated SEQ ID:6034 and SEQ ID:14864 respectively, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79869] Another function of VGAM2350 is therefore inhibition of Presenilin 2 (Alzheimer disease 4) (PSEN2, Accession NM_000447). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSEN2. Transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM2, Accession NM_004613) is another VGAM2350 host target gene. TGM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TGM2, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TGM2 BINDING SITE, designated SEQ ID:10955, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79870] Another function of VGAM2350 is therefore inhibition of Transglutaminase 2 (C polypeptide, protein-glutamine-gamma-glutamyltransferase) (TGM2, Accession NM_004613), a gene which catalyzes the cross-linking of proteins and the conjugation of polyamines to proteins. Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGM2. The function of TGM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM899.TIC (Accession NM_012455) is another VGAM2350 host target gene. TIC BINDING SITE1 and TIC BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TIC, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIC BINDING SITE1 and TIC BINDING

SITE2, designated SEQ ID:14826 and SEQ ID:14827 respectively, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79871] Another function of VGAM2350 is therefore inhibition of TIC (Accession NM_012455). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIC. Apg4B (Accession NM_013325) is another VGAM2350 host target gene. Apg4B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Apg4B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Apg4B BINDING SITE, designated SEQ ID:14976, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79872] Another function of VGAM2350 is therefore inhibition of Apg4B (Accession NM_013325). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Apg4B. Chromosome 11 Open Reading Frame 9 (C11orf9, Acces-

sion NM_013279) is another VGAM2350 host target gene. C11orf9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf9 BINDING SITE, designated SEQ ID:14945, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79873] Another function of VGAM2350 is therefore inhibition of Chromosome 11 Open Reading Frame 9 (C11orf9, Accession NM_013279). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf9. Calcium Channel, Voltage-dependent, Alpha 1H Subunit (CACNA1H, Accession NM_021098) is another VGAM2350 host target gene. CACNA1H BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CACNA1H, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CACNA1H BINDING SITE,

designated SEQ ID:22077, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79874] Another function of VGAM2350 is therefore inhibition of Calcium Channel, Voltage-dependent, Alpha 1H Subunit (CACNA1H, Accession NM_021098). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNA1H. Cat Eye Syndrome Chromosome Region, Candidate 7 (CECR7, Accession XM_086803) is another VGAM2350 host target gene. CECR7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CECR7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CECR7 BINDING SITE, designated SEQ ID:38878, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79875] Another function of VGAM2350 is therefore inhibition of Cat Eye Syndrome Chromosome Region, Candidate 7 (CECR7, Accession XM_086803). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with CECR7. Chorionic Gonadotropin, Beta Polypeptide 7 (CGB7, Accession NM_033142) is another VGAM2350 host target gene. CGB7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CGB7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CGB7 BINDING SITE, designated SEQ ID:26993, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79876] Another function of VGAM2350 is therefore inhibition of Chorionic Gonadotropin, Beta Polypeptide 7 (CGB7, Accession NM_033142). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGB7. CRMP5 (Accession NM_020134) is another VGAM2350 host target gene. CRMP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRMP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRMP5 BINDING SITE, designated SEQ

ID:21332, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79877] Another function of VGAM2350 is therefore inhibition of CRMP5 (Accession NM_020134). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRMP5. FLJ11160 (Accession NM_018344) is another VGAM2350 host target gene. FLJ11160 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11160 BINDING SITE, designated SEQ ID:20352, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79878] Another function of VGAM2350 is therefore inhibition of FLJ11160 (Accession NM_018344). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11160. FLJ12438 (Accession NM_021933) is another VGAM2350 host target gene. FLJ12438 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12438, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12438 BINDING SITE, designated SEQ ID:22455, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79879] Another function of VGAM2350 is therefore inhibition of FLJ12438 (Accession NM_021933). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12438. FLJ14957 (Accession NM_032866) is another VGAM2350 host target gene. FLJ14957 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14957, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14957 BINDING SITE, designated SEQ ID:26682, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79880] Another function of VGAM2350 is therefore inhibition of

FLJ14957 (Accession NM_032866). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14957. FLJ22195 (Accession NM_022758) is another VGAM2350 host target gene. FLJ22195 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22195 BINDING SITE, designated SEQ ID:22998, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79881] Another function of VGAM2350 is therefore inhibition of FLJ22195 (Accession NM_022758). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22195. FLJ23306 (Accession NM_024530) is another VGAM2350 host target gene. FLJ23306 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23306, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ23306 BINDING SITE, designated SEQ ID:23734, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79882] Another function of VGAM2350 is therefore inhibition of FLJ23306 (Accession NM_024530). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23306. Junctional Adhesion Molecule 1 (JAM1, Accession NM_144503) is another VGAM2350 host target gene. JAM1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by JAM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JAM1 BINDING SITE, designated SEQ ID:29339, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79883] Another function of VGAM2350 is therefore inhibition of Junctional Adhesion Molecule 1 (JAM1, Accession NM_144503). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAM1. K-ALPHA-1

(Accession XM_084866) is another VGAM2350 host target gene. K-ALPHA-1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by K-ALPHA-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of K-ALPHA-1 BINDING SITE, designated SEQ ID:37743, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79884] Another function of VGAM2350 is therefore inhibition of K-ALPHA-1 (Accession XM_084866). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with K-ALPHA-1. KIAA0544 (Accession XM_048119) is another VGAM2350 host target gene. KIAA0544 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0544, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0544 BINDING SITE, designated SEQ ID:35111, to the nucleotide sequence of VGAM2350 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5061.

[79885] Another function of VGAM2350 is therefore inhibition of KIAA0544 (Accession XM_048119). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0544. KIAA0789 (Accession XM_033113) is another VGAM2350 host target gene. KIAA0789 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0789, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0789 BINDING SITE, designated SEQ ID:31847, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79886] Another function of VGAM2350 is therefore inhibition of KIAA0789 (Accession XM_033113). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0789. KIAA0945 (Accession NM_014952) is another VGAM2350 host target gene. KIAA0945 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0945, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0945 BINDING SITE, designated SEQ ID:17295, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79887] Another function of VGAM2350 is therefore inhibition of KIAA0945 (Accession NM_014952). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0945. KIAA1055 (Accession XM_038509) is another VGAM2350 host target gene. KIAA1055 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1055, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1055 BINDING SITE, designated SEQ ID:32851, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79888] Another function of VGAM2350 is therefore inhibition of KIAA1055 (Accession XM_038509). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1055. KIAA1762 (Accession XM_033370) is another VGAM2350 host target gene. KIAA1762 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1762, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1762 BINDING SITE, designated SEQ ID:31912, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79889] Another function of VGAM2350 is therefore inhibition of KIAA1762 (Accession XM_033370). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1762. KIAA1906 (Accession XM_055095) is another VGAM2350 host target gene. KIAA1906 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1906 BINDING SITE, designated SEQ ID:36228, to the

nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79890] Another function of VGAM2350 is therefore inhibition of KIAA1906 (Accession XM_055095). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1906. Mitogen-activated Protein Kinase Kinase Kinase 3 (MAP3K3, Accession NM_002401) is another VGAM2350 host target gene. MAP3K3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K3 BINDING SITE, designated SEQ ID:8221, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79891] Another function of VGAM2350 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 3 (MAP3K3, Accession NM_002401). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K3. MDN1, Midasin Homolog (yeast) (MDN1, Acces-

sion XM_031539) is another VGAM2350 host target gene. MDN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MDN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MDN1 BINDING SITE, designated SEQ ID:31410, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79892] Another function of VGAM2350 is therefore inhibition of MDN1, Midasin Homolog (yeast) (MDN1, Accession XM_031539). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDN1. MGC13170 (Accession NM_032712) is another VGAM2350 host target gene. MGC13170 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC13170, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13170 BINDING SITE, designated SEQ ID:26433, to the nucleotide sequence of

VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79893] Another function of VGAM2350 is therefore inhibition of MGC13170 (Accession NM_032712). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13170. Neuronal Pentraxin Receptor (NPTXR, Accession NM_058178) is another VGAM2350 host target gene. NPTXR BINDING SITE1 and NPTXR BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NPTXR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPTXR BINDING SITE1 and NPTXR BINDING SITE2, designated SEQ ID:27733 and SEQ ID:15585 respectively, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79894] Another function of VGAM2350 is therefore inhibition of Neuronal Pentraxin Receptor (NPTXR, Accession NM_058178). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR. START Domain

Containing 7 (STARD7, Accession NM_020151) is another VGAM2350 host target gene. STARD7 BINDING SITE1 through STARD7 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by STARD7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STARD7 BINDING SITE1 through STARD7 BINDING SITE3, designated SEQ ID:21357, SEQ ID:21358 and SEQ ID:29260 respectively, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79895] Another function of VGAM2350 is therefore inhibition of START Domain Containing 7 (STARD7, Accession NM_020151). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STARD7. LOC120425 (Accession XM_058463) is another VGAM2350 host target gene. LOC120425 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120425, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of LOC120425 BINDING SITE, designated SEQ ID:36621, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79896] Another function of VGAM2350 is therefore inhibition of LOC120425 (Accession XM_058463). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120425. LOC146823 (Accession XM_097105) is another VGAM2350 host target gene. LOC146823 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146823, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146823 BINDING SITE, designated SEQ ID:40747, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79897] Another function of VGAM2350 is therefore inhibition of LOC146823 (Accession XM_097105). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146823. LOC150372 (Accession XM_086893) is an-

other VGAM2350 host target gene. LOC150372 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150372, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150372 BINDING SITE, designated SEQ ID:38941, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79898] Another function of VGAM2350 is therefore inhibition of LOC150372 (Accession XM_086893). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150372. LOC151176 (Accession XM_098016) is another VGAM2350 host target gene. LOC151176 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151176, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151176 BINDING SITE, designated SEQ ID:41314, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79899] Another function of VGAM2350 is therefore inhibition of LOC151176 (Accession XM_098016). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151176. LOC153577 (Accession XM_098394) is another VGAM2350 host target gene. LOC153577 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153577 BINDING SITE, designated SEQ ID:41644, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79900] Another function of VGAM2350 is therefore inhibition of LOC153577 (Accession XM_098394). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153577. LOC157653 (Accession XM_088353) is another VGAM2350 host target gene. LOC157653 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157653, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157653 BINDING SITE, designated SEQ ID:39634, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79901] Another function of VGAM2350 is therefore inhibition of LOC157653 (Accession XM_088353). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157653. LOC163682 (Accession XM_099402) is another VGAM2350 host target gene. LOC163682 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC163682, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163682 BINDING SITE, designated SEQ ID:42095, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79902] Another function of VGAM2350 is therefore inhibition of LOC163682 (Accession XM_099402). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC163682. LOC222681 (Accession XM_167116) is another VGAM2350 host target gene. LOC222681 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222681, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222681 BINDING SITE, designated SEQ ID:44615, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79903] Another function of VGAM2350 is therefore inhibition of LOC222681 (Accession XM_167116). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222681. LOC253216 (Accession XM_170765) is another VGAM2350 host target gene. LOC253216 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253216, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253216 BINDING SITE, designated SEQ ID:45518, to the nucleotide sequence of VGAM2350 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5061.

[79904] Another function of VGAM2350 is therefore inhibition of LOC253216 (Accession XM_170765). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253216. LOC257507 (Accession XM_175204) is another VGAM2350 host target gene. LOC257507 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257507, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257507 BINDING SITE, designated SEQ ID:46681, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79905] Another function of VGAM2350 is therefore inhibition of LOC257507 (Accession XM_175204). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257507. LOC257625 (Accession XM_175267) is another VGAM2350 host target gene. LOC257625 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257625, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257625 BINDING SITE, designated SEQ ID:46737, to the nucleotide sequence of VGAM2350 RNA, herein designated VGAM RNA, also designated SEQ ID:5061.

[79906] Another function of VGAM2350 is therefore inhibition of LOC257625 (Accession XM_175267). Accordingly, utilities of VGAM2350 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257625. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2351 (VGAM2351) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79907] VGAM2351 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2351 was detected is described hereinabove with reference to Figs. 1-8.

[79908] VGAM2351 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2.

VGAM2351 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79909] VGAM2351 gene encodes a VGAM2351 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2351 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2351 precursor RNA is designated SEQ ID:2337, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2337 is located at position 28694 relative to the genome of Equine Herpesvirus 2.

[79910] VGAM2351 precursor RNA folds onto itself, forming VGAM2351 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79911] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2351 folded precursor RNA into VGAM2351 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2351 RNA is designated SEQ ID:5062, and is provided hereinbelow with reference to the sequence listing part.

[79912] VGAM2351 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2351 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2351 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79913] VGAM2351 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2351 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2351 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2351 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2351 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79914] The complementary binding of VGAM2351 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2351 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2351 host target RNA into VGAM2351 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79915] It is appreciated that VGAM2351 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2351 host target genes. The mRNA of each one of this plurality of VGAM2351 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2351 RNA, herein designated VGAM RNA, and which when bound by VGAM2351 RNA causes inhibition of translation of respective one or more VGAM2351 host target proteins.

[79916] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2351 gene, herein designated VGAM GENE, on one or more VGAM2351 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[79917] It is yet further appreciated that a function of VGAM2351 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2351 correlate with, and may be deduced from, the identity of the host target genes which VGAM2351 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79918] Nucleotide sequences of the VGAM2351 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2351 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2351 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2351 are further described hereinbelow with reference to Table 1.

[79919] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2351 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2351 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79920] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2351 gene, herein designated VGAM is inhibition of expression of VGAM2351 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2351 correlate with, and may be deduced from, the identity of the target genes which VGAM2351 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79921] A Disintegrin-like and Metalloprotease (reprolysin type) with Thrombospondin Type 1 Motif, 4 (ADAMTS4, Accession NM_005099) is a VGAM2351 host target gene. ADAMTS4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADAMTS4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of ADAMTS4 BINDING SITE, designated SEQ ID:11569, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79922] A function of VGAM2351 is therefore inhibition of A Disintegrin-like and Metalloprotease (reprolysin type) with Thrombospondin Type 1 Motif, 4 (ADAMTS4, Accession NM_005099), a gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAMTS4. The function of ADAMTS4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM809.Activating Transcription Factor 7 (ATF7, Accession NM_006856) is another VGAM2351 host target gene. ATF7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATF7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATF7 BINDING SITE, designated SEQ ID:13725,

to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79923] Another function of VGAM2351 is therefore inhibition of Activating Transcription Factor 7 (ATF7, Accession NM_006856). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATF7. Glucose-6-phosphatase, Catalytic (glycogen storage disease type I, von Gierke disease) (G6PC, Accession NM_000151) is another VGAM2351 host target gene. G6PC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by G6PC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of G6PC BINDING SITE, designated SEQ ID:5658, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79924] Another function of VGAM2351 is therefore inhibition of Glucose-6-phosphatase, Catalytic (glycogen storage disease type I, von Gierke disease) (G6PC, Accession NM_000151). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with G6PC. Huntingtin (Huntington disease) (HD, Accession NM_002111) is another VGAM2351 host target gene. HD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HD BINDING SITE, designated SEQ ID:7897, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79925] Another function of VGAM2351 is therefore inhibition of Huntingtin (Huntington disease) (HD, Accession NM_002111). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HD. Interleukin-1 Receptor-associated Kinase 4 (IRAK4, Accession XM_028349) is another VGAM2351 host target gene. IRAK4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IRAK4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRAK4 BIND-

ING SITE, designated SEQ ID:30691, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79926] Another function of VGAM2351 is therefore inhibition of Interleukin-1 Receptor-associated Kinase 4 (IRAK4, Accession XM_028349), a gene which may function as an IRAK1 kinase, triggering a cascade of phosphorylation events. Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRAK4. The function of IRAK4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1291.NDRG Family Member 3 (NDRG3, Accession NM_032013) is another VGAM2351 host target gene. NDRG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NDRG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDRG3 BINDING SITE, designated SEQ ID:25726, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79927] Another function of VGAM2351 is therefore inhibition of NDRG Family Member 3 (NDRG3, Accession NM_032013). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDRG3. Regenerating Islet-derived-like, Pancreatic Stone Protein-like, Pancreatic Thread Protein-like (rat) (REGL, Accession NM_006508) is another VGAM2351 host target gene. REGL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by REGL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of REGL BINDING SITE, designated SEQ ID:13256, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79928] Another function of VGAM2351 is therefore inhibition of Regenerating Islet-derived-like, Pancreatic Stone Protein-like, Pancreatic Thread Protein-like (rat) (REGL, Accession NM_006508), a gene which is a member of REG family with unknown function. Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with REGL.

The function of REGL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.SMT3 Suppressor of Mif Two 3 Homolog 1 (yeast) (SMT3H1, Accession XM_009805) is another VGAM2351 host target gene. SMT3H1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMT3H1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMT3H1 BINDING SITE, designated SEQ ID:30126, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79929] Another function of VGAM2351 is therefore inhibition of SMT3 Suppressor of Mif Two 3 Homolog 1 (yeast) (SMT3H1, Accession XM_009805), a gene which is involved in the function and/or structure of the eukaryotic kinetochore. Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMT3H1. The function of SMT3H1 and its association with various diseases and clinical conditions, has been established by previous stud-

ies, as described hereinabove with reference to VGAM119.FLJ13102 (Accession NM_024887) is another VGAM2351 host target gene. FLJ13102 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13102, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13102 BINDING SITE, designated SEQ ID:24344, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79930] Another function of VGAM2351 is therefore inhibition of FLJ13102 (Accession NM_024887). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13102. FLJ20320 (Accession NM_017765) is another VGAM2351 host target gene. FLJ20320 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20320, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20320 BINDING SITE, designated SEQ ID:19384, to the nucleotide

sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79931] Another function of VGAM2351 is therefore inhibition of FLJ20320 (Accession NM_017765). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20320. FLJ20584 (Accession NM_017891) is another VGAM2351 host target gene. FLJ20584 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20584, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20584 BINDING SITE, designated SEQ ID:19562, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79932] Another function of VGAM2351 is therefore inhibition of FLJ20584 (Accession NM_017891). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20584. G Protein-coupled Receptor Kinase-interactor 1 (GIT1, Accession NM_014030) is another VGAM2351 host target gene. GIT1 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by GIT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GIT1 BINDING SITE, designated SEQ ID:15256, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79933] Another function of VGAM2351 is therefore inhibition of G Protein-coupled Receptor Kinase-interactor 1 (GIT1, Accession NM_014030). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GIT1. KIAA0980 (Accession NM_025176) is another VGAM2351 host target gene. KIAA0980 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0980, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0980 BINDING SITE, designated SEQ ID:24812, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79934] Another function of VGAM2351 is therefore inhibition of KIAA0980 (Accession NM_025176). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0980. KIAA1553 (Accession XM_166320) is another VGAM2351 host target gene. KIAA1553 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1553, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1553 BINDING SITE, designated SEQ ID:44144, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79935] Another function of VGAM2351 is therefore inhibition of KIAA1553 (Accession XM_166320). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1553. KIAA1854 (Accession XM_049884) is another VGAM2351 host target gene. KIAA1854 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1854, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1854 BINDING SITE, designated SEQ ID:35535, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79936] Another function of VGAM2351 is therefore inhibition of KIAA1854 (Accession XM_049884). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1854. Oxysterol Binding Protein-like 8 (OSBPL8, Accession NM_020841) is another VGAM2351 host target gene. OSBPL8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OSBPL8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL8 BINDING SITE, designated SEQ ID:21910, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79937] Another function of VGAM2351 is therefore inhibition of Oxysterol Binding Protein-like 8 (OSBPL8, Accession NM_020841). Accordingly, utilities of VGAM2351 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL8. PHRET1 (Accession NM_021200) is another VGAM2351 host target gene. PHRET1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PHRET1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PHRET1 BINDING SITE, designated SEQ ID:22178, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79938] Another function of VGAM2351 is therefore inhibition of PHRET1 (Accession NM_021200). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHRET1. Ubiquitin Specific Protease 2 (USP2, Accession NM_004205) is another VGAM2351 host target gene. USP2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by USP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

USP2 BINDING SITE, designated SEQ ID:10401, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79939] Another function of VGAM2351 is therefore inhibition of Ubiquitin Specific Protease 2 (USP2, Accession NM_004205). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP2. LOC130412 (Accession XM_065708) is another VGAM2351 host target gene. LOC130412 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC130412, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130412 BINDING SITE, designated SEQ ID:37293, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79940] Another function of VGAM2351 is therefore inhibition of LOC130412 (Accession XM_065708). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130412. LOC146337 (Accession XM_096982) is an-

other VGAM2351 host target gene. LOC146337 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146337, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146337 BINDING SITE, designated SEQ ID:40693, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79941] Another function of VGAM2351 is therefore inhibition of LOC146337 (Accession XM_096982). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146337. LOC152794 (Accession XM_087525) is another VGAM2351 host target gene. LOC152794 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152794 BINDING SITE, designated SEQ ID:39322, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79942] Another function of VGAM2351 is therefore inhibition of LOC152794 (Accession XM_087525). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152794. LOC206012 (Accession XM_116275) is another VGAM2351 host target gene. LOC206012 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC206012, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC206012 BINDING SITE, designated SEQ ID:43110, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79943] Another function of VGAM2351 is therefore inhibition of LOC206012 (Accession XM_116275). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC206012. LOC254251 (Accession XM_171088) is another VGAM2351 host target gene. LOC254251 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254251, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254251 BINDING SITE, designated SEQ ID:45901, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79944] Another function of VGAM2351 is therefore inhibition of LOC254251 (Accession XM_171088). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254251. LOC257480 (Accession XM_085456) is another VGAM2351 host target gene. LOC257480 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257480, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257480 BINDING SITE, designated SEQ ID:38146, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79945] Another function of VGAM2351 is therefore inhibition of LOC257480 (Accession XM_085456). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC257480. LOC257612 (Accession XM_175270) is another VGAM2351 host target gene. LOC257612 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257612, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257612 BINDING SITE, designated SEQ ID:46743, to the nucleotide sequence of VGAM2351 RNA, herein designated VGAM RNA, also designated SEQ ID:5062.

[79946] Another function of VGAM2351 is therefore inhibition of LOC257612 (Accession XM_175270). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257612. LOC91156 (Accession XM_036558) is another VGAM2351 host target gene. LOC91156 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91156, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91156 BINDING SITE, designated SEQ ID:32466, to the nucleotide sequence of VGAM2351 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5062.

[79947] Another function of VGAM2351 is therefore inhibition of LOC91156 (Accession XM_036558). Accordingly, utilities of VGAM2351 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91156. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2352 (VGAM2352) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[79948] VGAM2352 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2352 was detected is described hereinabove with reference to Figs. 1-8.

[79949] VGAM2352 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2352 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[79950] VGAM2352 gene encodes a VGAM2352 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2352 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2352 precursor RNA is designated SEQ ID:2338, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2338 is located at position 8029 relative to the genome of Equine Herpesvirus 2.

[79951] VGAM2352 precursor RNA folds onto itself, forming VGAM2352 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[79952] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2352 folded precursor RNA into VGAM2352 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2352 RNA is designated SEQ ID:5063, and is provided hereinbelow with reference to the sequence listing part.

[79953] VGAM2352 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2352 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2352 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[79954] VGAM2352 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2352 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2352 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2352 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2352 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[79955] The complementary binding of VGAM2352 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2352 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2352 host target RNA into VGAM2352 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[79956] It is appreciated that VGAM2352 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2352 host target genes. The mRNA of

each one of this plurality of VGAM2352 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2352 RNA, herein designated VGAM RNA, and which when bound by VGAM2352 RNA causes inhibition of translation of respective one or more VGAM2352 host target proteins.

[79957] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2352 gene, herein designated VGAM GENE, on one or more VGAM2352 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[79958] It is yet further appreciated that a function of VGAM2352 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2352 correlate with, and may be deduced from, the identity of the host target genes which VGAM2352 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[79959] Nucleotide sequences of the VGAM2352 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2352 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2352 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2352 are further described hereinbelow with reference to Table 1.

[79960] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2352 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2352 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[79961] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2352 gene, herein designated VGAM is inhibition of expression of VGAM2352 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2352 correlate with, and may be deduced from, the identity of the target genes which VGAM2352 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[79962] ATPase, Cu++ Transporting, Beta Polypeptide (Wilson disease) (ATP7B, Accession NM_000053) is a VGAM2352 host target gene. ATP7B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP7B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP7B BINDING SITE, designated SEQ ID:5503, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79963] A function of VGAM2352 is therefore inhibition of ATPase, Cu++ Transporting, Beta Polypeptide (Wilson disease)

(ATP7B, Accession NM_000053). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7B. Beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1, Accession NM_018644) is another VGAM2352 host target gene. B3GAT1 BINDING SITE1 and B3GAT1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by B3GAT1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B3GAT1 BINDING SITE1 and B3GAT1 BINDING SITE2, designated SEQ ID:20715 and SEQ ID:27627 respectively, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79964] Another function of VGAM2352 is therefore inhibition of Beta-1,3-glucuronyltransferase 1 (glucuronosyltransferase P) (B3GAT1, Accession NM_018644). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B3GAT1. CERD4 (Accession NM_012074) is another VGAM2352 host target gene.

CERD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CERD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CERD4 BINDING SITE, designated SEQ ID:14342, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79965] Another function of VGAM2352 is therefore inhibition of CERD4 (Accession NM_012074). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CERD4. Dihydropyrimidinase-like 3 (DPYSL3, Accession NM_001387) is another VGAM2352 host target gene. DPYSL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DPYSL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DPYSL3 BINDING SITE, designated SEQ ID:7069, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ

ID:5063.

[79966] Another function of VGAM2352 is therefore inhibition of Dihydropyrimidinase-like 3 (DPYSL3, Accession NM_001387), a gene which is a member of the dihydropyrimidinase family. Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPYSL3. The function of DPYSL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM24.Guanine Nucleotide Binding Protein (G protein), Beta Polypeptide 1 (GNB1, Accession NM_002074) is another VGAM2352 host target gene. GNB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNB1 BINDING SITE, designated SEQ ID:7848, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79967] Another function of VGAM2352 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Beta

Polypeptide 1 (GNB1, Accession NM_002074). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNB1. Interleukin 2 Receptor, Alpha (IL2RA, Accession NM_000417) is another VGAM2352 host target gene. IL2RA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL2RA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL2RA BINDING SITE, designated SEQ ID:5997, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79968] Another function of VGAM2352 is therefore inhibition of Interleukin 2 Receptor, Alpha (IL2RA, Accession NM_000417), a gene which plays a role in T cell mediated immune response. Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL2RA. The function of IL2RA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1168.Low Density Lipoprotein-related Protein 1

(alpha-2-macroglobulin receptor) (LRP1, Accession NM_002332) is another VGAM2352 host target gene. LRP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LRP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRP1 BINDING SITE, designated SEQ ID:8135, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79969] Another function of VGAM2352 is therefore inhibition of Low Density Lipoprotein-related Protein 1 (alpha-2-macroglobulin receptor) (LRP1, Accession NM_002332), a gene which is a recycling lipoprotein receptor with possible growth-modulating effects. Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRP1. The function of LRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM885.MAX Gene Associated (MGA, Accession XM_031689) is another VGAM2352 host target gene. MGA BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by MGA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGA BINDING SITE, designated SEQ ID:31453, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79970] Another function of VGAM2352 is therefore inhibition of MAX Gene Associated (MGA, Accession XM_031689), a gene which plays a role in the final steps of digestion of starch. Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGA. The function of MGA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2003.Moesin (MSN, Accession XM_013042) is another VGAM2352 host target gene. MSN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MSN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MSN BINDING SITE, designated SEQ

ID:30224, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79971] Another function of VGAM2352 is therefore inhibition of Moesin (MSN, Accession XM_013042), a gene which may have a role linking the cytoskeleton to the plasma membrane. Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSN. The function of MSN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM248.RAN Binding Protein 3 (RANBP3, Accession NM_003624) is another VGAM2352 host target gene. RANBP3 BINDING SITE1 and RANBP3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RANBP3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RANBP3 BINDING SITE1 and RANBP3 BINDING SITE2, designated SEQ ID:9687 and SEQ ID:14239 respectively, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ

ID:5063.

[79972] Another function of VGAM2352 is therefore inhibition of RAN Binding Protein 3 (RANBP3, Accession NM_003624). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RANBP3. Zinc Finger Protein 141 (clone pHZ-44) (ZNF141, Accession NM_003441) is another VGAM2352 host target gene. ZNF141 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF141, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF141 BINDING SITE, designated SEQ ID:9496, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79973] Another function of VGAM2352 is therefore inhibition of Zinc Finger Protein 141 (clone pHZ-44) (ZNF141, Accession NM_003441). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF141. AFAP (Accession NM_021638) is another VGAM2352 host target gene. AFAP BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by AFAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AFAP BINDING SITE, designated SEQ ID:22289, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79974] Another function of VGAM2352 is therefore inhibition of AFAP (Accession NM_021638). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AFAP. Discoidin Domain Receptor Family, Member 1 (DDR1, Accession NM_013993) is another VGAM2352 host target gene. DDR1 BINDING SITE1 through DDR1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DDR1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDR1 BINDING SITE1 through DDR1 BINDING SITE3, designated SEQ ID:15178, SEQ ID:15180 and SEQ ID:7677 respectively, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79975] Another function of VGAM2352 is therefore inhibition of Discoidin Domain Receptor Family, Member 1 (DDR1, Accession NM_013993). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDR1. FLJ12895 (Accession NM_023926) is another VGAM2352 host target gene. FLJ12895 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12895, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12895 BINDING SITE, designated SEQ ID:23403, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79976] Another function of VGAM2352 is therefore inhibition of FLJ12895 (Accession NM_023926). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12895. FLJ13150 (Accession NM_024813) is another VGAM2352 host target gene. FLJ13150 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13150, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13150 BINDING SITE, designated SEQ ID:24200, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79977] Another function of VGAM2352 is therefore inhibition of FLJ13150 (Accession NM_024813). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13150. FLJ20209 (Accession XM_098142) is another VGAM2352 host target gene. FLJ20209 BINDING SITE1 and FLJ20209 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ20209, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20209 BINDING SITE1 and FLJ20209 BINDING SITE2, designated SEQ ID:41402 and SEQ ID:41403 respectively, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79978] Another function of VGAM2352 is therefore inhibition of

FLJ20209 (Accession XM_098142). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20209. HIG2 (Accession NM_013332) is another VGAM2352 host target gene. HIG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HIG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HIG2 BINDING SITE, designated SEQ ID:14977, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79979] Another function of VGAM2352 is therefore inhibition of HIG2 (Accession NM_013332). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HIG2. KIAA0355 (Accession NM_014686) is another VGAM2352 host target gene. KIAA0355 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0355, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of KIAA0355 BINDING SITE, designated SEQ ID:16187, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79980] Another function of VGAM2352 is therefore inhibition of KIAA0355 (Accession NM_014686). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0355. KIAA0514 (Accession NM_014696) is another VGAM2352 host target gene. KIAA0514 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0514, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0514 BINDING SITE, designated SEQ ID:16200, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79981] Another function of VGAM2352 is therefore inhibition of KIAA0514 (Accession NM_014696). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0514. KIAA0545 (Accession XM_032278) is another

VGAM2352 host target gene. KIAA0545 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0545, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0545 BINDING SITE, designated SEQ ID:31633, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79982] Another function of VGAM2352 is therefore inhibition of KIAA0545 (Accession XM_032278). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0545. KIAA1272 (Accession XM_046600) is another VGAM2352 host target gene. KIAA1272 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1272, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1272 BINDING SITE, designated SEQ ID:34759, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79983] Another function of VGAM2352 is therefore inhibition of KIAA1272 (Accession XM_046600). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1272. KIAA1871 (Accession XM_028409) is another VGAM2352 host target gene. KIAA1871 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1871 BINDING SITE, designated SEQ ID:30702, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79984] Another function of VGAM2352 is therefore inhibition of KIAA1871 (Accession XM_028409). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1871. KIAA1879 (Accession XM_056635) is another VGAM2352 host target gene. KIAA1879 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1879, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1879 BINDING SITE, designated SEQ ID:36412, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79985] Another function of VGAM2352 is therefore inhibition of KIAA1879 (Accession XM_056635). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1879. Phosphate Cytidylyltransferase 2, Ethanolamine (PCYT2, Accession NM_002861) is another VGAM2352 host target gene. PCYT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCYT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCYT2 BINDING SITE, designated SEQ ID:8761, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79986] Another function of VGAM2352 is therefore inhibition of Phosphate Cytidylyltransferase 2, Ethanolamine (PCYT2, Accession NM_002861). Accordingly, utilities of

VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCYT2. Ubiquitin Specific Protease 22 (USP22, Accession XM_042698) is another VGAM2352 host target gene. USP22 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP22, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP22 BINDING SITE, designated SEQ ID:33750, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79987] Another function of VGAM2352 is therefore inhibition of Ubiquitin Specific Protease 22 (USP22, Accession XM_042698). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP22. LOC112476 (Accession NM_145239) is another VGAM2352 host target gene. LOC112476 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC112476, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112476 BINDING SITE, designated SEQ ID:29749, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79988] Another function of VGAM2352 is therefore inhibition of LOC112476 (Accession NM_145239). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112476. LOC144501 (Accession XM_096612) is another VGAM2352 host target gene. LOC144501 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144501, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144501 BINDING SITE, designated SEQ ID:40422, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79989] Another function of VGAM2352 is therefore inhibition of LOC144501 (Accession XM_096612). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC144501. LOC150935 (Accession XM_087049) is another VGAM2352 host target gene. LOC150935 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150935, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150935 BINDING SITE, designated SEQ ID:39018, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79990] Another function of VGAM2352 is therefore inhibition of LOC150935 (Accession XM_087049). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150935. LOC151178 (Accession XM_087117) is another VGAM2352 host target gene. LOC151178 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151178 BINDING SITE, designated SEQ ID:39068, to the nucleotide sequence of VGAM2352 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5063.

[79991] Another function of VGAM2352 is therefore inhibition of LOC151178 (Accession XM_087117). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151178. LOC155435 (Accession XM_088257) is another VGAM2352 host target gene. LOC155435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155435 BINDING SITE, designated SEQ ID:39567, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79992] Another function of VGAM2352 is therefore inhibition of LOC155435 (Accession XM_088257). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155435. LOC163115 (Accession XM_092010) is another VGAM2352 host target gene. LOC163115 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC163115, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163115 BINDING SITE, designated SEQ ID:40088, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79993] Another function of VGAM2352 is therefore inhibition of LOC163115 (Accession XM_092010). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163115. LOC163682 (Accession XM_099402) is another VGAM2352 host target gene. LOC163682 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC163682, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163682 BINDING SITE, designated SEQ ID:42083, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79994] Another function of VGAM2352 is therefore inhibition of LOC163682 (Accession XM_099402). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC163682. LOC197259 (Accession XM_113849) is another VGAM2352 host target gene. LOC197259 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197259 BINDING SITE, designated SEQ ID:42471, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79995] Another function of VGAM2352 is therefore inhibition of LOC197259 (Accession XM_113849). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197259. LOC201895 (Accession XM_114396) is another VGAM2352 host target gene. LOC201895 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201895, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201895 BINDING SITE, designated SEQ ID:42924, to

the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79996] Another function of VGAM2352 is therefore inhibition of LOC201895 (Accession XM_114396). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201895. LOC220758 (Accession XM_165466) is another VGAM2352 host target gene. LOC220758 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220758, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220758 BINDING SITE, designated SEQ ID:43641, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79997] Another function of VGAM2352 is therefore inhibition of LOC220758 (Accession XM_165466). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220758. LOC221272 (Accession XM_168050) is another VGAM2352 host target gene. LOC221272 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC221272, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221272 BINDING SITE, designated SEQ ID:44961, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79998] Another function of VGAM2352 is therefore inhibition of LOC221272 (Accession XM_168050). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221272. LOC221584 (Accession XM_168132) is another VGAM2352 host target gene. LOC221584 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221584, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221584 BINDING SITE, designated SEQ ID:45040, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[79999] Another function of VGAM2352 is therefore inhibition of LOC221584 (Accession XM_168132). Accordingly, utilities

of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221584. LOC254181 (Accession XM_174526) is another VGAM2352 host target gene. LOC254181 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254181, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254181 BINDING SITE, designated SEQ ID:46596, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[80000] Another function of VGAM2352 is therefore inhibition of LOC254181 (Accession XM_174526). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254181. LOC51152 (Accession NM_016181) is another VGAM2352 host target gene. LOC51152 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51152, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC51152 BINDING SITE, designated SEQ ID:18282, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[80001] Another function of VGAM2352 is therefore inhibition of LOC51152 (Accession NM_016181). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51152. LOC51580 (Accession NM_015874) is another VGAM2352 host target gene. LOC51580 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51580, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51580 BINDING SITE, designated SEQ ID:18009, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[80002] Another function of VGAM2352 is therefore inhibition of LOC51580 (Accession NM_015874). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51580. LOC56963 (Accession XM_049372) is another VGAM2352 host target gene. LOC56963 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC56963, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56963 BINDING SITE, designated SEQ ID:35398, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[80003] Another function of VGAM2352 is therefore inhibition of LOC56963 (Accession XM_049372). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56963. LOC90317 (Accession XM_030892) is another VGAM2352 host target gene. LOC90317 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90317, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90317 BINDING SITE, designated SEQ ID:31205, to the nucleotide sequence of VGAM2352 RNA, herein designated VGAM RNA, also designated SEQ ID:5063.

[80004] Another function of VGAM2352 is therefore inhibition of

LOC90317 (Accession XM_030892). Accordingly, utilities of VGAM2352 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90317. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2353 (VGAM2353) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80005] VGAM2353 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2353 was detected is described hereinabove with reference to Figs. 1-8.

[80006] VGAM2353 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2353 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80007] VGAM2353 gene encodes a VGAM2353 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2353 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2353 precursor RNA is designated SEQ ID:2339, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2339 is located at position 15043 relative to the genome of Equine Herpesvirus 2.

[80008] VGAM2353 precursor RNA folds onto itself, forming VGAM2353 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80009] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2353 folded precursor RNA into VGAM2353 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide se-

quence of VGAM2353 RNA is designated SEQ ID:5064, and is provided hereinbelow with reference to the sequence listing part.

[80010] VGAM2353 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2353 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2353 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80011] VGAM2353 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2353 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2353 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2353 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2353 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80012] The complementary binding of VGAM2353 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2353 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2353 host target RNA into VGAM2353 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80013] It is appreciated that VGAM2353 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2353 host target genes. The mRNA of each one of this plurality of VGAM2353 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2353 RNA, herein designated VGAM RNA, and which when bound by VGAM2353 RNA causes inhibition of translation of respective one or more VGAM2353 host target proteins.

[80014] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2353 gene, herein designated VGAM GENE, on one or more VGAM2353 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80015] It is yet further appreciated that a function of VGAM2353

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2353 correlate with, and may be deduced from, the identity of the host target genes which VGAM2353 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80016] Nucleotide sequences of the VGAM2353 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2353 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2353 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2353 are further described hereinbelow with reference to Table 1.

[80017] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2353 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2353 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80018] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2353 gene, herein designated VGAM is inhibition of expression of VGAM2353 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2353 correlate with, and may be deduced from, the identity of the target genes which VGAM2353 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80019] Aristaless-like Homeobox 3 (ALX3, Accession NM_006492) is a VGAM2353 host target gene. ALX3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ALX3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ALX3 BINDING SITE, designated SEQ ID:13223, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80020] A function of VGAM2353 is therefore inhibition of Aristaless-like Homeobox 3 (ALX3, Accession NM_006492), a gene which is involved in cell-type differentiation and development. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical

conditions associated with ALX3. The function of ALX3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.AT-binding Transcription Factor 1 (ATBF1, Accession NM_006885) is another VGAM2353 host target gene. ATBF1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ATBF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATBF1 BINDING SITE, designated SEQ ID:13749, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80021] Another function of VGAM2353 is therefore inhibition of AT-binding Transcription Factor 1 (ATBF1, Accession NM_006885). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATBF1. ATPase, Cu++ Transporting, Beta Polypeptide (Wilson disease) (ATP7B, Accession NM_000053) is another VGAM2353 host target gene. ATP7B BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by ATP7B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP7B BINDING SITE, designated SEQ ID:5507, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80022] Another function of VGAM2353 is therefore inhibition of ATPase, Cu++ Transporting, Beta Polypeptide (Wilson disease) (ATP7B, Accession NM_000053). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7B. AXL Receptor Tyrosine Kinase (AXL, Accession NM_001699) is another VGAM2353 host target gene. AXL BINDING SITE1 and AXL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AXL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE1 and AXL BINDING SITE2, designated SEQ ID:7424 and SEQ ID:22445 respectively, to the nucleotide sequence of VGAM2353 RNA,

herein designated VGAM RNA, also designated SEQ ID:5064.

[80023] Another function of VGAM2353 is therefore inhibition of AXL Receptor Tyrosine Kinase (AXL, Accession NM_001699). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL. Chromosome 1 Open Reading Frame 6 (C1orf6, Accession NM_020131) is another VGAM2353 host target gene. C1orf6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C1orf6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1orf6 BINDING SITE, designated SEQ ID:21329, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80024] Another function of VGAM2353 is therefore inhibition of Chromosome 1 Open Reading Frame 6 (C1orf6, Accession NM_020131), a gene which may link ataxin-1 with the chaperone and ubiquitin/proteasome pathways . Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with C1orf6. The function of C1orf6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1286.Citron (rho-interacting, serine/threonine kinase 21) (CIT, Accession XM_045786) is another VGAM2353 host target gene. CIT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CIT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CIT BINDING SITE, designated SEQ ID:34564, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80025] Another function of VGAM2353 is therefore inhibition of Citron (rho-interacting, serine/threonine kinase 21) (CIT, Accession XM_045786), a gene which is increased several-fold by coexpression of constitutively active Rho . Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIT. The function of CIT and its association with various diseases and clinical conditions, has been established by previous studies, as described here-

inabove with reference to VGAM393.Dopamine Beta-hydroxylase (dopamine beta-monooxygenase) (DBH, Accession NM_000787) is another VGAM2353 host target gene. DBH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DBH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DBH BINDING SITE, designated SEQ ID:6440, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80026] Another function of VGAM2353 is therefore inhibition of Dopamine Beta-hydroxylase (dopamine beta-monooxygenase) (DBH, Accession NM_000787), a gene which converts dopamine to norepinephrine . Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DBH. The function of DBH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1189.Forkhead Box E1 (thyroid transcription factor 2) (FOXE1, Accession NM_004473) is another VGAM2353 host target gene. FOXE1 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FOXE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOXE1 BINDING SITE, designated SEQ ID:10784, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80027] Another function of VGAM2353 is therefore inhibition of Forkhead Box E1 (thyroid transcription factor 2) (FOXE1, Accession NM_004473). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXE1. GRB2-associated Binding Protein 2 (GAB2, Accession NM_080491) is another VGAM2353 host target gene. GAB2 BINDING SITE1 and GAB2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GAB2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAB2 BINDING SITE1 and GAB2 BINDING SITE2, designated SEQ ID:27849 and SEQ ID:14654 respectively, to the nucleotide sequence of

VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80028] Another function of VGAM2353 is therefore inhibition of GRB2-associated Binding Protein 2 (GAB2, Accession NM_080491), a gene which act as adapters for transmitting various signals. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAB2. The function of GAB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM53.Host Cell Factor C1 (VP16-accessory protein) (HCFC1, Accession XM_048390) is another VGAM2353 host target gene. HCFC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCFC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCFC1 BINDING SITE, designated SEQ ID:35159, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80029] Another function of VGAM2353 is therefore inhibition of

Host Cell Factor C1 (VP16-accessory protein) (HCFC1, Accession XM_048390), a gene which is a host cell factor, has a role in cell proliferation and can form a complex with HSV VP16. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCFC1. The function of HCFC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM341.HERV-H LTR-associating 1 (HHLA1, Accession NM_005712) is another VGAM2353 host target gene. HHLA1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HHLA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HHLA1 BINDING SITE, designated SEQ ID:12263, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80030] Another function of VGAM2353 is therefore inhibition of HERV-H LTR-associating 1 (HHLA1, Accession NM_005712), a gene which has unknown function and

with low similarity to a region of S. cerevisiae WSC4. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HHLA1. The function of HHLA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM158.Hexokinase 2 (HK2, Accession NM_000189) is another VGAM2353 host target gene. HK2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HK2 BINDING SITE, designated SEQ ID:5690, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80031] Another function of VGAM2353 is therefore inhibition of Hexokinase 2 (HK2, Accession NM_000189), a gene which plays an important role in intracellular glucose metabolism by catalyzing the conversion of glucose to glucose-6-phosphate. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HK2. The function

of HK2 has been established by previous studies. Hexokinase II is the major hexokinase expressed in skeletal muscle. Insulin has been shown to increase transcription of this gene. Lehto et al. (1993) described the isolation of genomic clones for human hexokinase-2. These clones were isolated by screening a human placental genomic library with a rat hexokinase-2 cDNA clone. A genomic clone derived from this screening was used in fluorescence in situ hybridization studies and was found to map to human chromosome 2p13.1. The human HK2 genomic clones were also screened for dinucleotide repeats. Primers were selected to amplify an approximately 224-bp CA-repeat-rich region. This repeat region was highly polymorphic; the level of heterozygosity was 0.63 in Caucasians and 0.51 in Chinese subjects. Lehto et al. (1993) carried out linkage studies between this HK2 polymorphism and 9 markers on chromosome 2. No recombinants were observed between HK2 and TGFA (OMIM Ref. No. 190170) and D2S45; the most likely map order with respect to several chromosomal markers was determined. The HK2 gene is highly expressed in rapidly growing tumors to facilitate high rates of glucose catabolism. Mathupala et al. (1995) cloned and characterized the promoter

of the rat HK2 gene from a highly glycolytic hepatoma cell line (OMIM Ref. No. AS-30D). Mathupala et al. (1997) showed that the HK2 promoter contains functionally active response elements for p53 (OMIM Ref. No. 191170). Using coexpression assays, they showed that overexpression of a mutant p53 gene found in the tumor cell line significantly and reproducibly activated the HK2 promoter and increased HK2 gene expression. Mathupala et al. (1997) stated that theirs was the first report of a possible link between loss of cell cycle control in rapidly growing cells and their high glycolytic rate.

[80032] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[80033] Lehto, M.; Xiang, K.; Stoffel, M.; Espinosa, R., III; Groop, L. C.; Le Beau, M. M.; Bell, G. I. : Human hexokinase II: localization of the polymorphic gene to chromosome 2. Diabetologia 36: 1299-1302, 1993. ; and

[80034] Mathupala, S. P.; Heese, C.; Pedersen, P. L. : Glucose catabolism in cancer cells: the type II hexokinase promoter contains functionally active response elements for the tumor suppressor.

[80035] Further studies establishing the function and utilities of

HK2 are found in John Hopkins OMIM database record ID 601125, and in sited publications numbered 6874-6881 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411) is another VGAM2353 host target gene. HLCS BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HLCS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HLCS BINDING SITE, designated SEQ ID:5991, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80036] Another function of VGAM2353 is therefore inhibition of Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLCS. Insulin Receptor Substrate 1 (IRS1, Accession NM_005544) is another VGAM2353 host

target gene. IRS1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IRS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRS1 BINDING SITE, designated SEQ ID:12068, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80037] Another function of VGAM2353 is therefore inhibition of Insulin Receptor Substrate 1 (IRS1, Accession NM_005544), a gene which may mediate the control of various cellular processes by insulin. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRS1. The function of IRS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM281.Insulin Receptor Substrate 2 (IRS2, Accession XM_007095) is another VGAM2353 host target gene. IRS2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IRS2, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRS2 BINDING SITE, designated SEQ ID:30031, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80038] Another function of VGAM2353 is therefore inhibition of Insulin Receptor Substrate 2 (IRS2, Accession XM_007095), a gene which may mediate the control of various cellular processes by insulin. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRS2. The function of IRS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1217.Potassium Voltage-gated Channel, Shaw-related Subfamily, Member 3 (KCNC3, Accession NM_004977) is another VGAM2353 host target gene. KCNC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNC3 BINDING SITE, designated SEQ

ID:11421, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80039] Another function of VGAM2353 is therefore inhibition of Potassium Voltage-gated Channel, Shaw-related Subfamily, Member 3 (KCNC3, Accession NM_004977), a gene which mediates the voltage-dependent potassium ion permeability of excitable membranes. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNC3. The function of KCNC3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM476.Potassium Channel, Subfamily K, Member 4 (KCNK4, Accession NM_033310) is another VGAM2353 host target gene. KCNK4 BINDING SITE1 and KCNK4 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KCNK4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNK4 BINDING SITE1 and KCNK4 BINDING SITE2, designated SEQ ID:27151 and SEQ ID:27152 re-

spectively, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80040] Another function of VGAM2353 is therefore inhibition of Potassium Channel, Subfamily K, Member 4 (KCNK4, Accession NM_033310). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNK4. LIM Domain Only 2 (rhombotin-like 1) (LMO2, Accession NM_005574) is another VGAM2353 host target gene. LMO2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LMO2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LMO2 BINDING SITE, designated SEQ ID:12101, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80041] Another function of VGAM2353 is therefore inhibition of LIM Domain Only 2 (rhombotin-like 1) (LMO2, Accession NM_005574). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LMO2. LNK (Accession

NM_005475) is another VGAM2353 host target gene. LNK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LNK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LNK BINDING SITE, designated SEQ ID:11975, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80042] Another function of VGAM2353 is therefore inhibition of LNK (Accession NM_005475), a gene which links T-cell receptor activation signal to phospholipase c-gamma-1, grb-2 and phosphatidylinositol 3-kinase (by similarity). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LNK. The function of LNK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM115.Megakaryocyte-associated Tyrosine Kinase (MATK, Accession NM_139354) is another VGAM2353 host target gene. MATK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded

by MATK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MATK BINDING SITE, designated SEQ ID:29304, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80043] Another function of VGAM2353 is therefore inhibition of Megakaryocyte-associated Tyrosine Kinase (MATK, Accession NM_139354), a gene which can phosphorylate members of the SRC family of PTKs at the regulatory tyrosine residue. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MATK. The function of MATK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2173.Mannosyl (alpha-1,6-)-glycoprotein Beta-1,2-N-acetylglucosaminyltransferase (MGAT2, Accession NM_002408) is another VGAM2353 host target gene. MGAT2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGAT2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGAT2 BINDING SITE, designated SEQ ID:8232, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80044] Another function of VGAM2353 is therefore inhibition of Mannosyl (alpha-1,6-)-glycoprotein Beta-1,2-N-acetylglucosaminyltransferase (MGAT2, Accession NM_002408). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGAT2. Mucin and Cadherin-like (MUCDHL, Accession XM_113227) is another VGAM2353 host target gene. MUCDHL BINDING SITE1 and MUCDHL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MUCDHL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MUCDHL BINDING SITE1 and MUCDHL BINDING SITE2, designated SEQ ID:42209 and SEQ ID:25284 respectively, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ

ID:5064.

[80045] Another function of VGAM2353 is therefore inhibition of Mucin and Cadherin-like (MUCDHL, Accession XM_113227). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MUCDHL. Neurexin 2 (NRXN2, Accession NM_015080) is another VGAM2353 host target gene. NRXN2 BINDING SITE1 and NRXN2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NRXN2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NRXN2 BINDING SITE1 and NRXN2 BINDING SITE2, designated SEQ ID:17469 and SEQ ID:28985 respectively, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80046] Another function of VGAM2353 is therefore inhibition of Neurexin 2 (NRXN2, Accession NM_015080), a gene which may be involved in cell recognition, cell adhesion, and may mediate intracellular signaling. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

NRXN2. The function of NRXN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM178.Platelet-activating Factor Acetylhydrolase, Isoform Ib, Alpha Subunit 45kDa (PAFAH1B1, Accession NM_000430) is another VGAM2353 host target gene. PAFAH1B1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PAFAH1B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAFAH1B1 BINDING SITE, designated SEQ ID:6011, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80047] Another function of VGAM2353 is therefore inhibition of Platelet-activating Factor Acetylhydrolase, Isoform Ib, Alpha Subunit 45kDa (PAFAH1B1, Accession NM_000430). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAFAH1B1. poly(rC) Binding Protein 1 (PCBP1, Accession NM_006196) is another VGAM2353 host target gene. PCBP1 BINDING SITE is HOST TARGET

binding site found in the 5` untranslated region of mRNA encoded by PCBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCBP1 BINDING SITE, designated SEQ ID:12869, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80048] Another function of VGAM2353 is therefore inhibition of poly(rC) Binding Protein 1 (PCBP1, Accession NM_006196), a gene which binds preferentially to oligo dc. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCBP1. The function of PCBP1 has been established by previous studies. Leffers et al. (1995) described the cloning and characterization of 2 cDNAs for poly(rC)-binding proteins, called PCBP1 and PCBP2 (OMIM Ref. No. 601210) by them. The authors analyzed an EST database for sequences that were predicted to encode a protein with K-homologous (KH) domains. The 60- to 70-amino acid KH motifs are found in several putative nucleic acid binding proteins such as FMR1 (OMIM Ref. No. 309550) and HNRNPK (OMIM Ref. No. 600712) and

are thought to be involved in RNA binding. Using primers from 1 EST the authors produced a probe that was used to screen a cDNA library of transformed human amnion cells. The cDNA they isolated for PCBP1 encodes a putative 356-amino acid protein that contains 3 KH domains. It is 83% identical to PCBP2 at the DNA level and 90% homologous at the amino acid level. The PCBP1 protein is about 85% similar to the mouse hnRNP-X/mCTBP protein (Hahm et al., 1993). When expressed with a vaccinia virus system in transformed amnion cells, Leffers et al. (1995) found that both PCBP1 and PCBP2 bound poly(rC) when not phosphorylated; phosphorylated protein bound with much lower affinity. Transcripts of both PCBPs were detected in all the human tissues analyzed. Tommerup and Leffers (1996) mapped PCBP1 to 2p13-p12 by fluorescence in situ hybridization.

[80049] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[80050] Leffers, H.; Dejgaard, K.; Celis, J. E. : Characterisation of two major cellular poly(rC)-binding human proteins, each containing three K-homologous (KH) domains. Europ. J. Biochem. 230: 447-453, 1995. ; and

[80051] Tommerup, N.; Leffers, H. : Assignment of human KH-box-containing genes by in situ hybridization: HNRNPK maps to 9q21.32-q21.33, PCBP1 to 2p12-p13, and PCBP2 to 12q13.12-q13.13, distal t.

[80052] Further studies establishing the function and utilities of PCBP1 are found in John Hopkins OMIM database record ID 601209, and in sited publications numbered 6885-688 and 10050 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Protocadherin 9 (PCDH9, Accession XM_096054) is another VGAM2353 host target gene. PCDH9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PCDH9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH9 BINDING SITE, designated SEQ ID:40295, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80053] Another function of VGAM2353 is therefore inhibition of Protocadherin 9 (PCDH9, Accession XM_096054). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with PCDH9. Protein Kinase (cAMP-dependent, catalytic) Inhibitor Alpha (PKIA, Accession NM_006823) is another VGAM2353 host target gene. PKIA BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PKIA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PKIA BINDING SITE, designated SEQ ID:13701, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80054] Another function of VGAM2353 is therefore inhibition of Protein Kinase (cAMP-dependent, catalytic) Inhibitor Alpha (PKIA, Accession NM_006823). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKIA. RAD50 Homolog (S. cerevisiae) (RAD50, Accession NM_005732) is another VGAM2353 host target gene. RAD50 BINDING SITE1 and RAD50 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RAD50, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the comple-

mentarity of the nucleotide sequences of RAD50 BINDING SITE1 and RAD50 BINDING SITE2, designated SEQ ID:12295 and SEQ ID:28552 respectively, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80055] Another function of VGAM2353 is therefore inhibition of RAD50 Homolog (S. cerevisiae) (RAD50, Accession NM_005732), a gene which is involved in dna double-strand break repair (dsbr). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD50. The function of RAD50 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM132.Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977) is another VGAM2353 host target gene. SLC22A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC22A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC22A3 BINDING SITE, designated SEQ

ID:22505, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80056] Another function of VGAM2353 is therefore inhibition of Solute Carrier Family 22 (extraneuronal monoamine transporter), Member 3 (SLC22A3, Accession NM_021977), a gene which is a sodium-ion dependent, high affinity carnitine transporter. also transports organic cations without the involvement of sodium. involved in the active cellular uptake of carnitine. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC22A3. The function of SLC22A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2147.SMAC (Accession NM_138930) is another VGAM2353 host target gene. SMAC BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SMAC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMAC BINDING SITE, designated SEQ ID:29053, to the nucleotide sequence of

VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80057] Another function of VGAM2353 is therefore inhibition of SMAC (Accession NM_138930), a gene which promotes apoptosis via caspase activation. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMAC. The function of SMAC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.SMG1 (Accession NM_015092) is another VGAM2353 host target gene. SMG1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SMG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMG1 BINDING SITE, designated SEQ ID:17479, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80058] Another function of VGAM2353 is therefore inhibition of SMG1 (Accession NM_015092), a gene which acts as the target for the cell-cycle arrest and immunosuppressive ef-

fects. Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMG1. The function of SMG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM419.SRY (sex determining region Y)-box 10 (SOX10, Accession NM_006941) is another VGAM2353 host target gene. SOX10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SOX10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX10 BINDING SITE, designated SEQ ID:13824, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80059] Another function of VGAM2353 is therefore inhibition of SRY (sex determining region Y)-box 10 (SOX10, Accession NM_006941). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX10. SRP46 (Accession NM_032102) is another VGAM2353 host target gene.

SRP46 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SRP46, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SRP46 BINDING SITE, designated SEQ ID:25791, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80060] Another function of VGAM2353 is therefore inhibition of SRP46 (Accession NM_032102). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRP46. Transforming, Acidic Coiled-coil Containing Protein 1 (TACC1, Accession NM_006283) is another VGAM2353 host target gene. TACC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TACC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TACC1 BINDING SITE, designated SEQ ID:12967, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5064.

[80061] Another function of VGAM2353 is therefore inhibition of Transforming, Acidic Coiled-coil Containing Protein 1 (TACC1, Accession NM_006283). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TACC1. Thymidine Kinase 1, Soluble (TK1, Accession NM_003258) is another VGAM2353 host target gene. TK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TK1 BINDING SITE, designated SEQ ID:9270, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80062] Another function of VGAM2353 is therefore inhibition of Thymidine Kinase 1, Soluble (TK1, Accession NM_003258). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TK1. Vasoactive Intestinal Peptide Receptor 2 (VIPR2, Accession NM_003382) is another VGAM2353 host target gene. VIPR2 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VIPR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VIPR2 BINDING SITE, designated SEQ ID:9414, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80063] Another function of VGAM2353 is therefore inhibition of Vasoactive Intestinal Peptide Receptor 2 (VIPR2, Accession NM_003382). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIPR2. Bruno-like 6, RNA Binding Protein (Drosophila) (BRUNOL6, Accession NM_052840) is another VGAM2353 host target gene. BRUNOL6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BRUNOL6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRUNOL6 BINDING SITE, designated SEQ ID:27421, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ

ID:5064.

[80064] Another function of VGAM2353 is therefore inhibition of Bruno-like 6, RNA Binding Protein (Drosophila) (BRUNOL6, Accession NM_052840). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRUNOL6. Chromosome 21 Open Reading Frame 108 (C21orf108, Accession XM_114191) is another VGAM2353 host target gene. C21orf108 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C21orf108, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C21orf108 BINDING SITE, designated SEQ ID:42771, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80065] Another function of VGAM2353 is therefore inhibition of Chromosome 21 Open Reading Frame 108 (C21orf108, Accession XM_114191). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf108. CAPN13 (Accession NM_144575) is another

VGAM2353 host target gene. CAPN13 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CAPN13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAPN13 BINDING SITE, designated SEQ ID:29380, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80066] Another function of VGAM2353 is therefore inhibition of CAPN13 (Accession NM_144575). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAPN13. CDT1 (Accession XM_085327) is another VGAM2353 host target gene. CDT1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CDT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDT1 BINDING SITE, designated SEQ ID:38066, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80067] Another function of VGAM2353 is therefore inhibition of CDT1 (Accession XM_085327). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDT1. DKFZP434N1511 (Accession XM_166138) is another VGAM2353 host target gene. DKFZP434N1511 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434N1511, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434N1511 BINDING SITE, designated SEQ ID:43939, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80068] Another function of VGAM2353 is therefore inhibition of DKFZP434N1511 (Accession XM_166138). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434N1511. DKFZP586J1624 (Accession NM_015537) is another VGAM2353 host target gene. DKFZP586J1624 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

DKFZP586J1624, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586J1624 BINDING SITE, designated SEQ ID:17798, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80069] Another function of VGAM2353 is therefore inhibition of DKFZP586J1624 (Accession NM_015537). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586J1624. DKFZP727G051 (Accession XM_045308) is another VGAM2353 host target gene. DKFZP727G051 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP727G051, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP727G051 BINDING SITE, designated SEQ ID:34430, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80070] Another function of VGAM2353 is therefore inhibition of

DKFZP727G051 (Accession XM_045308). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP727G051. EHM2 (Accession NM_019114) is another VGAM2353 host target gene. EHM2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EHM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EHM2 BINDING SITE, designated SEQ ID:21190, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80071] Another function of VGAM2353 is therefore inhibition of EHM2 (Accession NM_019114). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHM2. Epsin 2 (EPN2, Accession NM_014964) is another VGAM2353 host target gene. EPN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of EPN2 BINDING SITE, designated SEQ ID:17348, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80072] Another function of VGAM2353 is therefore inhibition of Epsin 2 (EPN2, Accession NM_014964). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPN2. FLJ00001 (Accession XM_088525) is another VGAM2353 host target gene. FLJ00001 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00001, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00001 BINDING SITE, designated SEQ ID:39780, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80073] Another function of VGAM2353 is therefore inhibition of FLJ00001 (Accession XM_088525). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00001. FLJ13441 (Accession NM_023924) is another

VGAM2353 host target gene. FLJ13441 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13441, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13441 BINDING SITE, designated SEQ ID:23395, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80074] Another function of VGAM2353 is therefore inhibition of FLJ13441 (Accession NM_023924). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13441. FLJ20085 (Accession NM_017660) is another VGAM2353 host target gene. FLJ20085 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20085, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20085 BINDING SITE, designated SEQ ID:19186, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80075] Another function of VGAM2353 is therefore inhibition of FLJ20085 (Accession NM_017660). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20085. FLJ20898 (Accession NM_024600) is another VGAM2353 host target gene. FLJ20898 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20898, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20898 BINDING SITE, designated SEQ ID:23851, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80076] Another function of VGAM2353 is therefore inhibition of FLJ20898 (Accession NM_024600). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20898. FLJ22246 (Accession NM_025232) is another VGAM2353 host target gene. FLJ22246 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22246, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22246 BINDING SITE, designated SEQ ID:24909, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80077] Another function of VGAM2353 is therefore inhibition of FLJ22246 (Accession NM_025232). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22246. FLJ22408 (Accession NM_024794) is another VGAM2353 host target gene. FLJ22408 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22408, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22408 BINDING SITE, designated SEQ ID:24173, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80078] Another function of VGAM2353 is therefore inhibition of FLJ22408 (Accession NM_024794). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ22408. HRD1 (Accession XM_045498) is another VGAM2353 host target gene. HRD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HRD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRD1 BINDING SITE, designated SEQ ID:34473, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80079] Another function of VGAM2353 is therefore inhibition of HRD1 (Accession XM_045498). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRD1. HSPC195 (Accession XM_087785) is another VGAM2353 host target gene. HSPC195 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HSPC195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPC195 BINDING SITE, designated SEQ ID:39422, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5064.

[80080] Another function of VGAM2353 is therefore inhibition of HSPC195 (Accession XM_087785). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC195. KH-type Splicing Regulatory Protein (FUSE binding protein 2) (KHSRP, Accession NM_003685) is another VGAM2353 host target gene. KHSRP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KHSRP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KHSRP BINDING SITE, designated SEQ ID:9796, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80081] Another function of VGAM2353 is therefore inhibition of KH-type Splicing Regulatory Protein (FUSE binding protein 2) (KHSRP, Accession NM_003685). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KHSRP. KIAA0420 (Accession XM_032693) is another VGAM2353 host target gene. KIAA0420 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0420, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0420 BINDING SITE, designated SEQ ID:31728, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80082] Another function of VGAM2353 is therefore inhibition of KIAA0420 (Accession XM_032693). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0420. KIAA0513 (Accession NM_014732) is another VGAM2353 host target gene. KIAA0513 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0513, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0513 BINDING SITE, designated SEQ ID:16359, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80083] Another function of VGAM2353 is therefore inhibition of

KIAA0513 (Accession NM_014732). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513. KIAA0545 (Accession XM_032278) is another VGAM2353 host target gene. KIAA0545 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0545, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0545 BINDING SITE, designated SEQ ID:31632, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80084] Another function of VGAM2353 is therefore inhibition of KIAA0545 (Accession XM_032278). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0545. KIAA0668 (Accession XM_039332) is another VGAM2353 host target gene. KIAA0668 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0668, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0668 BINDING SITE, designated SEQ ID:33050, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80085] Another function of VGAM2353 is therefore inhibition of KIAA0668 (Accession XM_039332). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0668. KIAA0672 (Accession NM_014859) is another VGAM2353 host target gene. KIAA0672 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0672, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0672 BINDING SITE, designated SEQ ID:16920, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80086] Another function of VGAM2353 is therefore inhibition of KIAA0672 (Accession NM_014859). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0672. KIAA0987 (Accession NM_012307) is another

VGAM2353 host target gene. KIAA0987 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0987, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0987 BINDING SITE, designated SEQ ID:14677, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80087] Another function of VGAM2353 is therefore inhibition of KIAA0987 (Accession NM_012307). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0987. KIAA1170 (Accession XM_045907) is another VGAM2353 host target gene. KIAA1170 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1170, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1170 BINDING SITE, designated SEQ ID:34612, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80088] Another function of VGAM2353 is therefore inhibition of KIAA1170 (Accession XM_045907). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1170. KIAA1867 (Accession XM_170675) is another VGAM2353 host target gene. KIAA1867 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1867, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1867 BINDING SITE, designated SEQ ID:45455, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80089] Another function of VGAM2353 is therefore inhibition of KIAA1867 (Accession XM_170675). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1867. KIAA1904 (Accession XM_056282) is another VGAM2353 host target gene. KIAA1904 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1904, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1904 BINDING SITE, designated SEQ ID:36377, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80090] Another function of VGAM2353 is therefore inhibition of KIAA1904 (Accession XM_056282). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1904. KIAA1906 (Accession XM_055095) is another VGAM2353 host target gene. KIAA1906 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1906 BINDING SITE, designated SEQ ID:36231, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80091] Another function of VGAM2353 is therefore inhibition of KIAA1906 (Accession XM_055095). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1906. KIAA1924 (Accession XM_057091) is another VGAM2353 host target gene. KIAA1924 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1924, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1924 BINDING SITE, designated SEQ ID:36479, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80092] Another function of VGAM2353 is therefore inhibition of KIAA1924 (Accession XM_057091). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1924. LHPP (Accession NM_022126) is another VGAM2353 host target gene. LHPP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LHPP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LHPP BINDING SITE, designated SEQ ID:22678, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5064.

[80093] Another function of VGAM2353 is therefore inhibition of LHPP (Accession NM_022126). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHPP. Mannosidase, Beta A, Lysosomal-like (MANBAL, Accession NM_022077) is another VGAM2353 host target gene. MANBAL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MANBAL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MANBAL BINDING SITE, designated SEQ ID:22620, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80094] Another function of VGAM2353 is therefore inhibition of Mannosidase, Beta A, Lysosomal-like (MANBAL, Accession NM_022077). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MANBAL. Mitogen-activated Protein Kinase-activated Protein Kinase 2 (MAPKAPK2, Accession NM_004759) is another VGAM2353 host target

gene. MAPKAPK2 BINDING SITE1 and MAPKAPK2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MAPKAPK2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPKAPK2 BINDING SITE1 and MAPKAPK2 BINDING SITE2, designated SEQ ID:11150 and SEQ ID:26764 respectively, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80095] Another function of VGAM2353 is therefore inhibition of Mitogen-activated Protein Kinase-activated Protein Kinase 2 (MAPKAPK2, Accession NM_004759). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPKAPK2. NS1-BP (Accession XM_051877) is another VGAM2353 host target gene. NS1-BP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NS1-BP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NS1-BP BINDING SITE, designated SEQ ID:35913, to the nucleotide se-

quence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80096] Another function of VGAM2353 is therefore inhibition of NS1-BP (Accession XM_051877). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NS1-BP. OBTP (Accession NM_017601) is another VGAM2353 host target gene. OBTP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OBTP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OBTP BINDING SITE, designated SEQ ID:19080, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80097] Another function of VGAM2353 is therefore inhibition of OBTP (Accession NM_017601). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OBTP. Peptidyl Arginine Deiminase, Type I (PADI1, Accession XM_030498) is another VGAM2353 host target gene. PADI1 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by PADI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PADI1 BINDING SITE, designated SEQ ID:31055, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80098] Another function of VGAM2353 is therefore inhibition of Peptidyl Arginine Deiminase, Type I (PADI1, Accession XM_030498). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PADI1.

p21(CDKN1A)-activated Kinase 6 (PAK6, Accession NM_020168) is another VGAM2353 host target gene. PAK6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAK6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAK6 BINDING SITE, designated SEQ ID:21391, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80099] Another function of VGAM2353 is therefore inhibition of p21(CDKN1A)-activated Kinase 6 (PAK6, Accession NM_020168). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAK6. QKI (Accession XM_037438) is another VGAM2353 host target gene. QKI BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by QKI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of QKI BINDING SITE, designated SEQ ID:32619, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80100] Another function of VGAM2353 is therefore inhibition of QKI (Accession XM_037438). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with QKI. RAB3A Interacting Protein (rabin3)-like 1 (RAB3IL1, Accession NM_013401) is another VGAM2353 host target gene. RAB3IL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB3IL1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB3IL1 BINDING SITE, designated SEQ ID:15063, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80101] Another function of VGAM2353 is therefore inhibition of RAB3A Interacting Protein (rabin3)-like 1 (RAB3IL1, Accession NM_013401). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB3IL1. RAI (Accession NM_006663) is another VGAM2353 host target gene. RAI BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAI BINDING SITE, designated SEQ ID:13471, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80102] Another function of VGAM2353 is therefore inhibition of RAI (Accession NM_006663). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with RAI. Retinoic Acid Induced 17 (RAI17, Accession XM_166091) is another VGAM2353 host target gene. RAI17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAI17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAI17 BINDING SITE, designated SEQ ID:43862, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80103] Another function of VGAM2353 is therefore inhibition of Retinoic Acid Induced 17 (RAI17, Accession XM_166091). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI17. Rho-related BTB Domain Containing 1 (RHOBTB1, Accession XM_166144) is another VGAM2353 host target gene. RHOBTB1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RHOBTB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RHOBTB1

BINDING SITE, designated SEQ ID:43952, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80104] Another function of VGAM2353 is therefore inhibition of Rho-related BTB Domain Containing 1 (RHOBTB1, Accession XM_166144). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHOBTB1. SCAM-1 (Accession NM_005775) is another VGAM2353 host target gene. SCAM-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCAM-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAM-1 BINDING SITE, designated SEQ ID:12350, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80105] Another function of VGAM2353 is therefore inhibition of SCAM-1 (Accession NM_005775). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAM-1. Solute Carrier Family 26, Member 10 (SLC26A10, Ac-

cession NM_133489) is another VGAM2353 host target gene. SLC26A10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC26A10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC26A10 BINDING SITE, designated SEQ ID:28560, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80106] Another function of VGAM2353 is therefore inhibition of Solute Carrier Family 26, Member 10 (SLC26A10, Accession NM_133489). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC26A10. T-box 21 (TBX21, Accession NM_013351) is another VGAM2353 host target gene. TBX21 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBX21, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBX21 BINDING SITE, designated SEQ ID:14997, to the nucleotide sequence of

VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80107] Another function of VGAM2353 is therefore inhibition of T-box 21 (TBX21, Accession NM_013351). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBX21. Testis Expressed Sequence 27 (TEX27, Accession NM_021943) is another VGAM2353 host target gene. TEX27 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEX27, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEX27 BINDING SITE, designated SEQ ID:22460, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80108] Another function of VGAM2353 is therefore inhibition of Testis Expressed Sequence 27 (TEX27, Accession NM_021943). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEX27. Tubby Homolog (mouse) (TUB, Accession NM_003320) is another

VGAM2353 host target gene. TUB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUB BINDING SITE, designated SEQ ID:9324, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80109] Another function of VGAM2353 is therefore inhibition of Tubby Homolog (mouse) (TUB, Accession NM_003320). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUB. WSB1 (Accession NM_134264) is another VGAM2353 host target gene. WSB1 BINDING SITE1 and WSB1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WSB1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WSB1 BINDING SITE1 and WSB1 BINDING SITE2, designated SEQ ID:28617 and SEQ ID:28623 respectively, to the nucleotide sequence of VGAM2353 RNA, herein

designated VGAM RNA, also designated SEQ ID:5064.

[80110] Another function of VGAM2353 is therefore inhibition of WSB1 (Accession NM_134264). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WSB1. LOC115073 (Accession XM_055193) is another VGAM2353 host target gene. LOC115073 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC115073, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115073 BINDING SITE, designated SEQ ID:36242, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80111] Another function of VGAM2353 is therefore inhibition of LOC115073 (Accession XM_055193). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115073. LOC126917 (Accession XM_059091) is another VGAM2353 host target gene. LOC126917 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126917, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126917 BINDING SITE, designated SEQ ID:36871, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80112] Another function of VGAM2353 is therefore inhibition of LOC126917 (Accession XM_059091). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126917. LOC127702 (Accession XM_060619) is another VGAM2353 host target gene. LOC127702 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC127702, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127702 BINDING SITE, designated SEQ ID:37183, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80113] Another function of VGAM2353 is therefore inhibition of LOC127702 (Accession XM_060619). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC127702. LOC144347 (Accession XM_084832) is another VGAM2353 host target gene. LOC144347 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144347, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144347 BINDING SITE, designated SEQ ID:37724, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80114] Another function of VGAM2353 is therefore inhibition of LOC144347 (Accession XM_084832). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144347. LOC145438 (Accession XM_096781) is another VGAM2353 host target gene. LOC145438 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145438, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145438 BINDING SITE, designated SEQ ID:40537, to

the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80115] Another function of VGAM2353 is therefore inhibition of LOC145438 (Accession XM_096781). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145438. LOC145980 (Accession XM_096914) is another VGAM2353 host target gene. LOC145980 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145980, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145980 BINDING SITE, designated SEQ ID:40650, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80116] Another function of VGAM2353 is therefore inhibition of LOC145980 (Accession XM_096914). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145980. LOC146237 (Accession XM_096954) is another VGAM2353 host target gene. LOC146237 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC146237, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146237 BINDING SITE, designated SEQ ID:40669, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80117] Another function of VGAM2353 is therefore inhibition of LOC146237 (Accession XM_096954). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146237. LOC148014 (Accession XM_085999) is another VGAM2353 host target gene. LOC148014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148014 BINDING SITE, designated SEQ ID:38440, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80118] Another function of VGAM2353 is therefore inhibition of LOC148014 (Accession XM_085999). Accordingly, utilities

of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148014. LOC149182 (Accession XM_097605) is another VGAM2353 host target gene. LOC149182 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149182, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149182 BINDING SITE, designated SEQ ID:40971, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80119] Another function of VGAM2353 is therefore inhibition of LOC149182 (Accession XM_097605). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149182. LOC150208 (Accession XM_097841) is another VGAM2353 host target gene. LOC150208 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150208, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC150208 BINDING SITE, designated SEQ ID:41155, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80120] Another function of VGAM2353 is therefore inhibition of LOC150208 (Accession XM_097841). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150208. LOC151278 (Accession XM_087156) is another VGAM2353 host target gene. LOC151278 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151278, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151278 BINDING SITE, designated SEQ ID:39096, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80121] Another function of VGAM2353 is therefore inhibition of LOC151278 (Accession XM_087156). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151278. LOC155064 (Accession XM_088128) is another VGAM2353 host target gene. LOC155064 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC155064, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155064 BINDING SITE, designated SEQ ID:39530, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80122] Another function of VGAM2353 is therefore inhibition of LOC155064 (Accession XM_088128). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155064. LOC159199 (Accession XM_089441) is another VGAM2353 host target gene. LOC159199 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC159199, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159199 BINDING SITE, designated SEQ ID:39983, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80123] Another function of VGAM2353 is therefore inhibition of

LOC159199 (Accession XM_089441). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159199. LOC170127 (Accession XM_093116) is another VGAM2353 host target gene. LOC170127 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC170127, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC170127 BINDING SITE, designated SEQ ID:40176, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80124] Another function of VGAM2353 is therefore inhibition of LOC170127 (Accession XM_093116). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170127. LOC199786 (Accession XM_114021) is another VGAM2353 host target gene. LOC199786 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC199786 BINDING SITE, designated SEQ ID:42620, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80125] Another function of VGAM2353 is therefore inhibition of LOC199786 (Accession XM_114021). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199786. LOC200081 (Accession XM_114110) is another VGAM2353 host target gene. LOC200081 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200081, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200081 BINDING SITE, designated SEQ ID:42705, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80126] Another function of VGAM2353 is therefore inhibition of LOC200081 (Accession XM_114110). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200081. LOC200982 (Accession XM_117305) is an-

other VGAM2353 host target gene. LOC200982 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200982, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200982 BINDING SITE, designated SEQ ID:43376, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80127] Another function of VGAM2353 is therefore inhibition of LOC200982 (Accession XM_117305). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200982. LOC201229 (Accession XM_113925) is another VGAM2353 host target gene. LOC201229 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201229 BINDING SITE, designated SEQ ID:42543, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80128] Another function of VGAM2353 is therefore inhibition of LOC201229 (Accession XM_113925). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201229. LOC203378 (Accession XM_117541) is another VGAM2353 host target gene. LOC203378 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203378, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203378 BINDING SITE, designated SEQ ID:43555, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80129] Another function of VGAM2353 is therefore inhibition of LOC203378 (Accession XM_117541). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203378. LOC219920 (Accession XM_167787) is another VGAM2353 host target gene. LOC219920 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219920, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219920 BINDING SITE, designated SEQ ID:44809, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80130] Another function of VGAM2353 is therefore inhibition of LOC219920 (Accession XM_167787). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219920. LOC221399 (Accession XM_168134) is another VGAM2353 host target gene. LOC221399 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221399, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221399 BINDING SITE, designated SEQ ID:45052, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80131] Another function of VGAM2353 is therefore inhibition of LOC221399 (Accession XM_168134). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC221399. LOC221424 (Accession XM_168060) is another VGAM2353 host target gene. LOC221424 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221424, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221424 BINDING SITE, designated SEQ ID:44980, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80132] Another function of VGAM2353 is therefore inhibition of LOC221424 (Accession XM_168060). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221424. LOC221794 (Accession XM_168214) is another VGAM2353 host target gene. LOC221794 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221794 BINDING SITE, designated SEQ ID:45073, to the nucleotide sequence of VGAM2353 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5064.

[80133] Another function of VGAM2353 is therefore inhibition of LOC221794 (Accession XM_168214). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221794. LOC254351 (Accession XM_170774) is another VGAM2353 host target gene. LOC254351 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254351, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254351 BINDING SITE, designated SEQ ID:45542, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80134] Another function of VGAM2353 is therefore inhibition of LOC254351 (Accession XM_170774). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254351. LOC254617 (Accession XM_173236) is another VGAM2353 host target gene. LOC254617 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254617, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254617 BINDING SITE, designated SEQ ID:46519, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80135] Another function of VGAM2353 is therefore inhibition of LOC254617 (Accession XM_173236). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254617. LOC257354 (Accession XM_170810) is another VGAM2353 host target gene. LOC257354 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257354, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257354 BINDING SITE, designated SEQ ID:45581, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80136] Another function of VGAM2353 is therefore inhibition of LOC257354 (Accession XM_170810). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC257354. LOC51083 (Accession NM_015973) is another VGAM2353 host target gene. LOC51083 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51083, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51083 BINDING SITE, designated SEQ ID:18070, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80137] Another function of VGAM2353 is therefore inhibition of LOC51083 (Accession NM_015973). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51083. LOC92078 (Accession XM_042684) is another VGAM2353 host target gene. LOC92078 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92078, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92078 BINDING SITE, designated SEQ ID:33744, to the

nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80138] Another function of VGAM2353 is therefore inhibition of LOC92078 (Accession XM_042684). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92078. LOC92661 (Accession XM_046465) is another VGAM2353 host target gene. LOC92661 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92661, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92661 BINDING SITE, designated SEQ ID:34724, to the nucleotide sequence of VGAM2353 RNA, herein designated VGAM RNA, also designated SEQ ID:5064.

[80139] Another function of VGAM2353 is therefore inhibition of LOC92661 (Accession XM_046465). Accordingly, utilities of VGAM2353 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92661. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2354 (VGAM2354) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80140] VGAM2354 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2354 was detected is described hereinabove with reference to Figs. 1-8.

[80141] VGAM2354 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2354 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80142] VGAM2354 gene encodes a VGAM2354 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2354 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2354 precursor RNA is designated SEQ ID:2340, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2340 is located at position 18623 relative to the genome of Equine Herpesvirus 2.

[80143] VGAM2354 precursor RNA folds onto itself, forming VGAM2354 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80144] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2354 folded precursor RNA into VGAM2354 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2354 RNA is designated SEQ ID:5065, and is provided hereinbelow with reference to the sequence listing part.

[80145] VGAM2354 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2354 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2354 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80146] VGAM2354 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2354 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2354 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2354 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2354 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80147] The complementary binding of VGAM2354 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2354 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2354 host target RNA into VGAM2354 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80148] It is appreciated that VGAM2354 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2354 host target genes. The mRNA of each one of this plurality of VGAM2354 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2354 RNA, herein designated VGAM RNA, and which when bound by VGAM2354 RNA causes inhibition of translation of respective one or more VGAM2354 host target proteins.

[80149] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2354 gene, herein designated VGAM GENE, on one or more VGAM2354 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80150] It is yet further appreciated that a function of VGAM2354 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2354 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2354 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80151] Nucleotide sequences of the VGAM2354 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2354 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2354 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2354 are further described hereinbelow with reference to Table 1.

[80152] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2354 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2354 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80153] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2354 gene, herein designated VGAM is inhibition of expression of VGAM2354 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2354 correlate with, and may be deduced from, the identity of the target genes which VGAM2354

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80154] B-cell CLL/lymphoma 7B (BCL7B, Accession NM_001707) is a VGAM2354 host target gene. BCL7B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL7B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL7B BINDING SITE, designated SEQ ID:7433, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80155] A function of VGAM2354 is therefore inhibition of B-cell CLL/lymphoma 7B (BCL7B, Accession NM_001707), a gene which is of yet unknown fanction. Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL7B. The function of BCL7B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1189.Centrosomal Protein 1 (CEP1, Accession NM_007018) is another VGAM2354 host target gene. CEP1 BINDING SITE is HOST TARGET binding site found in the

5` untranslated region of mRNA encoded by CEP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CEP1 BINDING SITE, designated SEQ ID:13875, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80156] Another function of VGAM2354 is therefore inhibition of Centrosomal Protein 1 (CEP1, Accession NM_007018), a gene which mediates actin cytoskeleton reorganization at the plasma membrane. Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEP1. The function of CEP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1295.EH-domain Containing 4 (EHD4, Accession NM_139265) is another VGAM2354 host target gene. EHD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EHD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of EHD4 BINDING SITE, designated SEQ ID:29255, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80157] Another function of VGAM2354 is therefore inhibition of EH-domain Containing 4 (EHD4, Accession NM_139265). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHD4. Guanine Nucleotide Binding Protein (G protein), Alpha Inhibiting Activity Polypeptide 1 (GNAI1, Accession NM_002069) is another VGAM2354 host target gene. GNAI1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GNAI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNAI1 BINDING SITE, designated SEQ ID:7838, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80158] Another function of VGAM2354 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Alpha Inhibiting Activity Polypeptide 1 (GNAI1, Accession NM_002069), a gene which is involved as modulators or

transducers in various transmembrane signaling systems. Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNAI1. The function of GNAI1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM57.Histidine Ammonia-lyase (HAL, Accession NM_002108) is another VGAM2354 host target gene. HAL BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HAL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HAL BINDING SITE, designated SEQ ID:7889, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80159] Another function of VGAM2354 is therefore inhibition of Histidine Ammonia-lyase (HAL, Accession NM_002108). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAL. Huntingtin-associated Protein 1 (neuroan 1) (HAP1, Accession NM_003949) is another

VGAM2354 host target gene. HAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HAP1 BINDING SITE, designated SEQ ID:10073, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80160] Another function of VGAM2354 is therefore inhibition of Huntingtin-associated Protein 1 (neuroan 1) (HAP1, Accession NM_003949), a gene which functions as an adaptor protein using coiled coils to mediate interactions among cytoskeletal, vascular, and motor proteins. Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAP1. The function of HAP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM126.MAD, Mothers Against Decapentaplegic Homolog 2 (Drosophila) (MADH2, Accession NM_005901) is another VGAM2354 host target gene. MADH2 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by MADH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MADH2 BINDING SITE, designated SEQ ID:12521, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80161] Another function of VGAM2354 is therefore inhibition of MAD, Mothers Against Decapentaplegic Homolog 2 (Drosophila) (MADH2, Accession NM_005901). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADH2. Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 1 (p85 alpha) (PIK3R1, Accession XM_043865) is another VGAM2354 host target gene. PIK3R1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIK3R1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIK3R1 BINDING SITE, designated SEQ ID:34035, to the nucleotide sequence of VGAM2354 RNA,

herein designated VGAM RNA, also designated SEQ ID:5065.

[80162] Another function of VGAM2354 is therefore inhibition of Phosphoinositide-3-kinase, Regulatory Subunit, Polypeptide 1 (p85 alpha) (PIK3R1, Accession XM_043865), a gene which acts as an adapter, for the insulin-stimulated increase in glucose uptake and glycogen synthesis. Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3R1. The function of PIK3R1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM826.Regulator of G-protein Signalling 9 (RGS9, Accession NM_003835) is another VGAM2354 host target gene. RGS9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RGS9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RGS9 BINDING SITE, designated SEQ ID:9927, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80163] Another function of VGAM2354 is therefore inhibition of Regulator of G-protein Signalling 9 (RGS9, Accession NM_003835). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS9. Short Stature Homeobox 2 (SHOX2, Accession NM_006884) is another VGAM2354 host target gene. SHOX2 BINDING SITE1 and SHOX2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SHOX2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SHOX2 BINDING SITE1 and SHOX2 BINDING SITE2, designated SEQ ID:13747 and SEQ ID:8973 respectively, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80164] Another function of VGAM2354 is therefore inhibition of Short Stature Homeobox 2 (SHOX2, Accession NM_006884), a gene which may be a growth regulator and have a role in specifying neural systems. Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with SHOX2. The function of SHOX2 has been established by previous studies. Homeo box genes encode proteins containing a 60-amino acid residue motif that represents a DNA binding domain. They have been characterized extensively as transcriptional regulators involved in pattern formation in both invertebrate and vertebrate species. Embryonic development is mediated through an interactive network created by the overlapping expression patterns of a number of transcription factors including the homeo box gene superfamily. This dynamic scaffold provides positional information for cell determination and differentiation underlying developmental processes from the simple determination of body axis to the formation of complex body structures. This vital function of homeodomain proteins during embryonic development was initially elucidated in lower organisms. Later, several human genetic disorders were shown to be caused by aberrations in human homeo box genes: Waardenburg syndrome (PAX3; 606597), aniridia (PAX6; 607108), synpolydactyly (HOXD13; 142989), schizencephaly (EMX2; 600035), and Rieger syndrome (PITX2; 601542). SHOX (OMIM Ref. No. 312865) is a pseudoautosomal homeo box gene that is thought to be responsible for idiopathic short stature and

implicated to play a role in the short stature phenotype of Turner syndrome patients. This gene shows high homology to the murine og12 gene, which was consequently proposed as the putative mouse homolog of SHOX. The homeodomains of SHOX (also called PHOG) and og12 were shown to be identical, suggesting that the 2 proteins bind to equivalent DNA elements and therefore trigger similar physiologic pathways. Blaschke et al. (1998) reported the identification of a SHOX-related human gene, which they designated SHOT (for SHOX homologous gene on chromosome 3), that shows a much higher degree of homology to og12 than SHOX. Two different isoforms were isolated, SHOTa and SHOTb, which have identical homeodomains and share a C-terminal 14-amino acid residue motif characteristic for craniofacially expressed homeodomain proteins. The differences between SHOTa and SHOTb reside within the N-termini and an alternatively spliced exon in the C termini. In situ hybridization of og12 on sections from staged mouse embryos detected highly restricted transcripts in the developmental sinus venosus (aorta), female genitalia, diencephalon, mes- and myelencephalon, nasal capsula, palate, eyelid, and limbs. By fluorescence in situ hybridization (FISH), Blaschke et al. (1998)

mapped the human SHOT gene on 3q25-q26. By the same method, De Baere et al. (1998) confirmed the localization of SHOT on 3q25-q26.1. It has been suggested on the basis of chromosomal aberrations that the Cornelia de Lange syndrome (OMIM Ref. No. 122470) maps to 3q26.3. Blaschke et al. (1998) suggested that SHOT is a candidate gene for that disorder. By FISH, Blaschke et al. (1998) mapped the mouse og12 gene to chromosome 3 in a region that shows homology of synteny to human 3q.

[80165] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[80166] Blaschke, R. J.; Monaghan, A. P.; Schiller, S.; Schechinger, B.; Rao, E.; Padilla-Nash, H.; Ried, T.; Rappold, G. A. : SHOT, a SHOX-related homeobox gene, is implicated in craniofacial, brain, heart, and limb development. Proc. Nat. Acad. Sci. 95: 2406-2411, 1998. ; and

[80167] Clement-Jones, M.; Schiller, S.; Rao, E.; Blaschke, R. J.; Zuniga, A.; Zeller, R.; Robson, S. C.; Binder, G.; Glass, I.; Strachan, T.; Lindsay, S.; Rappold, G. A. : The short stature homeo.

[80168] Further studies establishing the function and utilities of SHOX2 are found in John Hopkins OMIM database record

ID 602504, and in sited publications numbered 10624-1062 and 9027 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.ABLIM (Accession NM_002313) is another VGAM2354 host target gene. ABLIM BINDING SITE1 and ABLIM BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ABLIM, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABLIM BINDING SITE1 and ABLIM BINDING SITE2, designated SEQ ID:8112 and SEQ ID:13545 respectively, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80169] Another function of VGAM2354 is therefore inhibition of ABLIM (Accession NM_002313). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABLIM. AD-020 (Accession XM_002161) is another VGAM2354 host target gene. AD-020 BINDING SITE1 and AD-020 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AD-020, corresponding to HOST TARGET binding sites such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AD-020 BINDING SITE1 and AD-020 BINDING SITE2, designated SEQ ID:29868 and SEQ ID:17541 respectively, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80170] Another function of VGAM2354 is therefore inhibition of AD-020 (Accession XM_002161). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AD-020. DKFZP586M1120 (Accession NM_031294) is another VGAM2354 host target gene. DKFZP586M1120 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586M1120, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586M1120 BINDING SITE, designated SEQ ID:25318, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80171] Another function of VGAM2354 is therefore inhibition of DKFZP586M1120 (Accession NM_031294). Accordingly,

utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586M1120. FLJ10769 (Accession NM_018210) is another VGAM2354 host target gene. FLJ10769 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10769, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10769 BINDING SITE, designated SEQ ID:20111, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80172] Another function of VGAM2354 is therefore inhibition of FLJ10769 (Accession NM_018210). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10769. FLJ20015 (Accession NM_018996) is another VGAM2354 host target gene. FLJ20015 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20015, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20015

BINDING SITE, designated SEQ ID:21069, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80173] Another function of VGAM2354 is therefore inhibition of FLJ20015 (Accession NM_018996). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20015. FLJ20420 (Accession NM_017812) is another VGAM2354 host target gene. FLJ20420 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20420, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20420 BINDING SITE, designated SEQ ID:19460, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80174] Another function of VGAM2354 is therefore inhibition of FLJ20420 (Accession NM_017812). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20420. Heart and Neural Crest Derivatives Expressed 1 (HAND1, Accession NM_004821) is another VGAM2354

host target gene. HAND1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HAND1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HAND1 BINDING SITE, designated SEQ ID:11236, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80175] Another function of VGAM2354 is therefore inhibition of Heart and Neural Crest Derivatives Expressed 1 (HAND1, Accession NM_004821). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAND1. KIAA0716 (Accession NM_014705) is another VGAM2354 host target gene. KIAA0716 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0716, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0716 BINDING SITE, designated SEQ ID:16245, to the nucleotide sequence of VGAM2354 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5065.

[80176] Another function of VGAM2354 is therefore inhibition of KIAA0716 (Accession NM_014705). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0716. KIAA1095 (Accession XM_041363) is another VGAM2354 host target gene. KIAA1095 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1095, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1095 BINDING SITE, designated SEQ ID:33505, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80177] Another function of VGAM2354 is therefore inhibition of KIAA1095 (Accession XM_041363). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1095. KIAA1416 (Accession XM_098762) is another VGAM2354 host target gene. KIAA1416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1416, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1416 BINDING SITE, designated SEQ ID:41798, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80178] Another function of VGAM2354 is therefore inhibition of KIAA1416 (Accession XM_098762). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1416. KIAA1582 (Accession XM_037262) is another VGAM2354 host target gene. KIAA1582 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1582, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1582 BINDING SITE, designated SEQ ID:32590, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80179] Another function of VGAM2354 is therefore inhibition of KIAA1582 (Accession XM_037262). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1582. KIAA1841 (Accession XM_087056) is another VGAM2354 host target gene. KIAA1841 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1841 BINDING SITE, designated SEQ ID:39024, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80180] Another function of VGAM2354 is therefore inhibition of KIAA1841 (Accession XM_087056). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1841. KIAA1889 (Accession XM_056298) is another VGAM2354 host target gene. KIAA1889 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1889, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1889 BINDING SITE, designated SEQ ID:36387, to the

nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80181] Another function of VGAM2354 is therefore inhibition of KIAA1889 (Accession XM_056298). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1889. MGC13183 (Accession NM_032358) is another VGAM2354 host target gene. MGC13183 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC13183, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC13183 BINDING SITE, designated SEQ ID:26144, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80182] Another function of VGAM2354 is therefore inhibition of MGC13183 (Accession NM_032358). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC13183. Olfactomedin 3 (OLFM3, Accession XM_088951) is another VGAM2354 host target gene. OLFM3 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by OLFM3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OLFM3 BINDING SITE, designated SEQ ID:39958, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80183] Another function of VGAM2354 is therefore inhibition of Olfactomedin 3 (OLFM3, Accession XM_088951). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OLFM3. Phosphodiesterase 10A (PDE10A, Accession NM_006661) is another VGAM2354 host target gene. PDE10A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE10A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE10A BINDING SITE, designated SEQ ID:13460, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80184] Another function of VGAM2354 is therefore inhibition of Phosphodiesterase 10A (PDE10A, Accession NM_006661). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE10A. Phosphodiesterase 4D Interacting Protein (myomegalin) (PDE4DIP, Accession NM_014644) is another VGAM2354 host target gene. PDE4DIP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE4DIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE4DIP BINDING SITE, designated SEQ ID:16049, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80185] Another function of VGAM2354 is therefore inhibition of Phosphodiesterase 4D Interacting Protein (myomegalin) (PDE4DIP, Accession NM_014644). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4DIP. SH3 Domain Binding Glutamic Acid-rich Protein Like (SH3BGRL, Accession XM_030373) is another

VGAM2354 host target gene. SH3BGRL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3BGRL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3BGRL BINDING SITE, designated SEQ ID:31023, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80186] Another function of VGAM2354 is therefore inhibition of SH3 Domain Binding Glutamic Acid-rich Protein Like (SH3BGRL, Accession XM_030373). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BGRL. Solute Carrier Family 31 (copper transporters), Member 2 (SLC31A2, Accession XM_011776) is another VGAM2354 host target gene. SLC31A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC31A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC31A2 BINDING SITE, designated SEQ ID:30192, to the nucleotide

sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80187] Another function of VGAM2354 is therefore inhibition of Solute Carrier Family 31 (copper transporters), Member 2 (SLC31A2, Accession XM_011776). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC31A2. Stanniocalcin 2 (STC2, Accession NM_003714) is another VGAM2354 host target gene. STC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STC2 BINDING SITE, designated SEQ ID:9811, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80188] Another function of VGAM2354 is therefore inhibition of Stanniocalcin 2 (STC2, Accession NM_003714). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STC2. TBLR1 (Accession NM_024665) is another VGAM2354 host target gene. TBLR1 BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by TBLR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBLR1 BINDING SITE, designated SEQ ID:23965, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80189] Another function of VGAM2354 is therefore inhibition of TBLR1 (Accession NM_024665). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBLR1. Transducer of ERBB2, 2 (TOB2, Accession XM_170995) is another VGAM2354 host target gene. TOB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOB2 BINDING SITE, designated SEQ ID:45761, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80190] Another function of VGAM2354 is therefore inhibition of

Transducer of ERBB2, 2 (TOB2, Accession XM_170995). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOB2. Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession XM_053740) is another VGAM2354 host target gene. TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TP53INP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2, designated SEQ ID:36115 and SEQ ID:27104 respectively, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80191] Another function of VGAM2354 is therefore inhibition of Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession XM_053740). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53INP1. LOC115110 (Accession XM_049825) is another VGAM2354 host target gene. LOC115110 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115110 BINDING SITE, designated SEQ ID:35504, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80192] Another function of VGAM2354 is therefore inhibition of LOC115110 (Accession XM_049825). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115110. LOC126669 (Accession XM_060121) is another VGAM2354 host target gene. LOC126669 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126669, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126669 BINDING SITE, designated SEQ ID:37155, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80193] Another function of VGAM2354 is therefore inhibition of

LOC126669 (Accession XM_060121). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126669. LOC127396 (Accession XM_059139) is another VGAM2354 host target gene. LOC127396 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC127396, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127396 BINDING SITE, designated SEQ ID:36895, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80194] Another function of VGAM2354 is therefore inhibition of LOC127396 (Accession XM_059139). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127396. LOC147671 (Accession XM_085844) is another VGAM2354 host target gene. LOC147671 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147671, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC147671 BINDING SITE, designated SEQ ID:38375, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80195] Another function of VGAM2354 is therefore inhibition of LOC147671 (Accession XM_085844). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147671. LOC150185 (Accession XM_097834) is another VGAM2354 host target gene. LOC150185 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150185, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150185 BINDING SITE, designated SEQ ID:41151, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80196] Another function of VGAM2354 is therefore inhibition of LOC150185 (Accession XM_097834). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150185. LOC154739 (Accession XM_098602) is an-

other VGAM2354 host target gene. LOC154739 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154739, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154739 BINDING SITE, designated SEQ ID:41712, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80197] Another function of VGAM2354 is therefore inhibition of LOC154739 (Accession XM_098602). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154739. LOC160717 (Accession XM_090457) is another VGAM2354 host target gene. LOC160717 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC160717, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC160717 BINDING SITE, designated SEQ ID:40009, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80198] Another function of VGAM2354 is therefore inhibition of LOC160717 (Accession XM_090457). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC160717. LOC169426 (Accession XM_108739) is another VGAM2354 host target gene. LOC169426 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC169426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169426 BINDING SITE, designated SEQ ID:42206, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80199] Another function of VGAM2354 is therefore inhibition of LOC169426 (Accession XM_108739). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169426. LOC200150 (Accession XM_114131) is another VGAM2354 host target gene. LOC200150 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200150, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200150 BINDING SITE, designated SEQ ID:42712, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80200] Another function of VGAM2354 is therefore inhibition of LOC200150 (Accession XM_114131). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200150. LOC219731 (Accession XM_167596) is another VGAM2354 host target gene. LOC219731 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219731, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219731 BINDING SITE, designated SEQ ID:44715, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80201] Another function of VGAM2354 is therefore inhibition of LOC219731 (Accession XM_167596). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC219731. LOC221069 (Accession XM_167676) is another VGAM2354 host target gene. LOC221069 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221069, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221069 BINDING SITE, designated SEQ ID:44767, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80202] Another function of VGAM2354 is therefore inhibition of LOC221069 (Accession XM_167676). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221069. LOC221294 (Accession XM_166297) is another VGAM2354 host target gene. LOC221294 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221294 BINDING SITE, designated SEQ ID:44112, to the nucleotide sequence of VGAM2354 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5065.

[80203] Another function of VGAM2354 is therefore inhibition of LOC221294 (Accession XM_166297). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221294. LOC221550 (Accession XM_166388) is another VGAM2354 host target gene. LOC221550 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221550, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221550 BINDING SITE, designated SEQ ID:44238, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80204] Another function of VGAM2354 is therefore inhibition of LOC221550 (Accession XM_166388). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221550. LOC222008 (Accession XM_168361) is another VGAM2354 host target gene. LOC222008 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222008, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222008 BINDING SITE, designated SEQ ID:45125, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80205] Another function of VGAM2354 is therefore inhibition of LOC222008 (Accession XM_168361). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222008. LOC222256 (Accession XM_168571) is another VGAM2354 host target gene. LOC222256 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222256, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222256 BINDING SITE, designated SEQ ID:45247, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80206] Another function of VGAM2354 is therefore inhibition of LOC222256 (Accession XM_168571). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC222256. LOC253263 (Accession XM_173102) is another VGAM2354 host target gene. LOC253263 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253263, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253263 BINDING SITE, designated SEQ ID:46359, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80207] Another function of VGAM2354 is therefore inhibition of LOC253263 (Accession XM_173102). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253263. LOC256021 (Accession XM_172884) is another VGAM2354 host target gene. LOC256021 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256021, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256021 BINDING SITE, designated SEQ ID:46163, to

the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80208] Another function of VGAM2354 is therefore inhibition of LOC256021 (Accession XM_172884). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256021. LOC256118 (Accession XM_174624) is another VGAM2354 host target gene. LOC256118 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256118, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256118 BINDING SITE, designated SEQ ID:46601, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80209] Another function of VGAM2354 is therefore inhibition of LOC256118 (Accession XM_174624). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256118. LOC257495 (Accession XM_175166) is another VGAM2354 host target gene. LOC257495 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC257495, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257495 BINDING SITE, designated SEQ ID:46655, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80210] Another function of VGAM2354 is therefore inhibition of LOC257495 (Accession XM_175166). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257495. LOC257576 (Accession XM_175254) is another VGAM2354 host target gene. LOC257576 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257576, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257576 BINDING SITE, designated SEQ ID:46715, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80211] Another function of VGAM2354 is therefore inhibition of LOC257576 (Accession XM_175254). Accordingly, utilities

of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257576. LOC92078 (Accession XM_042684) is another VGAM2354 host target gene. LOC92078 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92078, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92078 BINDING SITE, designated SEQ ID:33740, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80212] Another function of VGAM2354 is therefore inhibition of LOC92078 (Accession XM_042684). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92078. LOC92303 (Accession XM_044108) is another VGAM2354 host target gene. LOC92303 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92303, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC92303 BINDING SITE, designated SEQ ID:34133, to the nucleotide sequence of VGAM2354 RNA, herein designated VGAM RNA, also designated SEQ ID:5065.

[80213] Another function of VGAM2354 is therefore inhibition of LOC92303 (Accession XM_044108). Accordingly, utilities of VGAM2354 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92303. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2355 (VGAM2355) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80214] VGAM2355 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2355 was detected is described hereinabove with reference to Figs. 1-8.

[80215] VGAM2355 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2355 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80216] VGAM2355 gene encodes a VGAM2355 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2355 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2355 precursor RNA is designated SEQ ID:2341, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2341 is located at position 39033 relative to the genome of Equine Herpesvirus 2.

[80217] VGAM2355 precursor RNA folds onto itself, forming VGAM2355 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80218] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2355 folded precursor RNA into VGAM2355 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2355 RNA is designated SEQ ID:5066, and is provided hereinbelow with reference to the sequence listing part.

[80219] VGAM2355 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2355 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2355 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80220] VGAM2355 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2355 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2355 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2355 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2355 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80221] The complementary binding of VGAM2355 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2355 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2355 host target RNA into VGAM2355 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80222] It is appreciated that VGAM2355 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2355 host target genes. The mRNA of each one of this plurality of VGAM2355 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2355 RNA, herein designated VGAM RNA, and which when bound by VGAM2355 RNA causes inhibition of translation of respective one or more VGAM2355 host target proteins.

[80223] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2355 gene, herein designated VGAM GENE, on one or more VGAM2355 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80224] It is yet further appreciated that a function of VGAM2355 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2355 correlate with, and may be deduced from, the identity of the host target genes which VGAM2355 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80225] Nucleotide sequences of the VGAM2355 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2355 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2355 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2355 are further described hereinbelow with reference to Table 1.

[80226] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2355 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2355 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80227] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2355 gene, herein designated VGAM is inhibition of expression of VGAM2355 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2355 correlate with, and may be deduced from, the identity of the target genes which VGAM2355 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80228] Bromodomain Adjacent to Zinc Finger Domain, 2B (BAZ2B, Accession NM_013450) is a VGAM2355 host target gene. BAZ2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAZ2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAZ2B BINDING SITE, designated SEQ ID:15124, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80229] A function of VGAM2355 is therefore inhibition of Bromodomain Adjacent to Zinc Finger Domain, 2B (BAZ2B, Accession NM_013450). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAZ2B. G Protein-coupled Receptor 85 (GPR85, Accession NM_018970) is another VGAM2355 host target gene. GPR85 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPR85, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR85 BINDING SITE, designated SEQ ID:21042, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80230] Another function of VGAM2355 is therefore inhibition of G Protein-coupled Receptor 85 (GPR85, Accession NM_018970). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR85. Neurotrophic Tyrosine Kinase, Receptor, Type 2 (NTRK2, Accession NM_006180) is another VGAM2355 host target gene.

NTRK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NTRK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NTRK2 BINDING SITE, designated SEQ ID:12845, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80231] Another function of VGAM2355 is therefore inhibition of Neurotrophic Tyrosine Kinase, Receptor, Type 2 (NTRK2, Accession NM_006180), a gene which is involved in the development and/or maintenance of the nervous system. Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTRK2. The function of NTRK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM341.Ubiquitin-conjugating Enzyme E2L 3 (UBE2L3, Accession NM_003347) is another VGAM2355 host target gene. UBE2L3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

UBE2L3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE2L3 BINDING SITE, designated SEQ ID:9360, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80232] Another function of VGAM2355 is therefore inhibition of Ubiquitin-conjugating Enzyme E2L 3 (UBE2L3, Accession NM_003347), a gene which catalyzes the covalent attachment of ubiquitin to other proteins. Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE2L3. The function of UBE2L3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM215.DKFZP761G1913 (Accession NM_031474) is another VGAM2355 host target gene. DKFZP761G1913 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP761G1913, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the

nucleotide sequences of DKFZP761G1913 BINDING SITE, designated SEQ ID:25545, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80233] Another function of VGAM2355 is therefore inhibition of DKFZP761G1913 (Accession NM_031474). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP761G1913. Eukaryotic Translation Initiation Factor 5 (EIF5, Accession NM_001969) is another VGAM2355 host target gene. EIF5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF5 BINDING SITE, designated SEQ ID:7698, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80234] Another function of VGAM2355 is therefore inhibition of Eukaryotic Translation Initiation Factor 5 (EIF5, Accession NM_001969). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with EIF5. FLJ12586 (Accession NM_024620) is another VGAM2355 host target gene. FLJ12586 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12586, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12586 BINDING SITE, designated SEQ ID:23881, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80235] Another function of VGAM2355 is therefore inhibition of FLJ12586 (Accession NM_024620). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12586. FLJ14494 (Accession XM_165571) is another VGAM2355 host target gene. FLJ14494 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14494, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14494 BINDING SITE, designated SEQ ID:43693, to the nucleotide

sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80236] Another function of VGAM2355 is therefore inhibition of FLJ14494 (Accession XM_165571). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14494. HSPC031 (Accession NM_016101) is another VGAM2355 host target gene. HSPC031 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSPC031, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSPC031 BINDING SITE, designated SEQ ID:18184, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80237] Another function of VGAM2355 is therefore inhibition of HSPC031 (Accession NM_016101). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSPC031. KIAA1423 (Accession XM_029703) is another VGAM2355 host target gene. KIAA1423 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1423, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1423 BINDING SITE, designated SEQ ID:30919, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80238] Another function of VGAM2355 is therefore inhibition of KIAA1423 (Accession XM_029703). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1423. P21 (CDKN1A)-activated Kinase 2 (PAK2, Accession XM_039354) is another VGAM2355 host target gene. PAK2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PAK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAK2 BINDING SITE, designated SEQ ID:33062, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80239] Another function of VGAM2355 is therefore inhibition of P21 (CDKN1A)-activated Kinase 2 (PAK2, Accession

XM_039354). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAK2. Phosphatidylinositol-4-phosphate 5-kinase, Type II, Beta (PIP5K2B, Accession NM_003559) is another VGAM2355 host target gene. PIP5K2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIP5K2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIP5K2B BINDING SITE, designated SEQ ID:9606, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80240] Another function of VGAM2355 is therefore inhibition of Phosphatidylinositol-4-phosphate 5-kinase, Type II, Beta (PIP5K2B, Accession NM_003559). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIP5K2B. LOC134265 (Accession XM_059702) is another VGAM2355 host target gene. LOC134265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC134265, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC134265 BINDING SITE, designated SEQ ID:37075, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80241] Another function of VGAM2355 is therefore inhibition of LOC134265 (Accession XM_059702). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC134265. LOC144438 (Accession XM_084860) is another VGAM2355 host target gene. LOC144438 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144438, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144438 BINDING SITE, designated SEQ ID:37740, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80242] Another function of VGAM2355 is therefore inhibition of LOC144438 (Accession XM_084860). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC144438. LOC147071 (Accession XM_054031) is another VGAM2355 host target gene. LOC147071 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147071, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147071 BINDING SITE, designated SEQ ID:36133, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80243] Another function of VGAM2355 is therefore inhibition of LOC147071 (Accession XM_054031). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147071. LOC201173 (Accession XM_113312) is another VGAM2355 host target gene. LOC201173 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201173, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201173 BINDING SITE, designated SEQ ID:42212, to

the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80244] Another function of VGAM2355 is therefore inhibition of LOC201173 (Accession XM_113312). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201173. LOC51706 (Accession XM_046746) is another VGAM2355 host target gene. LOC51706 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51706, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51706 BINDING SITE, designated SEQ ID:34816, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80245] Another function of VGAM2355 is therefore inhibition of LOC51706 (Accession XM_046746). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51706. LOC91291 (Accession XM_037478) is another VGAM2355 host target gene. LOC91291 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by LOC91291, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91291 BINDING SITE, designated SEQ ID:32629, to the nucleotide sequence of VGAM2355 RNA, herein designated VGAM RNA, also designated SEQ ID:5066.

[80246] Another function of VGAM2355 is therefore inhibition of LOC91291 (Accession XM_037478). Accordingly, utilities of VGAM2355 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91291. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2356 (VGAM2356) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80247] VGAM2356 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2356 was detected is described hereinabove with reference to Figs. 1-8.

[80248] VGAM2356 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Equine Herpesvirus 2. VGAM2356 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80249] VGAM2356 gene encodes a VGAM2356 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2356 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2356 precursor RNA is designated SEQ ID:2342, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2342 is located at position 38873 relative to the genome of Equine Herpesvirus 2.

[80250] VGAM2356 precursor RNA folds onto itself, forming VGAM2356 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80251] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2356 folded precursor RNA into VGAM2356 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2356 RNA is designated SEQ ID:5067, and is provided hereinbelow with reference to the sequence listing part.

[80252] VGAM2356 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2356 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2356 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80253] VGAM2356 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2356 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2356 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2356 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2356 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80254] The complementary binding of VGAM2356 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2356 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2356

host target RNA into VGAM2356 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80255] It is appreciated that VGAM2356 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2356 host target genes. The mRNA of each one of this plurality of VGAM2356 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2356 RNA, herein designated VGAM RNA, and which when bound by VGAM2356 RNA causes inhibition of translation of respective one or more VGAM2356 host target proteins.

[80256] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2356 gene, herein designated VGAM GENE, on one or more VGAM2356 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80257] It is yet further appreciated that a function of VGAM2356 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2356 correlate with, and may be deduced from, the identity of the host target genes which VGAM2356 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80258] Nucleotide sequences of the VGAM2356 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2356 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2356 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2356 are further

described hereinbelow with reference to Table 1.

[80259] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2356 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2356 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80260] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2356 gene, herein designated VGAM is inhibition of expression of VGAM2356 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2356 correlate with, and may be deduced from, the identity of the target genes which VGAM2356 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80261] Dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD, Accession NM_004013) is a VGAM2356 host target gene. DMD BINDING SITE1 through DMD BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DMD, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of DMD BINDING SITE1 through DMD BINDING SITE3, designated SEQ ID:10196, SEQ ID:10223 and SEQ ID:10235 respectively, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80262] A function of VGAM2356 is therefore inhibition of Dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD, Accession NM_004013), a gene which muscular dystrophy . Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMD. The function of DMD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM218.Glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK, Accession NM_033508) is another VGAM2356 host target gene. GCK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GCK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GCK BINDING SITE, designated SEQ ID:27285, to the nucleotide se-

quence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80263] Another function of VGAM2356 is therefore inhibition of Glucokinase (hexokinase 4, maturity onset diabetes of the young 2) (GCK, Accession NM_033508), a gene which catalyzes the initial step in utilization of glucose by the beta-cell and liver at physiological glucose concentration. Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GCK. The function of GCK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1781.Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411) is another VGAM2356 host target gene. HLCS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HLCS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HLCS BINDING SITE, designated SEQ ID:5992, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM

RNA, also designated SEQ ID:5067.

[80264] Another function of VGAM2356 is therefore inhibition of Holocarboxylase Synthetase (biotin-[proprionyl-Coenzyme A-carboxylase (ATP-hydrolysing)] Ligase) (HLCS, Accession NM_000411). Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HLCS. Inositol Polyphosphate-5-phosphatase, 75kDa (INPP5B, Accession XM_170949) is another VGAM2356 host target gene. INPP5B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by INPP5B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of INPP5B BINDING SITE, designated SEQ ID:45736, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80265] Another function of VGAM2356 is therefore inhibition of Inositol Polyphosphate-5-phosphatase, 75kDa (INPP5B, Accession XM_170949), a gene which hydrolyzes the calcium-mobilizing second messenger ins(1,4,5)p3. Accordingly, utilities of VGAM2356 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with INPP5B. The function of INPP5B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM50.Mitogen-activated Protein Kinase Kinase Kinase 7 Interacting Protein 1 (MAP3K7IP1, Accession NM_006116) is another VGAM2356 host target gene. MAP3K7IP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K7IP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K7IP1 BINDING SITE, designated SEQ ID:12761, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80266] Another function of VGAM2356 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 7 Interacting Protein 1 (MAP3K7IP1, Accession NM_006116), a gene which may be an important signaling intermediate between tgfb receptors and map3k7/tak1. Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with MAP3K7IP1. The function of MAP3K7IP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM132.MCF.2 Cell Line Derived Transforming Sequence (MCF2, Accession NM_005369) is another VGAM2356 host target gene. MCF2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MCF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MCF2 BINDING SITE, designated SEQ ID:11841, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80267] Another function of VGAM2356 is therefore inhibition of MCF.2 Cell Line Derived Transforming Sequence (MCF2, Accession NM_005369), a gene which Cytoplasmic oncoprotein similar to vimentin. Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCF2. The function of MCF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM763.Placental Growth Factor, Vascular Endothelial Growth Factor-related Protein (PGF, Accession NM_002632) is another VGAM2356 host target gene. PGF BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PGF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PGF BINDING SITE, designated SEQ ID:8492, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80268] Another function of VGAM2356 is therefore inhibition of Placental Growth Factor, Vascular Endothelial Growth Factor-related Protein (PGF, Accession NM_002632), a gene which is a growth factor active in angiogenesis, and endothelial cell growth, stimulating cell proliferation and migration. it binds to receptor vegfr-1/fl. Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PGF. The function of PGF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1420.DEAD/H (Asp-Glu-Ala-Asp/His) Box

Polypeptide 17, 72kDa (DDX17, Accession NM_006386) is another VGAM2356 host target gene. DDX17 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DDX17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDX17 BINDING SITE, designated SEQ ID:13090, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80269] Another function of VGAM2356 is therefore inhibition of DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 17, 72kDa (DDX17, Accession NM_006386). Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX17. FLJ00024 (Accession XM_033361) is another VGAM2356 host target gene. FLJ00024 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ00024, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00024 BINDING SITE, designated SEQ ID:31896, to the nucleotide

sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80270] Another function of VGAM2356 is therefore inhibition of FLJ00024 (Accession XM_033361). Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00024. FLJ14871 (Accession NM_032854) is another VGAM2356 host target gene. FLJ14871 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ14871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14871 BINDING SITE, designated SEQ ID:26652, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80271] Another function of VGAM2356 is therefore inhibition of FLJ14871 (Accession NM_032854). Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14871. FLJ21687 (Accession NM_024859) is another VGAM2356 host target gene. FLJ21687 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ21687, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21687 BINDING SITE, designated SEQ ID:24292, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80272] Another function of VGAM2356 is therefore inhibition of FLJ21687 (Accession NM_024859). Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21687. KIAA1196 (Accession XM_028968) is another VGAM2356 host target gene. KIAA1196 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1196 BINDING SITE, designated SEQ ID:30823, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80273] Another function of VGAM2356 is therefore inhibition of KIAA1196 (Accession XM_028968). Accordingly, utilities

of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1196. Neuronal Pentraxin Receptor (NPTXR, Accession NM_058178) is another VGAM2356 host target gene. NPTXR BINDING SITE1 and NPTXR BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NPTXR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPTXR BINDING SITE1 and NPTXR BINDING SITE2, designated SEQ ID:27734 and SEQ ID:15586 respectively, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80274] Another function of VGAM2356 is therefore inhibition of Neuronal Pentraxin Receptor (NPTXR, Accession NM_058178). Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPTXR. LOC256222 (Accession XM_173177) is another VGAM2356 host target gene. LOC256222 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256222, corresponding to a HOST TARGET binding

site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256222 BINDING SITE, designated SEQ ID:46428, to the nucleotide sequence of VGAM2356 RNA, herein designated VGAM RNA, also designated SEQ ID:5067.

[80275] Another function of VGAM2356 is therefore inhibition of LOC256222 (Accession XM_173177). Accordingly, utilities of VGAM2356 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256222. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2357 (VGAM2357) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80276] VGAM2357 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2357 was detected is described hereinabove with reference to Figs. 1-8.

[80277] VGAM2357 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2.

VGAM2357 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80278] VGAM2357 gene encodes a VGAM2357 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2357 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2357 precursor RNA is designated SEQ ID:2343, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2343 is located at position 32894 relative to the genome of Equine Herpesvirus 2.

[80279] VGAM2357 precursor RNA folds onto itself, forming VGAM2357 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80280] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2357 folded precursor RNA into VGAM2357 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2357 RNA is designated SEQ ID:5068, and is provided hereinbelow with reference to the sequence listing part.

[80281] VGAM2357 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2357 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2357 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80282] VGAM2357 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2357 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2357 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2357 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2357 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80283] The complementary binding of VGAM2357 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2357 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2357 host target RNA into VGAM2357 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80284] It is appreciated that VGAM2357 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2357 host target genes. The mRNA of each one of this plurality of VGAM2357 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2357 RNA, herein designated VGAM RNA, and which when bound by VGAM2357 RNA causes inhibition of translation of respective one or more VGAM2357 host target proteins.

[80285] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2357 gene, herein designated VGAM GENE, on one or more VGAM2357 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80286] It is yet further appreciated that a function of VGAM2357 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2357 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2357 correlate with, and may be deduced from, the identity of the host target genes which VGAM2357 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80287] Nucleotide sequences of the VGAM2357 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2357 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2357 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2357 are further described hereinbelow with reference to Table 1.

[80288] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2357 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2357 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80289] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2357 gene, herein designated VGAM is inhibition of expression of VGAM2357 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2357 correlate with, and may be deduced from, the identity of the target genes which VGAM2357 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80290] ATP-binding Cassette, Sub-family E (OABP), Member 1 (ABCE1, Accession XM_003555) is a VGAM2357 host target gene. ABCE1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCE1 BINDING SITE, designated SEQ

ID:29939, to the nucleotide sequence of VGAM2357 RNA, herein designated VGAM RNA, also designated SEQ ID:5068.

[80291] A function of VGAM2357 is therefore inhibition of ATP-binding Cassette, Sub-family E (OABP), Member 1 (ABCE1, Accession XM_003555), a gene which a Ribonuclease L inhibitor. Accordingly, utilities of VGAM2357 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCE1. The function of ABCE1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1924.Procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 (PLOD2, Accession NM_000935) is another VGAM2357 host target gene. PLOD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLOD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLOD2 BINDING SITE, designated SEQ ID:6640, to the nucleotide sequence of VGAM2357 RNA, herein designated VGAM RNA, also designated SEQ

ID:5068.

[80292] Another function of VGAM2357 is therefore inhibition of Procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase) 2 (PLOD2, Accession NM_000935), a gene which catalyzes the formation of hydroxylysine in collagens. Accordingly, utilities of VGAM2357 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLOD2. The function of PLOD2 has been established by previous studies. Lysyl hydroxylase (EC 1.14.11.4) catalyzes the hydroxylation of lysyl residues in collagens. The active enzyme is a homodimer consisting of subunits with a molecular weight of about 85,000. Valtavaara et al. (1997) reported the isolation and characterization of cDNA clones for a novel isoform, which they called lysyl hydroxylase-2, symbolized PLOD2. The predicted 737-amino acid polypeptide includes an N-terminal signal peptide and has overall similarity of more than 75% to lysyl hydroxylase-1, or PLOD, from human and chicken. The similarity is even higher in the C-terminal region of the polypeptides. The PLOD2 gene contains 9 cysteines conserved in PLOD, in addition to conserved histidines in the putative active site. By Northern analysis, Valtavaara et al. (1997) detected a 4.2-kb tran-

script that was highly expressed in pancreas, skeletal muscle, heart, and placenta. Recombinant protein produced from cDNA using a baculovirus expression system yielded enzyme with lysyl hydroxylase activity in vitro. Animal model experiments lend further support to the function of PLOD2. Szpirer et al. (1997) mapped the PLOD2 gene to human chromosome 3 by somatic cell hybrid analysis and to 3q23-q24 by fluorescence in situ hybridization. The rat gene was mapped to chromosome 8 where the genes shared by human chromosome 3 are located. Sipila et al. (2000) mapped the mouse homolog to chromosome 9.

[80293] It is appreciated that the abovementioned animal model for PLOD2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[80294] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[80295] Valtavaara, M.; Papponen, H.; Pirttila, A.-M.; Hiltunen, K.; Helander, H.; Myllyla, R. : Cloning and characterization of a novel human lysyl hydroxylase isoform highly expressed in pancreas and muscle. J. Biol. Chem. 272: 6831-6834,

1997. ; and

[80296] Szpirer, C.; Szpirer, J.; Riviere, M.; Vanvooren, P.; Valtavaara, M.; Myllyla, R. : Localization of the gene encoding a novel isoform of lysyl hydroxylase. Mammalian Genome 8: 707-708, 1.

[80297] Further studies establishing the function and utilities of PLOD2 are found in John Hopkins OMIM database record ID 601865, and in sited publications numbered 6269-6271 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.DKFZP586P0123 (Accession XM_170681) is another VGAM2357 host target gene. DKFZP586P0123 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586P0123, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586P0123 BINDING SITE, designated SEQ ID:45462, to the nucleotide sequence of VGAM2357 RNA, herein designated VGAM RNA, also designated SEQ ID:5068.

[80298] Another function of VGAM2357 is therefore inhibition of DKFZP586P0123 (Accession XM_170681). Accordingly,

utilities of VGAM2357 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586P0123. Wingless-type MMTV Integration Site Family, Member 2B (WNT2B, Accession NM_004185) is another VGAM2357 host target gene. WNT2B BINDING SITE1 and WNT2B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WNT2B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT2B BINDING SITE1 and WNT2B BINDING SITE2, designated SEQ ID:10390 and SEQ ID:23691 respectively, to the nucleotide sequence of VGAM2357 RNA, herein designated VGAM RNA, also designated SEQ ID:5068.

[80299] Another function of VGAM2357 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 2B (WNT2B, Accession NM_004185). Accordingly, utilities of VGAM2357 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WNT2B. LOC220672 (Accession XM_017177) is another VGAM2357 host target gene. LOC220672 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC220672, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220672 BINDING SITE, designated SEQ ID:30306, to the nucleotide sequence of VGAM2357 RNA, herein designated VGAM RNA, also designated SEQ ID:5068.

[80300] Another function of VGAM2357 is therefore inhibition of LOC220672 (Accession XM_017177). Accordingly, utilities of VGAM2357 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220672. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2358 (VGAM2358) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80301] VGAM2358 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2358 was detected is described hereinabove with reference to Figs. 1-8.

[80302] VGAM2358 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Equine Herpesvirus 2. VGAM2358 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80303] VGAM2358 gene encodes a VGAM2358 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2358 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2358 precursor RNA is designated SEQ ID:2344, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2344 is located at position 44667 relative to the genome of Equine Herpesvirus 2.

[80304] VGAM2358 precursor RNA folds onto itself, forming VGAM2358 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80305] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2358 folded precursor RNA into VGAM2358 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2358 RNA is designated SEQ ID:5069, and is provided hereinbelow with reference to the sequence listing part.

[80306] VGAM2358 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2358 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2358 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80307] VGAM2358 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2358 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2358 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2358 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2358 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80308] The complementary binding of VGAM2358 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2358 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2358

host target RNA into VGAM2358 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80309] It is appreciated that VGAM2358 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2358 host target genes. The mRNA of each one of this plurality of VGAM2358 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2358 RNA, herein designated VGAM RNA, and which when bound by VGAM2358 RNA causes inhibition of translation of respective one or more VGAM2358 host target proteins.

[80310] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2358 gene, herein designated VGAM GENE, on one or more VGAM2358 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80311] It is yet further appreciated that a function of VGAM2358 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2358 correlate with, and may be deduced from, the identity of the host target genes which VGAM2358 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80312] Nucleotide sequences of the VGAM2358 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2358 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2358 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2358 are further

described hereinbelow with reference to Table 1.

[80313] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2358 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2358 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80314] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2358 gene, herein designated VGAM is inhibition of expression of VGAM2358 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2358 correlate with, and may be deduced from, the identity of the target genes which VGAM2358 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80315] Alcohol Dehydrogenase IB (class I), Beta Polypeptide (ADH1B, Accession XM_052365) is a VGAM2358 host target gene. ADH1B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADH1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of ADH1B BINDING SITE, designated SEQ ID:35962, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80316] A function of VGAM2358 is therefore inhibition of Alcohol Dehydrogenase IB (class I), Beta Polypeptide (ADH1B, Accession XM_052365), a gene which Alcohol dehydrogenase 2 (alcohol:NAD+ oxidoreductase) class I beta subunit. Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADH1B. The function of ADH1B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1805.Activation-induced Cytidine Deaminase (AICDA, Accession NM_020661) is another VGAM2358 host target gene. AICDA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AICDA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AICDA BINDING SITE, designated SEQ ID:21833, to the nucleotide sequence of

VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80317] Another function of VGAM2358 is therefore inhibition of Activation-induced Cytidine Deaminase (AICDA, Accession NM_020661), a gene which a member of the cytidine deaminase family. Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AICDA. The function of AICDA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM600.Amyloid Beta Precursor Protein (cytoplasmic tail) Binding Protein 2 (APPBP2, Accession NM_006380) is another VGAM2358 host target gene. APPBP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APPBP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APPBP2 BINDING SITE, designated SEQ ID:13085, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80318] Another function of VGAM2358 is therefore inhibition of

Amyloid Beta Precursor Protein (cytoplasmic tail) Binding Protein 2 (APPBP2, Accession NM_006380), a gene which interacts with the basolateral sorting signal of amyloid precursor protein. Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APPBP2. The function of APPBP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM525.ATPase, Ca++ Transporting, Plasma Membrane 4 (ATP2B4, Accession XM_046775) is another VGAM2358 host target gene. ATP2B4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ATP2B4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP2B4 BINDING SITE, designated SEQ ID:34825, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80319] Another function of VGAM2358 is therefore inhibition of ATPase, Ca++ Transporting, Plasma Membrane 4 (ATP2B4, Accession XM_046775). Accordingly, utilities of

VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP2B4. BRIP1 (Accession NM_032043) is another VGAM2358 host target gene. BRIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BRIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRIP1 BINDING SITE, designated SEQ ID:25758, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80320] Another function of VGAM2358 is therefore inhibition of BRIP1 (Accession NM_032043). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRIP1. Caspase 2, Apoptosis-related Cysteine Protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NM_032982) is another VGAM2358 host target gene. CASP2 BINDING SITE1 through CASP2 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CASP2, corresponding to HOST TARGET binding sites such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CASP2 BINDING SITE1 through CASP2 BINDING SITE4, designated SEQ ID:26856, SEQ ID:26861, SEQ ID:26866 and SEQ ID:6893 respectively, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80321] Another function of VGAM2358 is therefore inhibition of Caspase 2, Apoptosis-related Cysteine Protease (neural precursor cell expressed, developmentally down-regulated 2) (CASP2, Accession NM_032982), a gene which involves in the activation cascade of caspases responsible for apoptosis execution. Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP2. The function of CASP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM148.Core-binding Factor, Beta Subunit (CBFB, Accession NM_001755) is another VGAM2358 host target gene. CBFB BINDING SITE1 and CBFB BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CBFB, corresponding to HOST TAR-

GET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBFB BINDING SITE1 and CBFB BINDING SITE2, designated SEQ ID:7508 and SEQ ID:23149 respectively, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80322] Another function of VGAM2358 is therefore inhibition of Core-binding Factor, Beta Subunit (CBFB, Accession NM_001755), a gene which is beta subunit of the transcription factor CBF which causes leukemia. Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFB. The function of CBFB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM98.Coronin, Actin Binding Protein, 2B (CORO2B, Accession XM_035403) is another VGAM2358 host target gene. CORO2B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CORO2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of CORO2B BINDING SITE, designated SEQ ID:32257, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80323] Another function of VGAM2358 is therefore inhibition of Coronin, Actin Binding Protein, 2B (CORO2B, Accession XM_035403), a gene which may play a role in the reorganization of neuronal actin structure. Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CORO2B. The function of CORO2B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM923.Eukaryotic Translation Initiation Factor 1A (EIF1A, Accession XM_114147) is another VGAM2358 host target gene. EIF1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF1A BINDING SITE, designated SEQ ID:42728, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5069.

[80324] Another function of VGAM2358 is therefore inhibition of Eukaryotic Translation Initiation Factor 1A (EIF1A, Accession XM_114147), a gene which seems to be required for maximal rate of protein biosynthesis. Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF1A. The function of EIF1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM120.Homeo Box B3 (HOXB3, Accession NM_002146) is another VGAM2358 host target gene. HOXB3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HOXB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOXB3 BINDING SITE, designated SEQ ID:7923, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80325] Another function of VGAM2358 is therefore inhibition of Homeo Box B3 (HOXB3, Accession NM_002146). Accord-

ingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXB3. Immunoglobulin Superfamily Containing Leucine-rich Repeat (ISLR, Accession NM_005545) is another VGAM2358 host target gene. ISLR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ISLR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ISLR BINDING SITE, designated SEQ ID:12071, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80326] Another function of VGAM2358 is therefore inhibition of Immunoglobulin Superfamily Containing Leucine-rich Repeat (ISLR, Accession NM_005545). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ISLR. Melan-A (MLANA, Accession NM_005511) is another VGAM2358 host target gene. MLANA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MLANA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MLANA BINDING SITE, designated SEQ ID:12029, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80327] Another function of VGAM2358 is therefore inhibition of Melan-A (MLANA, Accession NM_005511). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLANA. V-myc Myelocytomatosis Viral Oncogene Homolog 2 (avian) (MYCL2, Accession NM_005377) is another VGAM2358 host target gene. MYCL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYCL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYCL2 BINDING SITE, designated SEQ ID:11858, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80328] Another function of VGAM2358 is therefore inhibition of V-myc Myelocytomatosis Viral Oncogene Homolog 2 (avian) (MYCL2, Accession NM_005377). Accordingly, util-

ities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYCL2. Serine (or cysteine) Proteinase Inhibitor, Clade D (heparin cofactor), Member 1 (SERPIND1, Accession NM_000185) is another VGAM2358 host target gene. SERPIND1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SERPIND1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERPIND1 BINDING SITE, designated SEQ ID:5687, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80329] Another function of VGAM2358 is therefore inhibition of Serine (or cysteine) Proteinase Inhibitor, Clade D (heparin cofactor), Member 1 (SERPIND1, Accession NM_000185). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPIND1. Solute Carrier Family 13 (sodium/sulfate symporters), Member 1 (SLC13A1, Accession NM_022444) is another VGAM2358 host target gene. SLC13A1 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by SLC13A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC13A1 BINDING SITE, designated SEQ ID:22776, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80330] Another function of VGAM2358 is therefore inhibition of Solute Carrier Family 13 (sodium/sulfate symporters), Member 1 (SLC13A1, Accession NM_022444). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC13A1. Surfeit 5 (SURF5, Accession NM_006752) is another VGAM2358 host target gene. SURF5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SURF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SURF5 BINDING SITE, designated SEQ ID:13607, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80331] Another function of VGAM2358 is therefore inhibition of Surfeit 5 (SURF5, Accession NM_006752). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SURF5. TRIM (Accession NM_016388) is another VGAM2358 host target gene. TRIM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM BINDING SITE, designated SEQ ID:18533, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80332] Another function of VGAM2358 is therefore inhibition of TRIM (Accession NM_016388), a gene which plays a role in recruiting signaling proteins to the plasma membrane upon T-cell receptor (TCR) complex activation in T cells. Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM. The function of TRIM and its association with various diseases and clinical conditions, has been established by previous studies, as described

hereinabove with reference to VGAM227.WAS Protein Family, Member 3 (WASF3, Accession NM_006646) is another VGAM2358 host target gene. WASF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WASF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WASF3 BINDING SITE, designated SEQ ID:13441, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80333] Another function of VGAM2358 is therefore inhibition of WAS Protein Family, Member 3 (WASF3, Accession NM_006646), a gene which stimulates actin polymerization. Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WASF3. The function of WASF3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1692.Williams-Beuren Syndrome Chromosome Region 1 (WBSCR1, Accession NM_022170) is another VGAM2358 host target gene. WBSCR1 BINDING SITE1 and

WBSCR1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WBSCR1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WBSCR1 BINDING SITE1 and WBSCR1 BINDING SITE2, designated SEQ ID:22727 and SEQ ID:25710 respectively, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80334] Another function of VGAM2358 is therefore inhibition of Williams-Beuren Syndrome Chromosome Region 1 (WBSCR1, Accession NM_022170), a gene which stimulates protein translation. Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR1. The function of WBSCR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM110.Collectin Sub-family Member 12 (COLEC12, Accession NM_030781) is another VGAM2358 host target gene. COLEC12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by COLEC12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COLEC12 BINDING SITE, designated SEQ ID:25073, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80335] Another function of VGAM2358 is therefore inhibition of Collectin Sub-family Member 12 (COLEC12, Accession NM_030781). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLEC12. CRMP5 (Accession NM_020134) is another VGAM2358 host target gene. CRMP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRMP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRMP5 BINDING SITE, designated SEQ ID:21331, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80336] Another function of VGAM2358 is therefore inhibition of

CRMP5 (Accession NM_020134). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRMP5. DDM36 (Accession NM_020962) is another VGAM2358 host target gene. DDM36 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DDM36, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDM36 BINDING SITE, designated SEQ ID:21957, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80337] Another function of VGAM2358 is therefore inhibition of DDM36 (Accession NM_020962). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDM36. FLJ11710 (Accession NM_024846) is another VGAM2358 host target gene. FLJ11710 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11710, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ11710 BINDING SITE, designated SEQ ID:24276, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80338] Another function of VGAM2358 is therefore inhibition of FLJ11710 (Accession NM_024846). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11710. FLJ12078 (Accession NM_024977) is another VGAM2358 host target gene. FLJ12078 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12078, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12078 BINDING SITE, designated SEQ ID:24535, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80339] Another function of VGAM2358 is therefore inhibition of FLJ12078 (Accession NM_024977). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12078. FLJ13910 (Accession NM_022780) is another

VGAM2358 host target gene. FLJ13910 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13910, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13910 BINDING SITE, designated SEQ ID:23054, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80340] Another function of VGAM2358 is therefore inhibition of FLJ13910 (Accession NM_022780). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13910. FLJ20651 (Accession NM_017919) is another VGAM2358 host target gene. FLJ20651 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20651, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20651 BINDING SITE, designated SEQ ID:19577, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80341] Another function of VGAM2358 is therefore inhibition of FLJ20651 (Accession NM_017919). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20651. FLJ20671 (Accession NM_017924) is another VGAM2358 host target gene. FLJ20671 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20671, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20671 BINDING SITE, designated SEQ ID:19593, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80342] Another function of VGAM2358 is therefore inhibition of FLJ20671 (Accession NM_017924). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20671. FLJ23024 (Accession NM_024936) is another VGAM2358 host target gene. FLJ23024 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23024, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23024 BINDING SITE, designated SEQ ID:24474, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80343] Another function of VGAM2358 is therefore inhibition of FLJ23024 (Accession NM_024936). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23024. FLJ23056 (Accession NM_024582) is another VGAM2358 host target gene. FLJ23056 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23056, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23056 BINDING SITE, designated SEQ ID:23809, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80344] Another function of VGAM2358 is therefore inhibition of FLJ23056 (Accession NM_024582). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ23056. Frequenin Homolog (Drosophila) (FREQ, Accession NM_014286) is another VGAM2358 host target gene. FREQ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FREQ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FREQ BINDING SITE, designated SEQ ID:15562, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80345] Another function of VGAM2358 is therefore inhibition of Frequenin Homolog (Drosophila) (FREQ, Accession NM_014286). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FREQ. GTP Binding Protein 1 (GTPBP1, Accession NM_004286) is another VGAM2358 host target gene. GTPBP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GTPBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTPBP1 BINDING SITE, designated SEQ ID:10497, to the nucleotide sequence of

VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80346] Another function of VGAM2358 is therefore inhibition of GTP Binding Protein 1 (GTPBP1, Accession NM_004286). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTPBP1. JM11 (Accession NM_033626) is another VGAM2358 host target gene. JM11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by JM11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JM11 BINDING SITE, designated SEQ ID:27330, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80347] Another function of VGAM2358 is therefore inhibition of JM11 (Accession NM_033626). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JM11. KIAA0026 (Accession NM_012286) is another VGAM2358 host target gene. KIAA0026 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by KIAA0026, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0026 BINDING SITE, designated SEQ ID:14616, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80348] Another function of VGAM2358 is therefore inhibition of KIAA0026 (Accession NM_012286). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0026. KIAA0152 (Accession NM_014730) is another VGAM2358 host target gene. KIAA0152 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0152, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0152 BINDING SITE, designated SEQ ID:16342, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80349] Another function of VGAM2358 is therefore inhibition of KIAA0152 (Accession NM_014730). Accordingly, utilities

of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0152. KIAA0285 (Accession NM_014807) is another VGAM2358 host target gene. KIAA0285 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0285, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0285 BINDING SITE, designated SEQ ID:16753, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80350] Another function of VGAM2358 is therefore inhibition of KIAA0285 (Accession NM_014807). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0285. KIAA0513 (Accession NM_014732) is another VGAM2358 host target gene. KIAA0513 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0513, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0513 BINDING SITE, designated SEQ ID:16365, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80351] Another function of VGAM2358 is therefore inhibition of KIAA0513 (Accession NM_014732). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513. KIAA0767 (Accession XM_027105) is another VGAM2358 host target gene. KIAA0767 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0767, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0767 BINDING SITE, designated SEQ ID:30410, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80352] Another function of VGAM2358 is therefore inhibition of KIAA0767 (Accession XM_027105). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0767. KIAA1200 (Accession XM_031054) is another VGAM2358 host target gene. KIAA1200 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1200, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1200 BINDING SITE, designated SEQ ID:31265, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80353] Another function of VGAM2358 is therefore inhibition of KIAA1200 (Accession XM_031054). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1200. KIAA1257 (Accession XM_031577) is another VGAM2358 host target gene. KIAA1257 BINDING SITE1 and KIAA1257 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1257, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1257 BINDING SITE1 and KIAA1257 BINDING SITE2, designated SEQ ID:31440 and SEQ ID:31441 respectively, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5069.

[80354] Another function of VGAM2358 is therefore inhibition of KIAA1257 (Accession XM_031577). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1257. KIAA1649 (Accession XM_040095) is another VGAM2358 host target gene. KIAA1649 BINDING SITE1 and KIAA1649 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1649, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1649 BINDING SITE1 and KIAA1649 BINDING SITE2, designated SEQ ID:33259 and SEQ ID:26111 respectively, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80355] Another function of VGAM2358 is therefore inhibition of KIAA1649 (Accession XM_040095). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1649. Kruppel-like Factor 12 (KLF12, Accession NM_016285) is another VGAM2358 host target gene.

KLF12 BINDING SITE1 and KLF12 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KLF12, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLF12 BINDING SITE1 and KLF12 BINDING SITE2, designated SEQ ID:18411 and SEQ ID:14120 respectively, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80356] Another function of VGAM2358 is therefore inhibition of Kruppel-like Factor 12 (KLF12, Accession NM_016285). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF12. Mannosidase, Beta A, Lysosomal-like (MANBAL, Accession NM_022077) is another VGAM2358 host target gene. MANBAL BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MANBAL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MANBAL BINDING SITE, designated SEQ ID:22622, to the nucleotide

sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80357] Another function of VGAM2358 is therefore inhibition of Mannosidase, Beta A, Lysosomal-like (MANBAL, Accession NM_022077). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MANBAL. MGC14836 (Accession NM_033412) is another VGAM2358 host target gene. MGC14836 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC14836, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC14836 BINDING SITE, designated SEQ ID:27237, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80358] Another function of VGAM2358 is therefore inhibition of MGC14836 (Accession NM_033412). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14836. MGC3222 (Accession NM_024334) is another VGAM2358 host target gene. MGC3222 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC3222, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC3222 BINDING SITE, designated SEQ ID:23642, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80359] Another function of VGAM2358 is therefore inhibition of MGC3222 (Accession NM_024334). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3222. moblak (Accession NM_130807) is another VGAM2358 host target gene. moblak BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by moblak, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of moblak BINDING SITE, designated SEQ ID:28313, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80360] Another function of VGAM2358 is therefore inhibition of

moblak (Accession NM_130807). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with moblak. NICE-3 (Accession NM_015449) is another VGAM2358 host target gene. NICE-3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NICE-3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NICE-3 BINDING SITE, designated SEQ ID:17735, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80361] Another function of VGAM2358 is therefore inhibition of NICE-3 (Accession NM_015449). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NICE-3. PILR(ALPHA) (Accession NM_013439) is another VGAM2358 host target gene. PILR(ALPHA) BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PILR(ALPHA), corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of PILR(ALPHA) BINDING SITE, designated SEQ ID:15103, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80362] Another function of VGAM2358 is therefore inhibition of PILR(ALPHA) (Accession NM_013439). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PILR(ALPHA). PIP3-E (Accession XM_039749) is another VGAM2358 host target gene. PIP3-E BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIP3-E, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIP3-E BINDING SITE, designated SEQ ID:33182, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80363] Another function of VGAM2358 is therefore inhibition of PIP3-E (Accession XM_039749). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIP3-E. Quiescin Q6 (QSCN6, Accession NM_002826) is another

VGAM2358 host target gene. QSCN6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by QSCN6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of QSCN6 BINDING SITE, designated SEQ ID:8699, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80364] Another function of VGAM2358 is therefore inhibition of Quiescin Q6 (QSCN6, Accession NM_002826). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with QSCN6. Rpo1-2 (Accession NM_019014) is another VGAM2358 host target gene. Rpo1-2 BINDING SITE1 and Rpo1-2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by Rpo1-2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rpo1-2 BINDING SITE1 and Rpo1-2 BINDING SITE2, designated SEQ ID:21100 and SEQ ID:25933 respectively, to the nucleotide sequence of VGAM2358 RNA,

herein designated VGAM RNA, also designated SEQ ID:5069.

[80365] Another function of VGAM2358 is therefore inhibition of Rpo1-2 (Accession NM_019014). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Rpo1-2. Solute Carrier Family 31 (copper transporters), Member 2 (SLC31A2, Accession XM_011776) is another VGAM2358 host target gene. SLC31A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC31A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC31A2 BINDING SITE, designated SEQ ID:30193, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80366] Another function of VGAM2358 is therefore inhibition of Solute Carrier Family 31 (copper transporters), Member 2 (SLC31A2, Accession XM_011776). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC31A2. Williams Beuren Syndrome Chromosome Region

20A (WBSCR20A, Accession NM_032158) is another VGAM2358 host target gene. WBSCR20A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by WBSCR20A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WB-SCR20A BINDING SITE, designated SEQ ID:25861, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80367] Another function of VGAM2358 is therefore inhibition of Williams Beuren Syndrome Chromosome Region 20A (WBSCR20A, Accession NM_032158). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR20A. ZFD25 (Accession NM_016220) is another VGAM2358 host target gene. ZFD25 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZFD25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZFD25 BINDING SITE, designated SEQ ID:18325, to the nucleotide sequence of

VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80368] Another function of VGAM2358 is therefore inhibition of ZFD25 (Accession NM_016220). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFD25. LOC113675 (Accession NM_138432) is another VGAM2358 host target gene. LOC113675 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC113675, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC113675 BINDING SITE, designated SEQ ID:28798, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80369] Another function of VGAM2358 is therefore inhibition of LOC113675 (Accession NM_138432). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113675. LOC115294 (Accession XM_054302) is another VGAM2358 host target gene. LOC115294 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC115294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115294 BINDING SITE, designated SEQ ID:36147, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80370] Another function of VGAM2358 is therefore inhibition of LOC115294 (Accession XM_054302). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115294. LOC130813 (Accession XM_065904) is another VGAM2358 host target gene. LOC130813 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130813, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130813 BINDING SITE, designated SEQ ID:37316, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80371] Another function of VGAM2358 is therefore inhibition of LOC130813 (Accession XM_065904). Accordingly, utilities

of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130813. LOC143241 (Accession NM_138812) is another VGAM2358 host target gene. LOC143241 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143241, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143241 BINDING SITE, designated SEQ ID:29037, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80372] Another function of VGAM2358 is therefore inhibition of LOC143241 (Accession NM_138812). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143241. LOC144248 (Accession XM_084786) is another VGAM2358 host target gene. LOC144248 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144248, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC144248 BINDING SITE, designated SEQ ID:37701, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80373] Another function of VGAM2358 is therefore inhibition of LOC144248 (Accession XM_084786). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144248. LOC144453 (Accession XM_084869) is another VGAM2358 host target gene. LOC144453 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144453, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144453 BINDING SITE, designated SEQ ID:37746, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80374] Another function of VGAM2358 is therefore inhibition of LOC144453 (Accession XM_084869). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144453. LOC144571 (Accession XM_096630) is another VGAM2358 host target gene. LOC144571 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144571, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144571 BINDING SITE, designated SEQ ID:40441, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80375] Another function of VGAM2358 is therefore inhibition of LOC144571 (Accession XM_096630). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144571. LOC144742 (Accession XM_084949) is another VGAM2358 host target gene. LOC144742 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144742, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144742 BINDING SITE, designated SEQ ID:37781, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80376] Another function of VGAM2358 is therefore inhibition of

LOC144742 (Accession XM_084949). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144742. LOC145216 (Accession XM_096730) is another VGAM2358 host target gene. LOC145216 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145216, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145216 BINDING SITE, designated SEQ ID:40508, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80377] Another function of VGAM2358 is therefore inhibition of LOC145216 (Accession XM_096730). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145216. LOC146909 (Accession XM_085634) is another VGAM2358 host target gene. LOC146909 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146909, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC146909 BINDING SITE, designated SEQ ID:38273, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80378] Another function of VGAM2358 is therefore inhibition of LOC146909 (Accession XM_085634). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146909. LOC148709 (Accession XM_086281) is another VGAM2358 host target gene. LOC148709 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148709, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148709 BINDING SITE, designated SEQ ID:38585, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80379] Another function of VGAM2358 is therefore inhibition of LOC148709 (Accession XM_086281). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148709. LOC150054 (Accession XM_097797) is an-

other VGAM2358 host target gene. LOC150054 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150054 BINDING SITE, designated SEQ ID:41127, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80380] Another function of VGAM2358 is therefore inhibition of LOC150054 (Accession XM_097797). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150054. LOC150319 (Accession XM_086816) is another VGAM2358 host target gene. LOC150319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150319, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150319 BINDING SITE, designated SEQ ID:38897, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80381] Another function of VGAM2358 is therefore inhibition of LOC150319 (Accession XM_086816). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150319. LOC151475 (Accession XM_098063) is another VGAM2358 host target gene. LOC151475 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151475, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151475 BINDING SITE, designated SEQ ID:41361, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80382] Another function of VGAM2358 is therefore inhibition of LOC151475 (Accession XM_098063). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151475. LOC152445 (Accession XM_098231) is another VGAM2358 host target gene. LOC152445 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152445, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152445 BINDING SITE, designated SEQ ID:41514, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80383] Another function of VGAM2358 is therefore inhibition of LOC152445 (Accession XM_098231). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152445. LOC153196 (Accession XM_098323) is another VGAM2358 host target gene. LOC153196 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153196 BINDING SITE, designated SEQ ID:41590, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80384] Another function of VGAM2358 is therefore inhibition of LOC153196 (Accession XM_098323). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC153196. LOC158310 (Accession XM_098919) is another VGAM2358 host target gene. LOC158310 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158310, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158310 BINDING SITE, designated SEQ ID:41951, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80385] Another function of VGAM2358 is therefore inhibition of LOC158310 (Accession XM_098919). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158310. LOC158382 (Accession XM_098931) is another VGAM2358 host target gene. LOC158382 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158382, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158382 BINDING SITE, designated SEQ ID:41968, to the nucleotide sequence of VGAM2358 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5069.

[80386] Another function of VGAM2358 is therefore inhibition of LOC158382 (Accession XM_098931). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158382. LOC169611 (Accession XM_095809) is another VGAM2358 host target gene. LOC169611 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC169611, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169611 BINDING SITE, designated SEQ ID:40289, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80387] Another function of VGAM2358 is therefore inhibition of LOC169611 (Accession XM_095809). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169611. LOC170082 (Accession XM_093092) is another VGAM2358 host target gene. LOC170082 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC170082, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC170082 BINDING SITE, designated SEQ ID:40172, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80388] Another function of VGAM2358 is therefore inhibition of LOC170082 (Accession XM_093092). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170082. LOC200059 (Accession XM_114104) is another VGAM2358 host target gene. LOC200059 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200059, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200059 BINDING SITE, designated SEQ ID:42701, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80389] Another function of VGAM2358 is therefore inhibition of LOC200059 (Accession XM_114104). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC200059. LOC200301 (Accession XM_114197) is another VGAM2358 host target gene. LOC200301 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200301 BINDING SITE, designated SEQ ID:42785, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80390] Another function of VGAM2358 is therefore inhibition of LOC200301 (Accession XM_114197). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200301. LOC220705 (Accession XM_166000) is another VGAM2358 host target gene. LOC220705 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220705, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220705 BINDING SITE, designated SEQ ID:43836, to

the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80391] Another function of VGAM2358 is therefore inhibition of LOC220705 (Accession XM_166000). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220705. LOC221354 (Accession XM_166468) is another VGAM2358 host target gene. LOC221354 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221354, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221354 BINDING SITE, designated SEQ ID:44394, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80392] Another function of VGAM2358 is therefore inhibition of LOC221354 (Accession XM_166468). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221354. LOC255454 (Accession XM_175124) is another VGAM2358 host target gene. LOC255454 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC255454, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255454 BINDING SITE, designated SEQ ID:46613, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80393] Another function of VGAM2358 is therefore inhibition of LOC255454 (Accession XM_175124). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255454. LOC255919 (Accession XM_170794) is another VGAM2358 host target gene. LOC255919 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255919, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255919 BINDING SITE, designated SEQ ID:45558, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80394] Another function of VGAM2358 is therefore inhibition of LOC255919 (Accession XM_170794). Accordingly, utilities

of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255919. LOC51008 (Accession NM_015947) is another VGAM2358 host target gene. LOC51008 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51008, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51008 BINDING SITE, designated SEQ ID:18066, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80395] Another function of VGAM2358 is therefore inhibition of LOC51008 (Accession NM_015947). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51008. LOC90141 (Accession XM_029373) is another VGAM2358 host target gene. LOC90141 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90141, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC90141 BINDING SITE, designated SEQ ID:30883, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80396] Another function of VGAM2358 is therefore inhibition of LOC90141 (Accession XM_029373). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90141. LOC90333 (Accession XM_030958) is another VGAM2358 host target gene. LOC90333 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90333 BINDING SITE, designated SEQ ID:31229, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80397] Another function of VGAM2358 is therefore inhibition of LOC90333 (Accession XM_030958). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90333. LOC90371 (Accession XM_031261) is another VGAM2358 host target gene. LOC90371 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90371, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90371 BINDING SITE, designated SEQ ID:31324, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80398] Another function of VGAM2358 is therefore inhibition of LOC90371 (Accession XM_031261). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90371. LOC91923 (Accession XM_041526) is another VGAM2358 host target gene. LOC91923 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91923, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91923 BINDING SITE, designated SEQ ID:33545, to the nucleotide sequence of VGAM2358 RNA, herein designated VGAM RNA, also designated SEQ ID:5069.

[80399] Another function of VGAM2358 is therefore inhibition of

LOC91923 (Accession XM_041526). Accordingly, utilities of VGAM2358 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91923. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2359 (VGAM2359) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80400] VGAM2359 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2359 was detected is described hereinabove with reference to Figs. 1-8.

[80401] VGAM2359 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2359 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80402] VGAM2359 gene encodes a VGAM2359 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2359 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2359 precursor RNA is designated SEQ ID:2345, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2345 is located at position 34353 relative to the genome of Equine Herpesvirus 2.

[80403] VGAM2359 precursor RNA folds onto itself, forming VGAM2359 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80404] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2359 folded precursor RNA into VGAM2359 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 57%) nucleotide se-

quence of VGAM2359 RNA is designated SEQ ID:5070, and is provided hereinbelow with reference to the sequence listing part.

[80405] VGAM2359 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2359 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2359 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80406] VGAM2359 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2359 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2359 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2359 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2359 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80407] The complementary binding of VGAM2359 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2359 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2359 host target RNA into VGAM2359 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80408] It is appreciated that VGAM2359 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2359 host target genes. The mRNA of each one of this plurality of VGAM2359 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2359 RNA, herein designated VGAM RNA, and which when bound by VGAM2359 RNA causes inhibition of translation of respective one or more VGAM2359 host target proteins.

[80409] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2359 gene, herein designated VGAM GENE, on one or more VGAM2359 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80410] It is yet further appreciated that a function of VGAM2359

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2359 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2359 correlate with, and may be deduced from, the identity of the host target genes which VGAM2359 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80411] Nucleotide sequences of the VGAM2359 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2359 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2359 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2359 are further described hereinbelow with reference to Table 1.

[80412] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2359 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2359 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80413] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2359 gene, herein designated VGAM is inhibition of expression of VGAM2359 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2359 correlate with, and may be deduced from, the identity of the target genes which VGAM2359 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80414] BTG Family, Member 2 (BTG2, Accession NM_006763) is a VGAM2359 host target gene. BTG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTG2 BINDING SITE, designated SEQ ID:13622, to the nucleotide sequence of VGAM2359 RNA, herein designated VGAM RNA, also designated SEQ ID:5070.

[80415] A function of VGAM2359 is therefore inhibition of BTG Family, Member 2 (BTG2, Accession NM_006763). Accordingly, utilities of VGAM2359 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTG2. Glutamate Receptor, Ionotropic, Kainate 3

(GRIK3, Accession NM_000831) is another VGAM2359 host target gene. GRIK3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRIK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRIK3 BINDING SITE, designated SEQ ID:6486, to the nucleotide sequence of VGAM2359 RNA, herein designated VGAM RNA, also designated SEQ ID:5070.

[80416] Another function of VGAM2359 is therefore inhibition of Glutamate Receptor, Ionotropic, Kainate 3 (GRIK3, Accession NM_000831). Accordingly, utilities of VGAM2359 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRIK3. MLL Septin-like Fusion (MSF, Accession XM_113892) is another VGAM2359 host target gene. MSF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MSF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MSF BINDING SITE, designated SEQ ID:42522, to the nucleotide sequence of

VGAM2359 RNA, herein designated VGAM RNA, also designated SEQ ID:5070.

[80417] Another function of VGAM2359 is therefore inhibition of MLL Septin-like Fusion (MSF, Accession XM_113892), a gene which plays a role in the cell cycle. Accordingly, utilities of VGAM2359 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSF. The function of MSF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM514.Zinc Finger Protein 36 (KOX 18) (ZNF36, Accession XM_168302) is another VGAM2359 host target gene. ZNF36 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF36, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF36 BINDING SITE, designated SEQ ID:45105, to the nucleotide sequence of VGAM2359 RNA, herein designated VGAM RNA, also designated SEQ ID:5070.

[80418] Another function of VGAM2359 is therefore inhibition of Zinc Finger Protein 36 (KOX 18) (ZNF36, Accession

XM_168302), a gene which may be involved in transcriptional regulation. Accordingly, utilities of VGAM2359 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF36. The function of ZNF36 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM804.KIAA0469 (Accession NM_014851) is another VGAM2359 host target gene. KIAA0469 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0469, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0469 BINDING SITE, designated SEQ ID:16888, to the nucleotide sequence of VGAM2359 RNA, herein designated VGAM RNA, also designated SEQ ID:5070.

[80419] Another function of VGAM2359 is therefore inhibition of KIAA0469 (Accession NM_014851). Accordingly, utilities of VGAM2359 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0469. SWI/SNF Related, Matrix Associated, Actin Dependent Regulator of Chromatin, Subfamily F, Member 1

(SMARCF1, Accession NM_018450) is another VGAM2359 host target gene. SMARCF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMARCF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMARCF1 BINDING SITE, designated SEQ ID:20518, to the nucleotide sequence of VGAM2359 RNA, herein designated VGAM RNA, also designated SEQ ID:5070.

[80420] Another function of VGAM2359 is therefore inhibition of SWI/SNF Related, Matrix Associated, Actin Dependent Regulator of Chromatin, Subfamily F, Member 1 (SMARCF1, Accession NM_018450). Accordingly, utilities of VGAM2359 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMARCF1. LOC115708 (Accession XM_056552) is another VGAM2359 host target gene. LOC115708 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115708, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC115708 BINDING SITE, designated SEQ ID:36403, to the nucleotide sequence of VGAM2359 RNA, herein designated VGAM RNA, also designated SEQ ID:5070.

[80421] Another function of VGAM2359 is therefore inhibition of LOC115708 (Accession XM_056552). Accordingly, utilities of VGAM2359 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115708. LOC51754 (Accession XM_048528) is another VGAM2359 host target gene. LOC51754 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51754, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51754 BINDING SITE, designated SEQ ID:35179, to the nucleotide sequence of VGAM2359 RNA, herein designated VGAM RNA, also designated SEQ ID:5070.

[80422] Another function of VGAM2359 is therefore inhibition of LOC51754 (Accession XM_048528). Accordingly, utilities of VGAM2359 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51754. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2360 (VGAM2360) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80423] VGAM2360 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2360 was detected is described hereinabove with reference to Figs. 1-8.

[80424] VGAM2360 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2360 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80425] VGAM2360 gene encodes a VGAM2360 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2360 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2360 precursor RNA is designated SEQ ID:2346, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2346 is located at position 40669 relative to the

genome of Equine Herpesvirus 2.

[80426] VGAM2360 precursor RNA folds onto itself, forming VGAM2360 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80427] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2360 folded precursor RNA into VGAM2360 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2360 RNA is designated SEQ ID:5071, and is provided hereinbelow with reference to the sequence listing part.

[80428] VGAM2360 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2360 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2360 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80429] VGAM2360 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2360 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2360 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2360 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2360 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80430] The complementary binding of VGAM2360 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2360 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2360 host target RNA into VGAM2360 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80431] It is appreciated that VGAM2360 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2360 host target genes. The mRNA of each one of this plurality of VGAM2360 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2360 RNA, herein designated VGAM RNA, and which when bound by VGAM2360 RNA causes inhibition of translation of respective one or more VGAM2360 host target proteins.

[80432] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2360 gene, herein designated VGAM GENE, on one or more VGAM2360 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80433] It is yet further appreciated that a function of VGAM2360 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2360 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2360

correlate with, and may be deduced from, the identity of the host target genes which VGAM2360 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80434] Nucleotide sequences of the VGAM2360 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2360 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2360 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2360 are further described hereinbelow with reference to Table 1.

[80435] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2360 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2360 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80436] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2360 gene, herein designated VGAM is inhibition of expression of VGAM2360 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2360 correlate with, and may be deduced

from, the identity of the target genes which VGAM2360 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80437] General Transcription Factor II, I (GTF2I, Accession NM_032999) is a VGAM2360 host target gene. GTF2I BINDING SITE1 and GTF2I BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GTF2I, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTF2I BINDING SITE1 and GTF2I BINDING SITE2, designated SEQ ID:26885 and SEQ ID:26889 respectively, to the nucleotide sequence of VGAM2360 RNA, herein designated VGAM RNA, also designated SEQ ID:5071.

[80438] A function of VGAM2360 is therefore inhibition of General Transcription Factor II, I (GTF2I, Accession NM_032999), a gene which interacts with the basal transcription machinery by coordinating the formation of a multiprotein complex at the c-fos promoter, and linking specific signal responsive activator complexes. Accordingly, utilities of VGAM2360 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2I.

The function of GTF2I and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM115.FLJ13441 (Accession NM_023924) is another VGAM2360 host target gene. FLJ13441 BINDING SITE1 and FLJ13441 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ13441, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13441 BINDING SITE1 and FLJ13441 BINDING SITE2, designated SEQ ID:23397 and SEQ ID:23398 respectively, to the nucleotide sequence of VGAM2360 RNA, herein designated VGAM RNA, also designated SEQ ID:5071.

[80439] Another function of VGAM2360 is therefore inhibition of FLJ13441 (Accession NM_023924). Accordingly, utilities of VGAM2360 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13441. KIAA1904 (Accession XM_056282) is another VGAM2360 host target gene. KIAA1904 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1904, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1904 BINDING SITE, designated SEQ ID:36376, to the nucleotide sequence of VGAM2360 RNA, herein designated VGAM RNA, also designated SEQ ID:5071.

[80440] Another function of VGAM2360 is therefore inhibition of KIAA1904 (Accession XM_056282). Accordingly, utilities of VGAM2360 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1904. POPX1 (Accession NM_014906) is another VGAM2360 host target gene. POPX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POPX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POPX1 BINDING SITE, designated SEQ ID:17120, to the nucleotide sequence of VGAM2360 RNA, herein designated VGAM RNA, also designated SEQ ID:5071.

[80441] Another function of VGAM2360 is therefore inhibition of POPX1 (Accession NM_014906). Accordingly, utilities of VGAM2360 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with POPX1. Solute Carrier Family 1 (glutamate transporter), Member 7 (SLC1A7, Accession NM_006671) is another VGAM2360 host target gene. SLC1A7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC1A7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC1A7 BINDING SITE, designated SEQ ID:13489, to the nucleotide sequence of VGAM2360 RNA, herein designated VGAM RNA, also designated SEQ ID:5071.

[80442] Another function of VGAM2360 is therefore inhibition of Solute Carrier Family 1 (glutamate transporter), Member 7 (SLC1A7, Accession NM_006671). Accordingly, utilities of VGAM2360 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC1A7. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2361 (VGAM2361) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[80443] VGAM2361 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2361 was detected is described hereinabove with reference to Figs. 1-8.

[80444] VGAM2361 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2361 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80445] VGAM2361 gene encodes a VGAM2361 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2361 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2361 precursor RNA is designated SEQ ID:2347, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2347 is located at position 23557 relative to the genome of Equine Herpesvirus 2.

[80446] VGAM2361 precursor RNA folds onto itself, forming VGAM2361 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80447] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2361 folded precursor RNA into VGAM2361 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2361 RNA is designated SEQ ID:5072, and is provided hereinbelow with reference to the sequence listing part.

[80448] VGAM2361 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2361 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2361 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80449] VGAM2361 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2361 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2361 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2361 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2361 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[80450] The complementary binding of VGAM2361 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2361 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2361 host target RNA into VGAM2361 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80451] It is appreciated that VGAM2361 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2361 host target genes. The mRNA of each one of this plurality of VGAM2361 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2361 RNA, herein designated VGAM RNA, and which when bound by VGAM2361 RNA causes inhibition of translation of respective one or more VGAM2361 host target proteins.

[80452] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2361 gene, herein designated VGAM GENE, on one

or more VGAM2361 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80453] It is yet further appreciated that a function of VGAM2361 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2361 correlate with, and may be deduced from, the identity of the host target genes which VGAM2361 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80454] Nucleotide sequences of the VGAM2361 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2361 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2361 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2361 are further described hereinbelow with reference to Table 1.

[80455] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2361 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2361 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80456] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2361 gene, herein designated VGAM is inhibition of expression of VGAM2361 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2361 correlate with, and may be deduced from, the identity of the target genes which VGAM2361 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80457] Amyloid Beta (A4) Precursor Protein-binding, Family A,

Member 2 (X11-like) (APBA2, Accession NM_005503) is a VGAM2361 host target gene. APBA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APBA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APBA2 BINDING SITE, designated SEQ ID:12017, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80458] A function of VGAM2361 is therefore inhibition of Amyloid Beta (A4) Precursor Protein-binding, Family A, Member 2 (X11-like) (APBA2, Accession NM_005503), a gene which interacts with and stabilisesthe Alzheimer's disease amyloid precursor protein (APP) and inhibits production of proteolytic APP fragments. Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APBA2. The function of APBA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM925.EphA8 (EPHA8, Accession NM_020526) is another VGAM2361 host target gene. EPHA8 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPHA8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPHA8 BINDING SITE, designated SEQ ID:21747, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80459] Another function of VGAM2361 is therefore inhibition of EphA8 (EPHA8, Accession NM_020526), a gene which Eph-related receptor tyrosine kinase A8. Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPHA8. The function of EPHA8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM494.Ellis Van Creveld Syndrome (EVC, Accession NM_014556) is another VGAM2361 host target gene. EVC BINDING SITE1 through EVC BINDING SITE8 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by EVC, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of EVC BINDING SITE1 through EVC BINDING SITE8, designated SEQ ID:15890, SEQ ID:15891, SEQ ID:15892, SEQ ID:15893, SEQ ID:15888, SEQ ID:15889, SEQ ID:15887 and SEQ ID:15886 respectively, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80460] Another function of VGAM2361 is therefore inhibition of Ellis Van Creveld Syndrome (EVC, Accession NM_014556). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC. Potassium Inwardly-rectifying Channel, Subfamily J, Member 10 (KCNJ10, Accession NM_002241) is another VGAM2361 host target gene. KCNJ10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCNJ10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNJ10 BINDING SITE, designated SEQ ID:8025, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80461] Another function of VGAM2361 is therefore inhibition of Potassium Inwardly-rectifying Channel, Subfamily J, Member 10 (KCNJ10, Accession NM_002241), a gene which may be responsible for potassium buffering action of glial cells in the brain. Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ10. The function of KCNJ10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM167.Potassium Voltage-gated Channel, KQT-like Subfamily, Member 1 (KCNQ1, Accession NM_000218) is another VGAM2361 host target gene. KCNQ1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNQ1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNQ1 BINDING SITE, designated SEQ ID:5724, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80462] Another function of VGAM2361 is therefore inhibition of Potassium Voltage-gated Channel, KQT-like Subfamily,

Member 1 (KCNQ1, Accession NM_000218), a gene which probably important in cardiac repolarization. associates with kcne1 (mink) to form the i(ks) cardiac potassium current. elicits a rapidly activating, k(+)-selective outward current. muscarinic agonist oxotremorine-m strongly suppresses kcnq1/kcne1 current in cho cells in which cloned kcnq1/kcne1 channels were coexpressed with m1 muscarinic receptors. may associate also with kcne3 (mirp2) to form the potassium channel that is important for cyclic amp-stimulated intestinal secretion of chloride io TISSUE:abondantly expressed in heart, pancreas, prostate, kidney, small intestine and peripheral blood leukocytes. less abondant in placenta, lung, spleen, colon, thymus, testis and ovaries. Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNQ1. The function of KCNQ1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM339.Loss of Heterozygosity, 11, Chromosomal Region 2, Gene A (LOH11CR2A, Accession NM_014622) is another VGAM2361 host target gene. LOH11CR2A BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOH11CR2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOH11CR2A BINDING SITE, designated SEQ ID:15988, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80463] Another function of VGAM2361 is therefore inhibition of Loss of Heterozygosity, 11, Chromosomal Region 2, Gene A (LOH11CR2A, Accession NM_014622). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOH11CR2A. Mitogen-activated Protein Kinase Kinase Kinase 14 (MAP3K14, Accession NM_003954) is another VGAM2361 host target gene. MAP3K14 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K14 BINDING SITE, designated SEQ ID:10091, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80464] Another function of VGAM2361 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 14 (MAP3K14, Accession NM_003954), a gene which is involved in the activation of nf-kappa-b and its transcriptional activity. induces the processing of nf-kappa-b 2/p100. could act in a receptor-selective manner (by similarity). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K14. The function of MAP3K14 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Neurotensin Receptor 1 (high affinity) (NTSR1, Accession NM_002531) is another VGAM2361 host target gene. NTSR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NTSR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NTSR1 BINDING SITE, designated SEQ ID:8369, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80465] Another function of VGAM2361 is therefore inhibition of Neurotensin Receptor 1 (high affinity) (NTSR1, Accession NM_002531), a gene which is associated with g proteins that activate a phosphatidylinositol- calcium second messenger system. Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTSR1. The function of NTSR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.SRY (sex determining region Y)-box 10 (SOX10, Accession NM_006941) is another VGAM2361 host target gene. SOX10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX10 BINDING SITE, designated SEQ ID:13823, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80466] Another function of VGAM2361 is therefore inhibition of SRY (sex determining region Y)-box 10 (SOX10, Accession

NM_006941). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX10. Sphingosine Kinase 2 (SPHK2, Accession NM_020126) is another VGAM2361 host target gene. SPHK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPHK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPHK2 BINDING SITE, designated SEQ ID:21313, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80467] Another function of VGAM2361 is therefore inhibition of Sphingosine Kinase 2 (SPHK2, Accession NM_020126). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPHK2. Collectin Sub-family Member 10 (C-type lectin) (COLEC10, Accession NM_006438) is another VGAM2361 host target gene. COLEC10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COLEC10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COLEC10 BINDING SITE, designated SEQ ID:13146, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80468] Another function of VGAM2361 is therefore inhibition of Collectin Sub-family Member 10 (C-type lectin) (COLEC10, Accession NM_006438). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COLEC10. DKFZP434L0117 (Accession NM_022778) is another VGAM2361 host target gene. DKFZP434L0117 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434L0117, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434L0117 BINDING SITE, designated SEQ ID:23051, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80469] Another function of VGAM2361 is therefore inhibition of DKFZP434L0117 (Accession NM_022778). Accordingly,

utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434L0117. FLJ20123 (Accession NM_017674) is another VGAM2361 host target gene. FLJ20123 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20123, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20123 BINDING SITE, designated SEQ ID:19218, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80470] Another function of VGAM2361 is therefore inhibition of FLJ20123 (Accession NM_017674). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20123. FLJ20160 (Accession NM_017694) is another VGAM2361 host target gene. FLJ20160 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20160

BINDING SITE, designated SEQ ID:19258, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80471] Another function of VGAM2361 is therefore inhibition of FLJ20160 (Accession NM_017694). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20160. KIAA0855 (Accession NM_015003) is another VGAM2361 host target gene. KIAA0855 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0855, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0855 BINDING SITE, designated SEQ ID:17372, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80472] Another function of VGAM2361 is therefore inhibition of KIAA0855 (Accession NM_015003). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0855. KIAA1086 (Accession XM_047610) is another VGAM2361 host target gene. KIAA1086 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1086, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1086 BINDING SITE, designated SEQ ID:35012, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80473] Another function of VGAM2361 is therefore inhibition of KIAA1086 (Accession XM_047610). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1086. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840) is another VGAM2361 host target gene. PPP1R16B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R16B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R16B BINDING SITE, designated SEQ ID:30775, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80474] Another function of VGAM2361 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R16B. Retinoic Acid Induced 1 (RAI1, Accession XM_016259) is another VGAM2361 host target gene. RAI1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAI1 BINDING SITE, designated SEQ ID:30253, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80475] Another function of VGAM2361 is therefore inhibition of Retinoic Acid Induced 1 (RAI1, Accession XM_016259). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI1. LOC112476 (Accession NM_145239) is another VGAM2361 host target gene. LOC112476 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

LOC112476, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112476 BINDING SITE, designated SEQ ID:29751, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80476] Another function of VGAM2361 is therefore inhibition of LOC112476 (Accession NM_145239). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112476. LOC149464 (Accession XM_097645) is another VGAM2361 host target gene. LOC149464 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149464, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149464 BINDING SITE, designated SEQ ID:40993, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80477] Another function of VGAM2361 is therefore inhibition of LOC149464 (Accession XM_097645). Accordingly, utilities

of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149464. LOC151959 (Accession XM_098144) is another VGAM2361 host target gene. LOC151959 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151959, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151959 BINDING SITE, designated SEQ ID:41408, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80478] Another function of VGAM2361 is therefore inhibition of LOC151959 (Accession XM_098144). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151959. LOC158969 (Accession XM_088728) is another VGAM2361 host target gene. LOC158969 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158969, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC158969 BINDING SITE, designated SEQ ID:39921, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80479] Another function of VGAM2361 is therefore inhibition of LOC158969 (Accession XM_088728). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158969. LOC166206 (Accession XM_093743) is another VGAM2361 host target gene. LOC166206 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC166206, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC166206 BINDING SITE, designated SEQ ID:40208, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80480] Another function of VGAM2361 is therefore inhibition of LOC166206 (Accession XM_093743). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC166206. LOC197196 (Accession XM_117003) is another VGAM2361 host target gene. LOC197196 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197196 BINDING SITE, designated SEQ ID:43202, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80481] Another function of VGAM2361 is therefore inhibition of LOC197196 (Accession XM_117003). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197196. LOC200081 (Accession XM_114110) is another VGAM2361 host target gene. LOC200081 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200081, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200081 BINDING SITE, designated SEQ ID:42704, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80482] Another function of VGAM2361 is therefore inhibition of

LOC200081 (Accession XM_114110). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200081. LOC220045 (Accession XM_167820) is another VGAM2361 host target gene. LOC220045 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220045, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220045 BINDING SITE, designated SEQ ID:44860, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80483] Another function of VGAM2361 is therefore inhibition of LOC220045 (Accession XM_167820). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220045. LOC221042 (Accession XM_167669) is another VGAM2361 host target gene. LOC221042 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221042, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC221042 BINDING SITE, designated SEQ ID:44757, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80484] Another function of VGAM2361 is therefore inhibition of LOC221042 (Accession XM_167669). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221042. LOC253842 (Accession XM_173230) is another VGAM2361 host target gene. LOC253842 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253842, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253842 BINDING SITE, designated SEQ ID:46502, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80485] Another function of VGAM2361 is therefore inhibition of LOC253842 (Accession XM_173230). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253842. LOC257479 (Accession XM_171548) is an-

other VGAM2361 host target gene. LOC257479 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257479, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257479 BINDING SITE, designated SEQ ID:46051, to the nucleotide sequence of VGAM2361 RNA, herein designated VGAM RNA, also designated SEQ ID:5072.

[80486] Another function of VGAM2361 is therefore inhibition of LOC257479 (Accession XM_171548). Accordingly, utilities of VGAM2361 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257479. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2362 (VGAM2362) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80487] VGAM2362 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2362 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[80488] VGAM2362 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2362 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80489] VGAM2362 gene encodes a VGAM2362 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2362 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2362 precursor RNA is designated SEQ ID:2348, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2348 is located at position 25075 relative to the genome of Equine Herpesvirus 2.

[80490] VGAM2362 precursor RNA folds onto itself, forming VGAM2362 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80491] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2362 folded precursor RNA into VGAM2362 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2362 RNA is designated SEQ ID:5073, and is provided hereinbelow with reference to the sequence listing part.

[80492] VGAM2362 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2362 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2362 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80493] VGAM2362 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2362 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2362 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2362 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2362 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80494] The complementary binding of VGAM2362 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2362 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2362 host target RNA into VGAM2362 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80495] It is appreciated that VGAM2362 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2362 host target genes. The mRNA of each one of this plurality of VGAM2362 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2362 RNA, herein designated VGAM RNA, and which when bound by VGAM2362 RNA causes inhibition of translation of respective one or more VGAM2362 host target proteins.

[80496] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2362 gene, herein designated VGAM GENE, on one or more VGAM2362 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80497] It is yet further appreciated that a function of VGAM2362 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2362 correlate with, and may be deduced from, the identity of the host target genes which VGAM2362 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80498] Nucleotide sequences of the VGAM2362 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2362 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2362 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2362 are further described hereinbelow with reference to Table 1.

[80499] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2362 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2362 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80500] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2362 gene, herein designated VGAM is inhibition of expression of VGAM2362 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2362 correlate with, and may be deduced from, the identity of the target genes which VGAM2362 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80501] Dolichyl-diphosphooligosaccharide-protein Glycosyltransferase (DDOST, Accession NM_005216) is a VGAM2362 host target gene. DDOST BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DDOST, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDOST BINDING SITE, designated SEQ ID:11712, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80502] A function of VGAM2362 is therefore inhibition of Dolichyl-diphosphooligosaccharide-protein Glycosyltransferase (DDOST, Accession NM_005216), a gene which transfers high-mannose oligosaccharides to nascent polypeptides. Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDOST. The function of DDOST has been established by previous studies. The enzyme oligosaccharyltransferase (dolichyl-diphosphooligosaccharide-protein glycosyltransferase (DDOST); EC 2.4.1.119) catalyzes the transfer of a high-mannose oligosaccharide from a dolichyl-linked oligosaccharide donor onto the asparagine acceptor site in nascent polypeptide chains across the membrane of the rough endoplasmic reticulum. Kelleher et al. (1992) reported that mammalian oligosaccharyltransferase activity is associated with a protein complex composed of ri-

bophorin I (OMIM Ref. No. 180470), ribophorin II (OMIM Ref. No. 180490), and a 48-kD protein, OST48.

[80503] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[80504] Kelleher, D. J.; Kreibich, G.; Gilmore, R. : Oligosaccharyl-transferase activity is associated with a protein complex composed of ribophorins I and II and a 48 kd protein. Cell 69: 55-65, 1992. ; and

[80505] Yamagata, T.; Tsuru, T.; Momoi, M. Y.; Suwa, K.; Nozaki, Y.; Mukasa, T.; Ohashi, H.; Fukushima, Y.; Momoi, T. : Genome organization of human 48-kDa oligosaccharyl-transferase (DDOST). Ge.

[80506] Further studies establishing the function and utilities of DDOST are found in John Hopkins OMIM database record ID 602202, and in sited publications numbered 2682 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Frizzled Homolog 1 (Drosophila) (FZD1, Accession NM_003505) is another VGAM2362 host target gene. FZD1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FZD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FZD1 BINDING SITE, designated SEQ ID:9595, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80507] Another function of VGAM2362 is therefore inhibition of Frizzled Homolog 1 (Drosophila) (FZD1, Accession NM_003505), a gene which may be involved in bone resorption; strongly similar to rat Fzd. Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FZD1. The function of FZD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM432.Histone Deacetylase 4 (HDAC4, Accession NM_006037) is another VGAM2362 host target gene. HDAC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HDAC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HDAC4 BINDING SITE, designated SEQ ID:12664, to the nucleotide sequence of VGAM2362 RNA,

herein designated VGAM RNA, also designated SEQ ID:5073.

[80508] Another function of VGAM2362 is therefore inhibition of Histone Deacetylase 4 (HDAC4, Accession NM_006037), a gene which is responsible for the deacetylation of lysine residues on the n-terminal part of the core histones and may mediate transcriptional regulation. Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HDAC4. The function of HDAC4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM264.Neuron Navigator 2 (NAV2, Accession XM_012028) is another VGAM2362 host target gene. NAV2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NAV2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAV2 BINDING SITE, designated SEQ ID:30204, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80509] Another function of VGAM2362 is therefore inhibition of

Neuron Navigator 2 (NAV2, Accession XM_012028), a gene which plays an important role in neuronal development, including neurite outgrowth. Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAV2. The function of NAV2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM481.Peroxisome Biogenesis Factor 10 (PEX10, Accession NM_002617) is another VGAM2362 host target gene. PEX10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PEX10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEX10 BINDING SITE, designated SEQ ID:8481, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80510] Another function of VGAM2362 is therefore inhibition of Peroxisome Biogenesis Factor 10 (PEX10, Accession NM_002617). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PEX10. Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769) is another VGAM2362 host target gene. C11orf11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf11 BINDING SITE, designated SEQ ID:44788, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80511] Another function of VGAM2362 is therefore inhibition of Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf11. DKFZp434F1719 (Accession NM_032248) is another VGAM2362 host target gene. DKFZp434F1719 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434F1719, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of DKFZp434F1719 BINDING SITE, designated SEQ ID:25990, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80512] Another function of VGAM2362 is therefore inhibition of DKFZp434F1719 (Accession NM_032248). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434F1719. FLJ20013 (Accession NM_017621) is another VGAM2362 host target gene. FLJ20013 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20013, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20013 BINDING SITE, designated SEQ ID:19122, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80513] Another function of VGAM2362 is therefore inhibition of FLJ20013 (Accession NM_017621). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20013. G Protein-coupled Receptor Kinase-interactor 2 (GIT2, Accession NM_014776) is another VGAM2362 host target gene. GIT2 BINDING SITE1 through GIT2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GIT2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GIT2 BINDING SITE1 through GIT2 BINDING SITE3, designated SEQ ID:16602, SEQ ID:27684 and SEQ ID:27697 respectively, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80514] Another function of VGAM2362 is therefore inhibition of G Protein-coupled Receptor Kinase-interactor 2 (GIT2, Accession NM_014776). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GIT2. IDN3 (Accession NM_015384) is another VGAM2362 host target gene. IDN3 BINDING SITE1 and IDN3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by IDN3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementar-

ity of the nucleotide sequences of IDN3 BINDING SITE1 and IDN3 BINDING SITE2, designated SEQ ID:17684 and SEQ ID:26105 respectively, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80515] Another function of VGAM2362 is therefore inhibition of IDN3 (Accession NM_015384). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IDN3. KIAA1884 (Accession XM_055539) is another VGAM2362 host target gene. KIAA1884 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1884, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1884 BINDING SITE, designated SEQ ID:36297, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80516] Another function of VGAM2362 is therefore inhibition of KIAA1884 (Accession XM_055539). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1884. KIAA1944 (Accession XM_062545) is another VGAM2362 host target gene. KIAA1944 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1944, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1944 BINDING SITE, designated SEQ ID:37231, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80517] Another function of VGAM2362 is therefore inhibition of KIAA1944 (Accession XM_062545). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1944. LOC151162 (Accession XM_098012) is another VGAM2362 host target gene. LOC151162 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151162 BINDING SITE, designated SEQ ID:41306, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80518] Another function of VGAM2362 is therefore inhibition of LOC151162 (Accession XM_098012). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151162. LOC203377 (Accession XM_117540) is another VGAM2362 host target gene. LOC203377 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203377, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203377 BINDING SITE, designated SEQ ID:43541, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80519] Another function of VGAM2362 is therefore inhibition of LOC203377 (Accession XM_117540). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203377. LOC221576 (Accession XM_168088) is another VGAM2362 host target gene. LOC221576 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221576, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221576 BINDING SITE, designated SEQ ID:45000, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80520] Another function of VGAM2362 is therefore inhibition of LOC221576 (Accession XM_168088). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC221576. LOC253573 (Accession XM_173110) is another VGAM2362 host target gene. LOC253573 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253573, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253573 BINDING SITE, designated SEQ ID:46366, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80521] Another function of VGAM2362 is therefore inhibition of LOC253573 (Accession XM_173110). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253573. LOC257515 (Accession XM_175211) is another VGAM2362 host target gene. LOC257515 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257515, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257515 BINDING SITE, designated SEQ ID:46684, to the nucleotide sequence of VGAM2362 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5073.

[80522] Another function of VGAM2362 is therefore inhibition of LOC257515 (Accession XM_175211). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257515. LOC257572 (Accession XM_175294) is another VGAM2362 host target gene. LOC257572 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257572, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257572 BINDING SITE, designated SEQ ID:46745, to the nucleotide sequence of VGAM2362 RNA, herein designated VGAM RNA, also designated SEQ ID:5073.

[80523] Another function of VGAM2362 is therefore inhibition of LOC257572 (Accession XM_175294). Accordingly, utilities of VGAM2362 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257572. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2363 (VGAM2363) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80524] VGAM2363 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2363 was detected is described hereinabove with reference to Figs. 1-8.

[80525] VGAM2363 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2. VGAM2363 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80526] VGAM2363 gene encodes a VGAM2363 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2363 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2363 precursor RNA is designated SEQ ID:2349, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2349 is located at position 40183 relative to the genome of Equine Herpesvirus 2.

[80527] VGAM2363 precursor RNA folds onto itself, forming

VGAM2363 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80528] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2363 folded precursor RNA into VGAM2363 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2363 RNA is designated SEQ ID:5074, and is provided hereinbelow with reference to the sequence listing part.

[80529] VGAM2363 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2363 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2363 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80530] VGAM2363 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2363 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2363 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2363 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2363 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80531] The complementary binding of VGAM2363 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2363 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2363 host target RNA into VGAM2363 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80532] It is appreciated that VGAM2363 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2363 host target genes. The mRNA of each one of this plurality of VGAM2363 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2363 RNA, herein designated VGAM RNA, and which when bound by VGAM2363 RNA causes inhibition of translation of respective one or more VGAM2363 host target proteins.

[80533] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2363 gene, herein designated VGAM GENE, on one or more VGAM2363 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80534] It is yet further appreciated that a function of VGAM2363 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2363 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2363 correlate with, and may be deduced from, the identity of the host target genes which VGAM2363 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[80535] Nucleotide sequences of the VGAM2363 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2363 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2363 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2363 are further described hereinbelow with reference to Table 1.

[80536] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2363 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2363 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80537] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2363 gene, herein designated VGAM is inhibition of expression of VGAM2363 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2363 correlate with, and may be deduced from, the identity of the target genes which VGAM2363 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[80538] Megakaryocyte-associated Tyrosine Kinase (MATK, Accession NM_002378) is a VGAM2363 host target gene. MATK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MATK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MATK BINDING SITE, designated SEQ ID:8194, to the nucleotide sequence of VGAM2363 RNA, herein designated VGAM RNA, also designated SEQ ID:5074.

[80539] A function of VGAM2363 is therefore inhibition of Megakaryocyte-associated Tyrosine Kinase (MATK, Accession NM_002378), a gene which can phosphorylate members of the SRC family of PTKs at the regulatory tyrosine residue. Accordingly, utilities of VGAM2363 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MATK. The function of MATK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2173.Fatty Acid Desaturase 2 (FADS2, Accession NM_004265) is another VGAM2363 host target gene. FADS2 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FADS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FADS2 BINDING SITE, designated SEQ ID:10469, to the nucleotide sequence of VGAM2363 RNA, herein designated VGAM RNA, also designated SEQ ID:5074.

[80540] Another function of VGAM2363 is therefore inhibition of Fatty Acid Desaturase 2 (FADS2, Accession NM_004265). Accordingly, utilities of VGAM2363 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FADS2. FK506 Binding Protein 9, 63 KDa (FKBP9, Accession XM_168403) is another VGAM2363 host target gene. FKBP9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FKBP9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FKBP9 BINDING SITE, designated SEQ ID:45146, to the nucleotide sequence of VGAM2363 RNA, herein designated VGAM RNA, also designated SEQ ID:5074.

[80541] Another function of VGAM2363 is therefore inhibition of FK506 Binding Protein 9, 63 KDa (FKBP9, Accession XM_168403). Accordingly, utilities of VGAM2363 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKBP9. KIAA0318 (Accession XM_044334) is another VGAM2363 host target gene. KIAA0318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0318 BINDING SITE, designated SEQ ID:34187, to the nucleotide sequence of VGAM2363 RNA, herein designated VGAM RNA, also designated SEQ ID:5074.

[80542] Another function of VGAM2363 is therefore inhibition of KIAA0318 (Accession XM_044334). Accordingly, utilities of VGAM2363 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0318. KIAA1524 (Accession XM_056015) is another VGAM2363 host target gene. KIAA1524 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1524, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1524 BINDING SITE, designated SEQ ID:36360, to the nucleotide sequence of VGAM2363 RNA, herein designated VGAM RNA, also designated SEQ ID:5074.

[80543] Another function of VGAM2363 is therefore inhibition of KIAA1524 (Accession XM_056015). Accordingly, utilities of VGAM2363 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1524. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2364 (VGAM2364) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80544] VGAM2364 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2364 was detected is described hereinabove with reference to Figs. 1-8.

[80545] VGAM2364 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Equine Herpesvirus 2.

VGAM2364 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80546] VGAM2364 gene encodes a VGAM2364 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2364 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2364 precursor RNA is designated SEQ ID:2350, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2350 is located at position 23189 relative to the genome of Equine Herpesvirus 2.

[80547] VGAM2364 precursor RNA folds onto itself, forming VGAM2364 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80548] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2364 folded precursor RNA into VGAM2364 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM2364 RNA is designated SEQ ID:5075, and is provided hereinbelow with reference to the sequence listing part.

[80549] VGAM2364 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2364 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2364 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80550] VGAM2364 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2364 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2364 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2364 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2364 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80551] The complementary binding of VGAM2364 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2364 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2364 host target RNA into VGAM2364 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80552] It is appreciated that VGAM2364 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2364 host target genes. The mRNA of each one of this plurality of VGAM2364 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2364 RNA, herein designated VGAM RNA, and which when bound by VGAM2364 RNA causes inhibition of translation of respective one or more VGAM2364 host target proteins.

[80553] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2364 gene, herein designated VGAM GENE, on one or more VGAM2364 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80554] It is yet further appreciated that a function of VGAM2364 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of viral infection by Equine Herpesvirus 2. Specific functions, and accordingly utilities, of VGAM2364 correlate with, and may be deduced from, the identity of the host target genes which VGAM2364 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80555] Nucleotide sequences of the VGAM2364 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2364 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2364 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2364 are further described hereinbelow with reference to Table 1.

[80556] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2364 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2364 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80557] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2364 gene, herein designated VGAM is inhibition of expression of VGAM2364 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2364 correlate with, and may be deduced from, the identity of the target genes which VGAM2364 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80558] ATP-binding Cassette, Sub-family D (ALD), Member 4 (ABCD4, Accession NM_020326) is a VGAM2364 host target gene. ABCD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCD4 BINDING SITE, designated SEQ

ID:21590, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80559] A function of VGAM2364 is therefore inhibition of ATP-binding Cassette, Sub-family D (ALD), Member 4 (ABCD4, Accession NM_020326), a gene which Putative peroxisomal ATP binding cassette transporter. Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCD4. The function of ABCD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1924.Cadherin, EGF LAG Seven-pass G-type Receptor 1 (flamingo homolog, Drosophila) (CELSR1, Accession NM_014246) is another VGAM2364 host target gene. CELSR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CELSR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CELSR1 BINDING SITE, designated SEQ ID:15512, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5075.

[80560] Another function of VGAM2364 is therefore inhibition of Cadherin, EGF LAG Seven-pass G-type Receptor 1 (flamingo homolog, Drosophila) (CELSR1, Accession NM_014246), a gene which is involved in contact-mediated communication. Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CELSR1. The function of CELSR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM459.Hydroxysteroid (17-beta) Dehydrogenase 1 (HSD17B1, Accession NM_000413) is another VGAM2364 host target gene. HSD17B1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HSD17B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSD17B1 BINDING SITE, designated SEQ ID:5995, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80561] Another function of VGAM2364 is therefore inhibition of

Hydroxysteroid (17-beta) Dehydrogenase 1 (HSD17B1, Accession NM_000413). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSD17B1. Integrin, Alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4, Accession NM_000885) is another VGAM2364 host target gene. ITGA4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ITGA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA4 BINDING SITE, designated SEQ ID:6581, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80562] Another function of VGAM2364 is therefore inhibition of Integrin, Alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) (ITGA4, Accession NM_000885), a gene which recognizes one or more domains within the alternatively spliced cs-1 and cs-5 regions of fibronectin. Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA4. The function of ITGA4 and its association with

various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1096.Myelin Basic Protein (MBP, Accession XM_117096) is another VGAM2364 host target gene. MBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MBP BINDING SITE, designated SEQ ID:43220, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80563] Another function of VGAM2364 is therefore inhibition of Myelin Basic Protein (MBP, Accession XM_117096), a gene which Myelin basic protein; a constituent of myelin, plays a role in nerve function. Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBP. The function of MBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.PR Domain Containing 2, with ZNF Domain (PRDM2, Accession NM_015866) is another VGAM2364

host target gene. PRDM2 BINDING SITE1 and PRDM2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PRDM2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRDM2 BINDING SITE1 and PRDM2 BINDING SITE2, designated SEQ ID:18000 and SEQ ID:14532 respectively, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80564] Another function of VGAM2364 is therefore inhibition of PR Domain Containing 2, with ZNF Domain (PRDM2, Accession NM_015866), a gene which plays a role in transcriptional regulation during neuronal differentiation and pathogenesis of retinoblastoma. Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDM2. The function of PRDM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM120.Synaptogyrin 1 (SYNGR1, Accession NM_004711) is another VGAM2364 host target gene. SYNGR1 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by SYNGR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYNGR1 BINDING SITE, designated SEQ ID:11064, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80565] Another function of VGAM2364 is therefore inhibition of Synaptogyrin 1 (SYNGR1, Accession NM_004711), a gene which belongs to transmembrane synaptic vesicle protein and may function in membrane recycling. Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYNGR1. The function of SYNGR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM107.FLJ11053 (Accession XM_114194) is another VGAM2364 host target gene. FLJ11053 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ11053, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11053 BINDING SITE, designated SEQ ID:42777, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80566] Another function of VGAM2364 is therefore inhibition of FLJ11053 (Accession XM_114194). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11053. FLJ11539 (Accession NM_024748) is another VGAM2364 host target gene. FLJ11539 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ11539, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11539 BINDING SITE, designated SEQ ID:24087, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80567] Another function of VGAM2364 is therefore inhibition of FLJ11539 (Accession NM_024748). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ11539. FLJ12505 (Accession NM_024749) is another VGAM2364 host target gene. FLJ12505 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12505, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12505 BINDING SITE, designated SEQ ID:24093, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80568] Another function of VGAM2364 is therefore inhibition of FLJ12505 (Accession NM_024749). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12505. FLJ14129 (Accession NM_030895) is another VGAM2364 host target gene. FLJ14129 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14129, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14129 BINDING SITE, designated SEQ ID:25163, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM

RNA, also designated SEQ ID:5075.

[80569] Another function of VGAM2364 is therefore inhibition of FLJ14129 (Accession NM_030895). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14129. FLJ20004 (Accession XM_170889) is another VGAM2364 host target gene. FLJ20004 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20004, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20004 BINDING SITE, designated SEQ ID:45644, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80570] Another function of VGAM2364 is therefore inhibition of FLJ20004 (Accession XM_170889). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20004. FLJ21709 (Accession XM_085480) is another VGAM2364 host target gene. FLJ21709 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21709, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21709 BINDING SITE, designated SEQ ID:38171, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80571] Another function of VGAM2364 is therefore inhibition of FLJ21709 (Accession XM_085480). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21709. KIAA0084 (Accession XM_042841) is another VGAM2364 host target gene. KIAA0084 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0084, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0084 BINDING SITE, designated SEQ ID:33804, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80572] Another function of VGAM2364 is therefore inhibition of KIAA0084 (Accession XM_042841). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0084. KIAA0376 (Accession XM_037759) is another VGAM2364 host target gene. KIAA0376 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0376, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0376 BINDING SITE, designated SEQ ID:32673, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80573] Another function of VGAM2364 is therefore inhibition of KIAA0376 (Accession XM_037759). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0376. Kruppel-like Factor 5 (intestinal) (KLF5, Accession NM_001730) is another VGAM2364 host target gene. KLF5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KLF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLF5 BINDING SITE, designated SEQ ID:7462,

to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80574] Another function of VGAM2364 is therefore inhibition of Kruppel-like Factor 5 (intestinal) (KLF5, Accession NM_001730). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF5. MGC15631 (Accession NM_032753) is another VGAM2364 host target gene. MGC15631 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC15631, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15631 BINDING SITE, designated SEQ ID:26493, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80575] Another function of VGAM2364 is therefore inhibition of MGC15631 (Accession NM_032753). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15631. MGC20727 (Accession NM_052853) is another VGAM2364 host target gene. MGC20727 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC20727, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC20727 BINDING SITE, designated SEQ ID:27436, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80576] Another function of VGAM2364 is therefore inhibition of MGC20727 (Accession NM_052853). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC20727. MGC2605 (Accession NM_032304) is another VGAM2364 host target gene. MGC2605 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC2605, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2605 BINDING SITE, designated SEQ ID:26086, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80577] Another function of VGAM2364 is therefore inhibition of

MGC2605 (Accession NM_032304). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2605. PP1665 (Accession NM_030792) is another VGAM2364 host target gene. PP1665 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PP1665, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP1665 BINDING SITE, designated SEQ ID:25090, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80578] Another function of VGAM2364 is therefore inhibition of PP1665 (Accession NM_030792). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1665. Phosphatidylserine Synthase 2 (PTDSS2, Accession NM_030783) is another VGAM2364 host target gene. PTDSS2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PTDSS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of PTDSS2 BINDING SITE, designated SEQ ID:25076, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80579] Another function of VGAM2364 is therefore inhibition of Phosphatidylserine Synthase 2 (PTDSS2, Accession NM_030783). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTDSS2. SAST (Accession XM_032034) is another VGAM2364 host target gene. SAST BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SAST, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SAST BINDING SITE, designated SEQ ID:31539, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80580] Another function of VGAM2364 is therefore inhibition of SAST (Accession XM_032034). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SAST.

SSH2 (Accession XM_030846) is another VGAM2364 host target gene. SSH2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SSH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SSH2 BINDING SITE, designated SEQ ID:31179, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80581] Another function of VGAM2364 is therefore inhibition of SSH2 (Accession XM_030846). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSH2. U5-116KD (Accession NM_004247) is another VGAM2364 host target gene. U5-116KD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by U5-116KD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of U5-116KD BINDING SITE, designated SEQ ID:10437, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA,

also designated SEQ ID:5075.

[80582] Another function of VGAM2364 is therefore inhibition of U5-116KD (Accession NM_004247). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with U5-116KD. LOC130074 (Accession XM_072228) is another VGAM2364 host target gene. LOC130074 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC130074, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC130074 BINDING SITE, designated SEQ ID:37471, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80583] Another function of VGAM2364 is therefore inhibition of LOC130074 (Accession XM_072228). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC130074. LOC146506 (Accession XM_085489) is another VGAM2364 host target gene. LOC146506 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146506, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146506 BINDING SITE, designated SEQ ID:38179, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80584] Another function of VGAM2364 is therefore inhibition of LOC146506 (Accession XM_085489). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146506. LOC147229 (Accession XM_085742) is another VGAM2364 host target gene. LOC147229 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147229 BINDING SITE, designated SEQ ID:38317, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80585] Another function of VGAM2364 is therefore inhibition of LOC147229 (Accession XM_085742). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC147229. LOC150244 (Accession XM_086856) is another VGAM2364 host target gene. LOC150244 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150244, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150244 BINDING SITE, designated SEQ ID:38920, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80586] Another function of VGAM2364 is therefore inhibition of LOC150244 (Accession XM_086856). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150244. LOC257426 (Accession XM_039451) is another VGAM2364 host target gene. LOC257426 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257426 BINDING SITE, designated SEQ ID:33099, to

the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80587] Another function of VGAM2364 is therefore inhibition of LOC257426 (Accession XM_039451). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257426. LOC51608 (Accession XM_033102) is another VGAM2364 host target gene. LOC51608 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51608, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51608 BINDING SITE, designated SEQ ID:31840, to the nucleotide sequence of VGAM2364 RNA, herein designated VGAM RNA, also designated SEQ ID:5075.

[80588] Another function of VGAM2364 is therefore inhibition of LOC51608 (Accession XM_033102). Accordingly, utilities of VGAM2364 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51608. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2365 (VGAM2365) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80589] VGAM2365 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2365 was detected is described hereinabove with reference to Figs. 1-8.

[80590] VGAM2365 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2365 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80591] VGAM2365 gene encodes a VGAM2365 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2365 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2365 precursor RNA is designated SEQ ID:2351, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2351 is located at position 185947 relative to the genome of Rat Cytomegalovirus.

[80592] VGAM2365 precursor RNA folds onto itself, forming VGAM2365 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80593] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2365 folded precursor RNA into VGAM2365 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2365 RNA is designated SEQ ID:5076, and is provided hereinbelow with reference to the sequence listing part.

[80594] VGAM2365 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2365 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2365 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80595] VGAM2365 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2365 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2365 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2365 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2365 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80596] The complementary binding of VGAM2365 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2365 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2365 host target RNA into VGAM2365 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80597] It is appreciated that VGAM2365 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2365 host target genes. The mRNA of each one of this plurality of VGAM2365 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2365 RNA, herein designated VGAM RNA, and which when bound by VGAM2365 RNA causes inhibition of translation of respective one or more VGAM2365 host target proteins.

[80598] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2365 gene, herein designated VGAM GENE, on one or more VGAM2365 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80599] It is yet further appreciated that a function of VGAM2365 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2365 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2365 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80600] Nucleotide sequences of the VGAM2365 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2365 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2365 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2365 are further described hereinbelow with reference to Table 1.

[80601] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2365 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2365 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80602] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2365 gene, herein designated VGAM is inhibition of expression of VGAM2365 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2365 correlate with, and may be deduced from, the identity of the target genes which VGAM2365

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80603] Polycystic Kidney and Hepatic Disease 1 (autosomal recessive) (PKHD1, Accession NM_138694) is a VGAM2365 host target gene. PKHD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PKHD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PKHD1 BINDING SITE, designated SEQ ID:28946, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80604] A function of VGAM2365 is therefore inhibition of Polycystic Kidney and Hepatic Disease 1 (autosomal recessive) (PKHD1, Accession NM_138694). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKHD1. RAD17 Homolog (S. pombe) (RAD17, Accession NM_133340) is another VGAM2365 host target gene. RAD17 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAD17, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD17 BINDING SITE, designated SEQ ID:28482, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80605] Another function of VGAM2365 is therefore inhibition of RAD17 Homolog (S. pombe) (RAD17, Accession NM_133340), a gene which may have a role in DNA damage-dependent and DNA replication-dependent cell cycle checkpoints. Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD17. The function of RAD17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM209.Solute Carrier Family 25 (mitochondrial carrier; ornithine transporter) Member 15 (SLC25A15, Accession NM_014252) is another VGAM2365 host target gene. SLC25A15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC25A15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of SLC25A15 BINDING SITE, designated SEQ ID:15524, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80606] Another function of VGAM2365 is therefore inhibition of Solute Carrier Family 25 (mitochondrial carrier; ornithine transporter) Member 15 (SLC25A15, Accession NM_014252), a gene which participates theornithine transport across inner mitochondrial membrane, from the cytoplasm to the matrix. Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC25A15. The function of SLC25A15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM172.Solute Carrier Family 38, Member 2 (SLC38A2, Accession NM_018976) is another VGAM2365 host target gene. SLC38A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC38A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of SLC38A2 BINDING SITE, designated SEQ ID:21050, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80607] Another function of VGAM2365 is therefore inhibition of Solute Carrier Family 38, Member 2 (SLC38A2, Accession NM_018976), a gene which is an amino acid transporter. Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC38A2. The function of SLC38A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.ARNTL2 (Accession NM_020183) is another VGAM2365 host target gene. ARNTL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARNTL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARNTL2 BINDING SITE, designated SEQ ID:21410, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80608] Another function of VGAM2365 is therefore inhibition of ARNTL2 (Accession NM_020183). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARNTL2. Chromosome 20 Open Reading Frame 7 (C20orf7, Accession NM_024120) is another VGAM2365 host target gene. C20orf7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf7 BINDING SITE, designated SEQ ID:23572, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80609] Another function of VGAM2365 is therefore inhibition of Chromosome 20 Open Reading Frame 7 (C20orf7, Accession NM_024120). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf7. CDA02 (Accession XM_042168) is another VGAM2365 host target gene. CDA02 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

CDA02, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDA02 BINDING SITE, designated SEQ ID:33702, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80610] Another function of VGAM2365 is therefore inhibition of CDA02 (Accession XM_042168). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDA02. Death-associated Protein Kinase 2 (DAPK2, Accession NM_014326) is another VGAM2365 host target gene. DAPK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DAPK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAPK2 BINDING SITE, designated SEQ ID:15637, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80611] Another function of VGAM2365 is therefore inhibition of

Death-associated Protein Kinase 2 (DAPK2, Accession NM_014326). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAPK2. DKFZP586I2223 (Accession NM_015438) is another VGAM2365 host target gene. DKFZP586I2223 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586I2223, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586I2223 BINDING SITE, designated SEQ ID:17733, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80612] Another function of VGAM2365 is therefore inhibition of DKFZP586I2223 (Accession NM_015438). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586I2223. FLJ10803 (Accession NM_018224) is another VGAM2365 host target gene. FLJ10803 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10803, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10803 BINDING SITE, designated SEQ ID:20157, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80613] Another function of VGAM2365 is therefore inhibition of FLJ10803 (Accession NM_018224). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10803. FLJ13031 (Accession NM_024688) is another VGAM2365 host target gene. FLJ13031 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13031, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13031 BINDING SITE, designated SEQ ID:23998, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80614] Another function of VGAM2365 is therefore inhibition of FLJ13031 (Accession NM_024688). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ13031. FLJ32762 (Accession NM_145023) is another VGAM2365 host target gene. FLJ32762 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ32762, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32762 BINDING SITE, designated SEQ ID:29636, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80615] Another function of VGAM2365 is therefore inhibition of FLJ32762 (Accession NM_145023). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32762. KIAA1946 (Accession XM_092459) is another VGAM2365 host target gene. KIAA1946 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1946, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1946 BINDING SITE, designated SEQ ID:40119, to the nucleotide sequence of VGAM2365 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5076.

[80616] Another function of VGAM2365 is therefore inhibition of KIAA1946 (Accession XM_092459). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1946. MGC16142 (Accession NM_032763) is another VGAM2365 host target gene. MGC16142 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC16142, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16142 BINDING SITE, designated SEQ ID:26508, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80617] Another function of VGAM2365 is therefore inhibition of MGC16142 (Accession NM_032763). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16142. Nuclear Receptor Coactivator 2 (NCOA2, Accession NM_006540) is another VGAM2365 host target gene. NCOA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

NCOA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOA2 BINDING SITE, designated SEQ ID:13297, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80618] Another function of VGAM2365 is therefore inhibition of Nuclear Receptor Coactivator 2 (NCOA2, Accession NM_006540). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA2. Signal Sequence Receptor, Alpha (translocon-associated protein alpha) (SSR1, Accession NM_003144) is another VGAM2365 host target gene. SSR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SSR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SSR1 BINDING SITE, designated SEQ ID:9114, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80619] Another function of VGAM2365 is therefore inhibition of

Signal Sequence Receptor, Alpha (translocon-associated protein alpha) (SSR1, Accession NM_003144). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSR1. Unc-5 Homolog D (C. elegans) (UNC5D, Accession NM_080872) is another VGAM2365 host target gene. UNC5D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UNC5D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UNC5D BINDING SITE, designated SEQ ID:28114, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80620] Another function of VGAM2365 is therefore inhibition of Unc-5 Homolog D (C. elegans) (UNC5D, Accession NM_080872). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC5D. LOC203369 (Accession XM_114689) is another VGAM2365 host target gene. LOC203369 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by LOC203369, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203369 BINDING SITE, designated SEQ ID:43033, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80621] Another function of VGAM2365 is therefore inhibition of LOC203369 (Accession XM_114689). Accordingly, utilities of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203369. LOC206480 (Accession XM_121360) is another VGAM2365 host target gene. LOC206480 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC206480, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC206480 BINDING SITE, designated SEQ ID:43614, to the nucleotide sequence of VGAM2365 RNA, herein designated VGAM RNA, also designated SEQ ID:5076.

[80622] Another function of VGAM2365 is therefore inhibition of LOC206480 (Accession XM_121360). Accordingly, utilities

of VGAM2365 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC206480. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2366 (VGAM2366) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80623] VGAM2366 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2366 was detected is described hereinabove with reference to Figs. 1-8.

[80624] VGAM2366 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2366 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80625] VGAM2366 gene encodes a VGAM2366 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2366 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2366 precursor RNA is designated SEQ ID:2352, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2352 is located at position 183326 relative to the genome of Rat Cytomegalovirus.

[80626] VGAM2366 precursor RNA folds onto itself, forming VGAM2366 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80627] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2366 folded precursor RNA into VGAM2366 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2366 RNA is designated SEQ ID:5077, and

is provided hereinbelow with reference to the sequence listing part.

[80628] VGAM2366 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2366 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2366 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80629] VGAM2366 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2366 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2366 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2366 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2366 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80630] The complementary binding of VGAM2366 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2366 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2366 host target RNA into VGAM2366 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80631] It is appreciated that VGAM2366 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2366 host target genes. The mRNA of each one of this plurality of VGAM2366 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2366 RNA, herein designated VGAM RNA, and which when bound by VGAM2366 RNA causes inhibition of translation of respective one or more VGAM2366 host target proteins.

[80632] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2366 gene, herein designated VGAM GENE, on one or more VGAM2366 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80633] It is yet further appreciated that a function of VGAM2366 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2366 correlate with, and may be deduced from, the identity of the host target genes which VGAM2366 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80634] Nucleotide sequences of the VGAM2366 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2366 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2366 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2366 are further described hereinbelow with reference to Table 1.

[80635] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2366 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2366 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80636] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2366 gene, herein designated VGAM is inhibition of expression of VGAM2366 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2366 correlate with, and may be deduced from, the identity of the target genes which VGAM2366 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80637] ATP-binding Cassette, Sub-family C (CFTR/MRP), Member 5 (ABCC5, Accession NM_005688) is a VGAM2366 host target gene. ABCC5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCC5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCC5 BINDING SITE, designated SEQ ID:12248, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80638] A function of VGAM2366 is therefore inhibition of ATP-binding Cassette, Sub-family C (CFTR/MRP), Member 5 (ABCC5, Accession NM_005688), a gene which acts as a multispecific organic anion pump which can transport nucleotide analogs. Accordingly, utilities of VGAM2366 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC5. The function of ABCC5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1744.ADP-ribosyltransferase (NAD+; poly (ADP-ribose) Polymerase) (ADPRT, Accession NM_001618) is another VGAM2366 host target gene. ADPRT BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ADPRT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADPRT BINDING SITE, designated SEQ ID:7324, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80639] Another function of VGAM2366 is therefore inhibition of ADP-ribosyltransferase (NAD+; poly (ADP-ribose) Polymerase) (ADPRT, Accession NM_001618), a gene which catalyzes addition of mono-ADP-ribose to arginine residues of proteins, inhibits Pol II transcription. Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with ADPRT. The function of ADPRT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM506.Insulin Receptor Substrate 2 (IRS2, Accession XM_007095) is another VGAM2366 host target gene. IRS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IRS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRS2 BINDING SITE, designated SEQ ID:30029, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80640] Another function of VGAM2366 is therefore inhibition of Insulin Receptor Substrate 2 (IRS2, Accession XM_007095), a gene which may mediate the control of various cellular processes by insulin. Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRS2. The function of IRS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM1217.Neuropeptide Y Receptor Y2 (NPY2R, Accession NM_000910) is another VGAM2366 host target gene. NPY2R BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NPY2R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPY2R BINDING SITE, designated SEQ ID:6612, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80641] Another function of VGAM2366 is therefore inhibition of Neuropeptide Y Receptor Y2 (NPY2R, Accession NM_000910), a gene which stimulates intracellular calcium flux and may modulate psychomotor activity, food intake, endocrine secretion and vasoconstriction. Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPY2R. The function of NPY2R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM309.Prominin-like 1 (mouse) (PROML1, Accession NM_006017) is another

VGAM2366 host target gene. PROML1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PROML1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PROML1 BINDING SITE, designated SEQ ID:12635, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80642] Another function of VGAM2366 is therefore inhibition of Prominin-like 1 (mouse) (PROML1, Accession NM_006017), a gene which is a Transmembrane protein. Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROML1. The function of PROML1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM905.Transmembrane Protein 2 (TMEM2, Accession NM_013390) is another VGAM2366 host target gene. TMEM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TMEM2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TMEM2 BINDING SITE, designated SEQ ID:15042, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80643] Another function of VGAM2366 is therefore inhibition of Transmembrane Protein 2 (TMEM2, Accession NM_013390). Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TMEM2. FLJ13491 (Accession NM_024623) is another VGAM2366 host target gene. FLJ13491 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13491, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13491 BINDING SITE, designated SEQ ID:23888, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80644] Another function of VGAM2366 is therefore inhibition of FLJ13491 (Accession NM_024623). Accordingly, utilities of

VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13491. KIAA0125 (Accession XM_018203) is another VGAM2366 host target gene. KIAA0125 BINDING SITE1 and KIAA0125 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0125, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0125 BINDING SITE1 and KIAA0125 BINDING SITE2, designated SEQ ID:30347 and SEQ ID:16692 respectively, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80645] Another function of VGAM2366 is therefore inhibition of KIAA0125 (Accession XM_018203). Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0125. KIAA0469 (Accession NM_014851) is another VGAM2366 host target gene. KIAA0469 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0469, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0469 BINDING SITE, designated SEQ ID:16890, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80646] Another function of VGAM2366 is therefore inhibition of KIAA0469 (Accession NM_014851). Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0469. KIAA1005 (Accession XM_051197) is another VGAM2366 host target gene. KIAA1005 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1005, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1005 BINDING SITE, designated SEQ ID:35778, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80647] Another function of VGAM2366 is therefore inhibition of KIAA1005 (Accession XM_051197). Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1005. PP1628 (Accession NM_025201) is another VGAM2366 host target gene. PP1628 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PP1628, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP1628 BINDING SITE, designated SEQ ID:24858, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80648] Another function of VGAM2366 is therefore inhibition of PP1628 (Accession NM_025201). Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1628. Thioesterase, Adipose Associated (THEA, Accession XM_038922) is another VGAM2366 host target gene. THEA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by THEA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of THEA BINDING SITE, designated SEQ ID:32952, to the nucleotide sequence of VGAM2366 RNA, herein

designated VGAM RNA, also designated SEQ ID:5077.

[80649] Another function of VGAM2366 is therefore inhibition of Thioesterase, Adipose Associated (THEA, Accession XM_038922). Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with THEA. LOC128338 (Accession XM_059238) is another VGAM2366 host target gene. LOC128338 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC128338, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC128338 BINDING SITE, designated SEQ ID:36927, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80650] Another function of VGAM2366 is therefore inhibition of LOC128338 (Accession XM_059238). Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128338. LOC146713 (Accession XM_097071) is another VGAM2366 host target gene. LOC146713 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC146713, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146713 BINDING SITE, designated SEQ ID:40714, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80651] Another function of VGAM2366 is therefore inhibition of LOC146713 (Accession XM_097071). Accordingly, utilities of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146713. LOC220070 (Accession NM_145308) is another VGAM2366 host target gene. LOC220070 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220070, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220070 BINDING SITE, designated SEQ ID:29820, to the nucleotide sequence of VGAM2366 RNA, herein designated VGAM RNA, also designated SEQ ID:5077.

[80652] Another function of VGAM2366 is therefore inhibition of LOC220070 (Accession NM_145308). Accordingly, utilities

of VGAM2366 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220070. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2367 (VGAM2367) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80653] VGAM2367 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2367 was detected is described hereinabove with reference to Figs. 1-8.

[80654] VGAM2367 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2367 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80655] VGAM2367 gene encodes a VGAM2367 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2367 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2367 precursor RNA is designated SEQ ID:2353, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2353 is located at position 207957 relative to the genome of Rat Cytomegalovirus.

[80656] VGAM2367 precursor RNA folds onto itself, forming VGAM2367 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80657] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2367 folded precursor RNA into VGAM2367 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2367 RNA is designated SEQ ID:5078, and

is provided hereinbelow with reference to the sequence listing part.

[80658] VGAM2367 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2367 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2367 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80659] VGAM2367 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2367 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2367 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2367 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2367 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80660] The complementary binding of VGAM2367 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2367 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2367 host target RNA into VGAM2367 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80661] It is appreciated that VGAM2367 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2367 host target genes. The mRNA of each one of this plurality of VGAM2367 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2367 RNA, herein designated VGAM RNA, and which when bound by VGAM2367 RNA causes inhibition of translation of respective one or more VGAM2367 host target proteins.

[80662] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2367 gene, herein designated VGAM GENE, on one or more VGAM2367 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80663] It is yet further appreciated that a function of VGAM2367 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2367 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2367 correlate with, and may be deduced from, the identity of the host target genes which VGAM2367 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80664] Nucleotide sequences of the VGAM2367 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2367 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2367 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2367 are further described hereinbelow with reference to Table 1.

[80665] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2367 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2367 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80666] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2367 gene, herein designated VGAM is inhibition of expression of VGAM2367 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2367 correlate with, and may be deduced from, the identity of the target genes which VGAM2367 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80667] A Kinase (PRKA) Anchor Protein 2 (AKAP2, Accession NM_007203) is a VGAM2367 host target gene. AKAP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKAP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP2 BINDING SITE, designated SEQ ID:14058, to the nucleotide sequence of VGAM2367 RNA, herein designated VGAM RNA, also designated SEQ ID:5078.

[80668] A function of VGAM2367 is therefore inhibition of A Kinase (PRKA) Anchor Protein 2 (AKAP2, Accession NM_007203), a gene which binds to regulatory subunit (rii) of protein kinase a. Accordingly, utilities of VGAM2367 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP2.

The function of AKAP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM18.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2368 (VGAM2368) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80669] VGAM2368 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2368 was detected is described hereinabove with reference to Figs. 1-8.

[80670] VGAM2368 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2368 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80671] VGAM2368 gene encodes a VGAM2368 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2368 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2368 precursor RNA is designated SEQ ID:2354, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2354 is located at position 223088 relative to the genome of Rat Cytomegalovirus.

[80672] VGAM2368 precursor RNA folds onto itself, forming VGAM2368 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80673] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2368 folded precursor RNA into VGAM2368 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide se-

quence of VGAM2368 RNA is designated SEQ ID:5079, and is provided hereinbelow with reference to the sequence listing part.

[80674] VGAM2368 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2368 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2368 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80675] VGAM2368 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2368 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2368 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2368 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2368 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80676] The complementary binding of VGAM2368 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2368 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2368 host target RNA into VGAM2368 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80677] It is appreciated that VGAM2368 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2368 host target genes. The mRNA of each one of this plurality of VGAM2368 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2368 RNA, herein designated VGAM RNA, and which when bound by VGAM2368 RNA causes inhibition of translation of respective one or more VGAM2368 host target proteins.

[80678] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2368 gene, herein designated VGAM GENE, on one or more VGAM2368 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80679] It is yet further appreciated that a function of VGAM2368

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2368 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2368 correlate with, and may be deduced from, the identity of the host target genes which VGAM2368 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80680] Nucleotide sequences of the VGAM2368 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2368 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2368 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2368 are further described hereinbelow with reference to Table 1.

[80681] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2368 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2368 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80682] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2368 gene, herein designated VGAM is inhibition of expression of VGAM2368 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2368 correlate with, and may be deduced from, the identity of the target genes which VGAM2368 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80683] Apolipoprotein L, 6 (APOL6, Accession NM_030641) is a VGAM2368 host target gene. APOL6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by APOL6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APOL6 BINDING SITE, designated SEQ ID:24968, to the nucleotide sequence of VGAM2368 RNA, herein designated VGAM RNA, also designated SEQ ID:5079.

[80684] A function of VGAM2368 is therefore inhibition of Apolipoprotein L, 6 (APOL6, Accession NM_030641). Accordingly, utilities of VGAM2368 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APOL6. Fig. 1 further provides a concep-

tual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2369 (VGAM2369) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80685] VGAM2369 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2369 was detected is described hereinabove with reference to Figs. 1-8.

[80686] VGAM2369 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2369 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80687] VGAM2369 gene encodes a VGAM2369 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2369 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2369 precursor RNA is designated SEQ ID:2355, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2355 is located at position 208920 relative to the genome of Rat Cytomegalovirus.

[80688] VGAM2369 precursor RNA folds onto itself, forming VGAM2369 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80689] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2369 folded precursor RNA into VGAM2369 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2369 RNA is designated SEQ ID:5080, and is provided hereinbelow with reference to the sequence listing part.

[80690] VGAM2369 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2369 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2369 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80691] VGAM2369 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2369 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2369 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2369 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2369 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80692] The complementary binding of VGAM2369 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2369 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2369 host target RNA into VGAM2369 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80693] It is appreciated that VGAM2369 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2369 host target genes. The mRNA of each one of this plurality of VGAM2369 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2369 RNA, herein designated VGAM RNA, and which when bound by VGAM2369 RNA causes inhibition of translation of respective one or more

VGAM2369 host target proteins.

[80694] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2369 gene, herein designated VGAM GENE, on one or more VGAM2369 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80695] It is yet further appreciated that a function of VGAM2369 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Spe-

cific functions, and accordingly utilities, of VGAM2369 correlate with, and may be deduced from, the identity of the host target genes which VGAM2369 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80696] Nucleotide sequences of the VGAM2369 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2369 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2369 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2369 are further described hereinbelow with reference to Table 1.

[80697] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2369 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2369 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80698] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2369 gene, herein designated VGAM is inhibition of expression of VGAM2369 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2369 correlate with, and may be deduced from, the identity of the target genes which VGAM2369 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80699] Numb Homolog (Drosophila) (NUMB, Accession NM_003744) is a VGAM2369 host target gene. NUMB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUMB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUMB BINDING SITE, designated SEQ ID:9831, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80700] A function of VGAM2369 is therefore inhibition of Numb Homolog (Drosophila) (NUMB, Accession NM_003744), a gene which may act in generating asymmetric cell division during neurogenesisand is strongly similar to murine Numb. Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUMB. The function of NUMB and its association with various diseases and clinical conditions, has been established by previous studies, as de-

scribed hereinabove with reference to VGAM2322.Protocadherin Alpha 1 (PCDHA1, Accession NM_018900) is another VGAM2369 host target gene. PCDHA1 BINDING SITE1 and PCDHA1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDHA1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA1 BINDING SITE1 and PCDHA1 BINDING SITE2, designated SEQ ID:20860 and SEQ ID:25379 respectively, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80701] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha 1 (PCDHA1, Accession NM_018900). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA1. Protocadherin Alpha 10 (PCDHA10, Accession NM_018901) is another VGAM2369 host target gene. PCDHA10 BINDING SITE1 and PCDHA10 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDHA10, corresponding to HOST TARGET binding sites such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA10 BINDING SITE1 and PCDHA10 BINDING SITE2, designated SEQ ID:20870 and SEQ ID:20880 respectively, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80702] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha 10 (PCDHA10, Accession NM_018901). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA10. Protocadherin Alpha 13 (PCDHA13, Accession NM_018904) is another VGAM2369 host target gene. PCDHA13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHA13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA13 BINDING SITE, designated SEQ ID:20901, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80703] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha 13 (PCDHA13, Accession

NM_018904). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA13. Protocadherin Alpha 2 (PCDHA2, Accession NM_018905) is another VGAM2369 host target gene. PCDHA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA2 BINDING SITE, designated SEQ ID:20911, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80704] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha 2 (PCDHA2, Accession NM_018905). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA2. Protocadherin Alpha 3 (PCDHA3, Accession NM_018906) is another VGAM2369 host target gene. PCDHA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA3 BINDING SITE, designated SEQ ID:20921, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80705] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha 3 (PCDHA3, Accession NM_018906). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA3. Protocadherin Alpha 4 (PCDHA4, Accession NM_018907) is another VGAM2369 host target gene. PCDHA4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA4 BINDING SITE, designated SEQ ID:20931, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80706] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha 4 (PCDHA4, Accession NM_018907). Accordingly, utilities of VGAM2369 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with PCDHA4. Protocadherin Alpha 5 (PCDHA5, Accession NM_018908) is another VGAM2369 host target gene. PCDHA5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA5 BINDING SITE, designated SEQ ID:20941, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80707] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha 5 (PCDHA5, Accession NM_018908). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA5. Protocadherin Alpha 6 (PCDHA6, Accession NM_018909) is another VGAM2369 host target gene. PCDHA6 BINDING SITE1 and PCDHA6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDHA6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of PCDHA6 BINDING SITE1 and PCDHA6 BINDING SITE2, designated SEQ ID:20951 and SEQ ID:25583 respectively, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80708] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha 6 (PCDHA6, Accession NM_018909). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA6. Protocadherin Alpha 8 (PCDHA8, Accession NM_018911) is another VGAM2369 host target gene. PCDHA8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHA8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA8 BINDING SITE, designated SEQ ID:20971, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80709] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha 8 (PCDHA8, Accession NM_018911). Accordingly, utilities of VGAM2369 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with PCDHA8. Protocadherin Alpha 9 (PCDHA9, Accession NM_031857) is another VGAM2369 host target gene. PCDHA9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHA9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHA9 BINDING SITE, designated SEQ ID:25596, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80710] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha 9 (PCDHA9, Accession NM_031857), a gene which is a calcium-dependent cell-adhesion protein. Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHA9. The function of PCDHA9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM71.Protocadherin Alpha Subfamily C, 1 (PCDHAC1, Accession NM_018898) is another VGAM2369 host target

gene. PCDHAC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHAC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHAC1 BINDING SITE, designated SEQ ID:20840, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80711] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha Subfamily C, 1 (PCDHAC1, Accession NM_018898). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHAC1. Protocadherin Alpha Subfamily C, 2 (PCDHAC2, Accession NM_018899) is another VGAM2369 host target gene. PCDHAC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHAC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHAC2 BINDING SITE, designated SEQ ID:20850, to the nucleotide sequence of VGAM2369 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5080.

[80712] Another function of VGAM2369 is therefore inhibition of Protocadherin Alpha Subfamily C, 2 (PCDHAC2, Accession NM_018899). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHAC2. FHR5 (Accession NM_030787) is another VGAM2369 host target gene. FHR5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FHR5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FHR5 BINDING SITE, designated SEQ ID:25082, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80713] Another function of VGAM2369 is therefore inhibition of FHR5 (Accession NM_030787). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHR5. FLJ10511 (Accession NM_018120) is another VGAM2369 host target gene. FLJ10511 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10511, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10511 BINDING SITE, designated SEQ ID:19897, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80714] Another function of VGAM2369 is therefore inhibition of FLJ10511 (Accession NM_018120). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10511. FLJ13962 (Accession NM_024862) is another VGAM2369 host target gene. FLJ13962 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13962, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13962 BINDING SITE, designated SEQ ID:24296, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80715] Another function of VGAM2369 is therefore inhibition of FLJ13962 (Accession NM_024862). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ13962. LOC143785 (Accession XM_084635) is another VGAM2369 host target gene. LOC143785 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143785, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143785 BINDING SITE, designated SEQ ID:37631, to the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80716] Another function of VGAM2369 is therefore inhibition of LOC143785 (Accession XM_084635). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143785. LOC152215 (Accession XM_087407) is another VGAM2369 host target gene. LOC152215 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152215, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152215 BINDING SITE, designated SEQ ID:39224, to

the nucleotide sequence of VGAM2369 RNA, herein designated VGAM RNA, also designated SEQ ID:5080.

[80717] Another function of VGAM2369 is therefore inhibition of LOC152215 (Accession XM_087407). Accordingly, utilities of VGAM2369 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152215. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2370 (VGAM2370) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80718] VGAM2370 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2370 was detected is described hereinabove with reference to Figs. 1-8.

[80719] VGAM2370 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2370 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80720] VGAM2370 gene encodes a VGAM2370 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2370 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2370 precursor RNA is designated SEQ ID:2356, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2356 is located at position 217655 relative to the genome of Rat Cytomegalovirus.

[80721] VGAM2370 precursor RNA folds onto itself, forming VGAM2370 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80722] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2370 folded precursor RNA into VGAM2370 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2370 RNA is designated SEQ ID:5081, and is provided hereinbelow with reference to the sequence listing part.

[80723] VGAM2370 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2370 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2370 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80724] VGAM2370 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2370 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2370 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2370 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2370 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80725] The complementary binding of VGAM2370 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2370 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2370 host target RNA into VGAM2370 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80726] It is appreciated that VGAM2370 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2370 host target genes. The mRNA of each one of this plurality of VGAM2370 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2370 RNA, herein designated VGAM RNA, and which when bound by VGAM2370 RNA causes inhibition of translation of respective one or more VGAM2370 host target proteins.

[80727] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2370 gene, herein designated VGAM GENE, on one or more VGAM2370 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80728] It is yet further appreciated that a function of VGAM2370 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2370 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2370 correlate with, and may be deduced from, the identity of the host target genes which VGAM2370 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80729] Nucleotide sequences of the VGAM2370 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2370 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2370 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2370 are further described hereinbelow with reference to Table 1.

[80730] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2370 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2370 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80731] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2370 gene, herein designated VGAM is inhibition of expression of VGAM2370 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2370 correlate with, and may be deduced from, the identity of the target genes which VGAM2370 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80732] Collagen, Type IV, Alpha 1 (COL4A1, Accession NM_001845) is a VGAM2370 host target gene. COL4A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL4A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL4A1 BINDING SITE, designated SEQ ID:7580, to the nucleotide sequence of VGAM2370 RNA, herein designated VGAM RNA, also designated SEQ ID:5081.

[80733] A function of VGAM2370 is therefore inhibition of Colla-

gen, Type IV, Alpha 1 (COL4A1, Accession NM_001845), a gene which is a member of a subfamily of collagen extracellular matrix proteins. Accordingly, utilities of VGAM2370 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL4A1. The function of COL4A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1645.Catenin (cadherin-associated protein), Alpha 2 (CTNNA2, Accession NM_004389) is another VGAM2370 host target gene. CTNNA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CTNNA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTNNA2 BINDING SITE, designated SEQ ID:10617, to the nucleotide sequence of VGAM2370 RNA, herein designated VGAM RNA, also designated SEQ ID:5081.

[80734] Another function of VGAM2370 is therefore inhibition of Catenin (cadherin-associated protein), Alpha 2 (CTNNA2, Accession NM_004389), a gene which is involved in the cytoplasmic anchorage of cell-cell and cell-substrate ad-

hesion molecules. Accordingly, utilities of VGAM2370 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTNNA2. The function of CTNNA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM877.Catenin (cadherin-associated protein), Delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2, Accession NM_001332) is another VGAM2370 host target gene. CTNND2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CTNND2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CTNND2 BINDING SITE, designated SEQ ID:7015, to the nucleotide sequence of VGAM2370 RNA, herein designated VGAM RNA, also designated SEQ ID:5081.

[80735] Another function of VGAM2370 is therefore inhibition of Catenin (cadherin-associated protein), Delta 2 (neural plakophilin-related arm-repeat protein) (CTNND2, Accession NM_001332), a gene which interacts with presenilin 1 (PSEN1) and is a member of the plakoglobin/armadillo

family. Accordingly, utilities of VGAM2370 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CTNND2. The function of CTNND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2235.FKSG28 (Accession NM_030929) is another VGAM2370 host target gene. FKSG28 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FKSG28, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FKSG28 BINDING SITE, designated SEQ ID:25201, to the nucleotide sequence of VGAM2370 RNA, herein designated VGAM RNA, also designated SEQ ID:5081.

[80736] Another function of VGAM2370 is therefore inhibition of FKSG28 (Accession NM_030929). Accordingly, utilities of VGAM2370 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKSG28. Myristoylated Alanine-rich Protein Kinase C Substrate (MARCKS, Accession NM_002356) is another VGAM2370 host target gene. MARCKS BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MARCKS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MARCKS BINDING SITE, designated SEQ ID:8169, to the nucleotide sequence of VGAM2370 RNA, herein designated VGAM RNA, also designated SEQ ID:5081.

[80737] Another function of VGAM2370 is therefore inhibition of Myristoylated Alanine-rich Protein Kinase C Substrate (MARCKS, Accession NM_002356). Accordingly, utilities of VGAM2370 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MARCKS. NPD009 (Accession XM_170795) is another VGAM2370 host target gene. NPD009 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NPD009, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPD009 BINDING SITE, designated SEQ ID:45565, to the nucleotide sequence of VGAM2370 RNA, herein designated VGAM RNA, also designated SEQ ID:5081.

[80738] Another function of VGAM2370 is therefore inhibition of NPD009 (Accession XM_170795). Accordingly, utilities of VGAM2370 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPD009. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2371 (VGAM2371) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80739] VGAM2371 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2371 was detected is described hereinabove with reference to Figs. 1-8.

[80740] VGAM2371 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2371 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80741] VGAM2371 gene encodes a VGAM2371 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2371 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2371 precursor RNA is designated SEQ ID:2357, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2357 is located at position 183987 relative to the genome of Rat Cytomegalovirus.

[80742] VGAM2371 precursor RNA folds onto itself, forming VGAM2371 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80743] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2371 folded precursor RNA into VGAM2371 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 60%) nucleotide sequence of VGAM2371 RNA is designated SEQ ID:5082, and is provided hereinbelow with reference to the sequence listing part.

[80744] VGAM2371 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2371 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2371 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80745] VGAM2371 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2371 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2371 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2371 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2371 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80746] The complementary binding of VGAM2371 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2371 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2371 host target RNA into VGAM2371 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80747] It is appreciated that VGAM2371 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2371 host target genes. The mRNA of each one of this plurality of VGAM2371 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2371 RNA, herein designated VGAM RNA, and which when bound by VGAM2371 RNA causes inhibition of translation of respective one or more VGAM2371 host target proteins.

[80748] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2371 gene, herein designated VGAM GENE, on one or more VGAM2371 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80749] It is yet further appreciated that a function of VGAM2371 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2371 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2371 correlate with, and may be deduced from, the identity of the host target genes which VGAM2371 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80750] Nucleotide sequences of the VGAM2371 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2371 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2371 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2371 are further described hereinbelow with reference to Table 1.

[80751] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2371 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2371 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[80752] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2371 gene, herein designated VGAM is inhibition of expression of VGAM2371 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2371 correlate with, and may be deduced from, the identity of the target genes which VGAM2371 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80753] UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 1 (B4GALT1, Accession NM_001497) is a VGAM2371 host target gene. B4GALT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by B4GALT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B4GALT1 BINDING SITE, designated SEQ ID:7246, to the nucleotide sequence of VGAM2371 RNA, herein designated VGAM RNA, also designated SEQ ID:5082.

[80754] A function of VGAM2371 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 1 (B4GALT1, Accession NM_001497). Accordingly,

utilities of VGAM2371 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT1. IRTA2 (Accession NM_031281) is another VGAM2371 host target gene. IRTA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IRTA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRTA2 BINDING SITE, designated SEQ ID:25299, to the nucleotide sequence of VGAM2371 RNA, herein designated VGAM RNA, also designated SEQ ID:5082.

[80755] Another function of VGAM2371 is therefore inhibition of IRTA2 (Accession NM_031281), a gene which binds to the fc region of immunoglobulins gamma low affinity receptor. Accordingly, utilities of VGAM2371 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRTA2. The function of IRTA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.KIAA1318 (Accession XM_041080) is another VGAM2371 host target gene. KIAA1318 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by KIAA1318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1318 BINDING SITE, designated SEQ ID:33433, to the nucleotide sequence of VGAM2371 RNA, herein designated VGAM RNA, also designated SEQ ID:5082.

[80756] Another function of VGAM2371 is therefore inhibition of KIAA1318 (Accession XM_041080). Accordingly, utilities of VGAM2371 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1318. MOST2 (Accession NM_020250) is another VGAM2371 host target gene. MOST2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MOST2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MOST2 BINDING SITE, designated SEQ ID:21554, to the nucleotide sequence of VGAM2371 RNA, herein designated VGAM RNA, also designated SEQ ID:5082.

[80757] Another function of VGAM2371 is therefore inhibition of

MOST2 (Accession NM_020250). Accordingly, utilities of VGAM2371 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOST2. LOC158364 (Accession XM_088546) is another VGAM2371 host target gene. LOC158364 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158364, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158364 BINDING SITE, designated SEQ ID:39818, to the nucleotide sequence of VGAM2371 RNA, herein designated VGAM RNA, also designated SEQ ID:5082.

[80758] Another function of VGAM2371 is therefore inhibition of LOC158364 (Accession XM_088546). Accordingly, utilities of VGAM2371 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158364. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2372 (VGAM2372) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[80759] VGAM2372 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2372 was detected is described hereinabove with reference to Figs. 1-8.

[80760] VGAM2372 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2372 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80761] VGAM2372 gene encodes a VGAM2372 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2372 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2372 precursor RNA is designated SEQ ID:2358, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2358 is located at position 208652 relative to the genome of Rat Cytomegalovirus.

[80762] VGAM2372 precursor RNA folds onto itself, forming VGAM2372 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80763] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2372 folded precursor RNA into VGAM2372 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 51%) nucleotide sequence of VGAM2372 RNA is designated SEQ ID:5083, and is provided hereinbelow with reference to the sequence listing part.

[80764] VGAM2372 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2372 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2372 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80765] VGAM2372 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2372 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2372 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2372 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2372 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[80766] The complementary binding of VGAM2372 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2372 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2372 host target RNA into VGAM2372 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80767] It is appreciated that VGAM2372 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2372 host target genes. The mRNA of each one of this plurality of VGAM2372 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2372 RNA, herein designated VGAM RNA, and which when bound by VGAM2372 RNA causes inhibition of translation of respective one or more VGAM2372 host target proteins.

[80768] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2372 gene, herein designated VGAM GENE, on one

or more VGAM2372 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80769] It is yet further appreciated that a function of VGAM2372 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2372 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2372 correlate with, and may be deduced from, the identity of the host target genes which VGAM2372 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80770] Nucleotide sequences of the VGAM2372 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2372 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2372 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2372 are further described hereinbelow with reference to Table 1.

[80771] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2372 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2372 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80772] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2372 gene, herein designated VGAM is inhibition of expression of VGAM2372 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2372 correlate with, and may be deduced from, the identity of the target genes which VGAM2372 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80773] Dystrophin (muscular dystrophy, Duchenne and Becker

types) (DMD, Accession NM_000109) is a VGAM2372 host target gene. DMD BINDING SITE1 through DMD BINDING SITE13 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DMD, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DMD BINDING SITE1 through DMD BINDING SITE13, designated SEQ ID:5573, SEQ ID:10156, SEQ ID:10163, SEQ ID:10209, SEQ ID:10214, SEQ ID:10225, SEQ ID:10169, SEQ ID:10177, SEQ ID:10182, SEQ ID:10187, SEQ ID:10198, SEQ ID:10204 and SEQ ID:10237 respectively, to the nucleotide sequence of VGAM2372 RNA, herein designated VGAM RNA, also designated SEQ ID:5083.

[80774] A function of VGAM2372 is therefore inhibition of Dystrophin (muscular dystrophy, Duchenne and Becker types) (DMD, Accession NM_000109), a gene which muscular dystrophy . Accordingly, utilities of VGAM2372 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMD. The function of DMD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to

VGAM218.Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_000793) is another VGAM2372 host target gene. DIO2 BINDING SITE1 and DIO2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DIO2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DIO2 BINDING SITE1 and DIO2 BINDING SITE2, designated SEQ ID:6462 and SEQ ID:15173 respectively, to the nucleotide sequence of VGAM2372 RNA, herein designated VGAM RNA, also designated SEQ ID:5083.

[80775] Another function of VGAM2372 is therefore inhibition of Deiodinase, Iodothyronine, Type II (DIO2, Accession NM_000793). Accordingly, utilities of VGAM2372 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIO2. FLJ14906 (Accession NM_032859) is another VGAM2372 host target gene. FLJ14906 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of FLJ14906 BINDING SITE, designated SEQ ID:26661, to the nucleotide sequence of VGAM2372 RNA, herein designated VGAM RNA, also designated SEQ ID:5083.

[80776] Another function of VGAM2372 is therefore inhibition of FLJ14906 (Accession NM_032859). Accordingly, utilities of VGAM2372 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14906. PRO1584 (Accession NM_018586) is another VGAM2372 host target gene. PRO1584 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1584, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1584 BINDING SITE, designated SEQ ID:20662, to the nucleotide sequence of VGAM2372 RNA, herein designated VGAM RNA, also designated SEQ ID:5083.

[80777] Another function of VGAM2372 is therefore inhibition of PRO1584 (Accession NM_018586). Accordingly, utilities of VGAM2372 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1584. LOC203078 (Accession XM_114625) is another

VGAM2372 host target gene. LOC203078 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203078, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203078 BINDING SITE, designated SEQ ID:43006, to the nucleotide sequence of VGAM2372 RNA, herein designated VGAM RNA, also designated SEQ ID:5083.

[80778] Another function of VGAM2372 is therefore inhibition of LOC203078 (Accession XM_114625). Accordingly, utilities of VGAM2372 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203078. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2373 (VGAM2373) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80779] VGAM2373 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2373 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[80780] VGAM2373 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2373 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80781] VGAM2373 gene encodes a VGAM2373 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2373 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2373 precursor RNA is designated SEQ ID:2359, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2359 is located at position 222910 relative to the genome of Rat Cytomegalovirus.

[80782] VGAM2373 precursor RNA folds onto itself, forming VGAM2373 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80783] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2373 folded precursor RNA into VGAM2373 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2373 RNA is designated SEQ ID:5084, and is provided hereinbelow with reference to the sequence listing part.

[80784] VGAM2373 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2373 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2373 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80785] VGAM2373 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2373 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2373 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2373 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2373 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80786] The complementary binding of VGAM2373 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2373 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2373 host target RNA into VGAM2373 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80787] It is appreciated that VGAM2373 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2373 host target genes. The mRNA of each one of this plurality of VGAM2373 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2373 RNA, herein designated VGAM RNA, and which when bound by VGAM2373 RNA causes inhibition of translation of respective one or more VGAM2373 host target proteins.

[80788] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2373 gene, herein designated VGAM GENE, on one or more VGAM2373 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80789] It is yet further appreciated that a function of VGAM2373 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2373 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2373 correlate with, and may be deduced from, the identity of the host target genes which VGAM2373 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80790] Nucleotide sequences of the VGAM2373 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2373 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2373 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2373 are further described hereinbelow with reference to Table 1.

[80791] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2373 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2373 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80792] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2373 gene, herein designated VGAM is inhibition of expression of VGAM2373 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2373 correlate with, and may be deduced from, the identity of the target genes which VGAM2373 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80793] LIM Domain Kinase 1 (LIMK1, Accession NM_002314) is a VGAM2373 host target gene. LIMK1 BINDING SITE1 and LIMK1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LIMK1, corresponding to HOST TARGET binding sites such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIMK1 BINDING SITE1 and LIMK1 BINDING SITE2, designated SEQ ID:8127 and SEQ ID:18804 respectively, to the nucleotide sequence of VGAM2373 RNA, herein designated VGAM RNA, also designated SEQ ID:5084.

[80794] A function of VGAM2373 is therefore inhibition of LIM Domain Kinase 1 (LIMK1, Accession NM_002314). Accordingly, utilities of VGAM2373 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIMK1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2374 (VGAM2374) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80795] VGAM2374 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2374 was detected is described hereinabove with reference to Figs. 1-8.

[80796] VGAM2374 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Rat Cytomegalovirus. VGAM2374 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80797] VGAM2374 gene encodes a VGAM2374 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2374 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2374 precursor RNA is designated SEQ ID:2360, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2360 is located at position 203878 relative to the genome of Rat Cytomegalovirus.

[80798] VGAM2374 precursor RNA folds onto itself, forming VGAM2374 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80799] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2374 folded precursor RNA into VGAM2374 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM2374 RNA is designated SEQ ID:5085, and is provided hereinbelow with reference to the sequence listing part.

[80800] VGAM2374 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2374 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2374 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80801] VGAM2374 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2374 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2374 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2374 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2374 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80802] The complementary binding of VGAM2374 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2374 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2374

host target RNA into VGAM2374 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80803] It is appreciated that VGAM2374 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2374 host target genes. The mRNA of each one of this plurality of VGAM2374 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2374 RNA, herein designated VGAM RNA, and which when bound by VGAM2374 RNA causes inhibition of translation of respective one or more VGAM2374 host target proteins.

[80804] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2374 gene, herein designated VGAM GENE, on one or more VGAM2374 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80805] It is yet further appreciated that a function of VGAM2374 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2374 correlate with, and may be deduced from, the identity of the host target genes which VGAM2374 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80806] Nucleotide sequences of the VGAM2374 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2374 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2374 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2374 are further

described hereinbelow with reference to Table 1.

[80807] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2374 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2374 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80808] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2374 gene, herein designated VGAM is inhibition of expression of VGAM2374 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2374 correlate with, and may be deduced from, the identity of the target genes which VGAM2374 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80809] Caspase 10, Apoptosis-related Cysteine Protease (CASP10, Accession NM_032976) is a VGAM2374 host target gene. CASP10 BINDING SITE1 and CASP10 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CASP10, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of CASP10 BINDING SITE1 and CASP10 BINDING SITE2, designated SEQ ID:26832 and SEQ ID:26835 respectively, to the nucleotide sequence of VGAM2374 RNA, herein designated VGAM RNA, also designated SEQ ID:5085.

[80810] A function of VGAM2374 is therefore inhibition of Caspase 10, Apoptosis-related Cysteine Protease (CASP10, Accession NM_032976), a gene which is one aspartate-specific cysteine protease and important in death receptor signaling or other cellular processes. Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CASP10. The function of CASP10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.Protein Kinase, CGMP-dependent, Type I (PRKG1, Accession NM_006258) is another VGAM2374 host target gene. PRKG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKG1 BINDING SITE,

designated SEQ ID:12937, to the nucleotide sequence of VGAM2374 RNA, herein designated VGAM RNA, also designated SEQ ID:5085.

[80811] Another function of VGAM2374 is therefore inhibition of Protein Kinase, CGMP-dependent, Type I (PRKG1, Accession NM_006258), a gene which relaxes vascular smooth muscle and inhibits platelet aggregation. Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKG1. The function of PRKG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1571.TNF Receptor-associated Factor 5 (TRAF5, Accession NM_004619) is another VGAM2374 host target gene. TRAF5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRAF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRAF5 BINDING SITE, designated SEQ ID:10962, to the nucleotide sequence of VGAM2374 RNA, herein designated VGAM RNA, also designated SEQ ID:5085.

[80812] Another function of VGAM2374 is therefore inhibition of TNF Receptor-associated Factor 5 (TRAF5, Accession NM_004619), a gene which Member of a family of proteins that interact with TNF receptors; binds the lymphotoxin beta receptor (LTBR). Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRAF5. The function of TRAF5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM76.Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, Gamma Polypeptide (YWHAG, Accession NM_012479) is another VGAM2374 host target gene. YWHAG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by YWHAG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of YWHAG BINDING SITE, designated SEQ ID:14856, to the nucleotide sequence of VGAM2374 RNA, herein designated VGAM RNA, also designated SEQ ID:5085.

[80813] Another function of VGAM2374 is therefore inhibition of

Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase Activation Protein, Gamma Polypeptide (YWHAG, Accession NM_012479), a gene which mediates mitogenic signals of PDGF in vascular smooth muscle cells. Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment of diseases and clinical conditions associated with YWHAG. The function of YWHAG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM180.FLJ10097 (Accession XM_043653) is another VGAM2374 host target gene. FLJ10097 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10097, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10097 BINDING SITE, designated SEQ ID:33987, to the nucleotide sequence of VGAM2374 RNA, herein designated VGAM RNA, also designated SEQ ID:5085.

[80814] Another function of VGAM2374 is therefore inhibition of FLJ10097 (Accession XM_043653). Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ10097. KIAA0884 (Accession XM_046660) is another VGAM2374 host target gene. KIAA0884 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0884, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0884 BINDING SITE, designated SEQ ID:34777, to the nucleotide sequence of VGAM2374 RNA, herein designated VGAM RNA, also designated SEQ ID:5085.

[80815] Another function of VGAM2374 is therefore inhibition of KIAA0884 (Accession XM_046660). Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0884. KIAA1058 (Accession XM_090586) is another VGAM2374 host target gene. KIAA1058 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1058, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1058 BINDING SITE, designated SEQ ID:40011, to the

nucleotide sequence of VGAM2374 RNA, herein designated VGAM RNA, also designated SEQ ID:5085.

[80816] Another function of VGAM2374 is therefore inhibition of KIAA1058 (Accession XM_090586). Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1058. LANO (Accession NM_025168) is another VGAM2374 host target gene. LANO BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LANO, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LANO BINDING SITE, designated SEQ ID:24803, to the nucleotide sequence of VGAM2374 RNA, herein designated VGAM RNA, also designated SEQ ID:5085.

[80817] Another function of VGAM2374 is therefore inhibition of LANO (Accession NM_025168). Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LANO. PAIP1 (Accession XM_039946) is another VGAM2374 host target gene. PAIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by PAIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAIP1 BINDING SITE, designated SEQ ID:33234, to the nucleotide sequence of VGAM2374 RNA, herein designated VGAM RNA, also designated SEQ ID:5085.

[80818] Another function of VGAM2374 is therefore inhibition of PAIP1 (Accession XM_039946). Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAIP1. Ubiquitin Specific Protease 25 (USP25, Accession NM_013396) is another VGAM2374 host target gene. USP25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USP25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP25 BINDING SITE, designated SEQ ID:15047, to the nucleotide sequence of VGAM2374 RNA, herein designated VGAM RNA, also designated SEQ ID:5085.

[80819] Another function of VGAM2374 is therefore inhibition of

Ubiquitin Specific Protease 25 (USP25, Accession NM_013396). Accordingly, utilities of VGAM2374 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP25. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2375 (VGAM2375) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80820] VGAM2375 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2375 was detected is described hereinabove with reference to Figs. 1-8.

[80821] VGAM2375 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2375 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80822] VGAM2375 gene encodes a VGAM2375 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2375 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2375 precursor RNA is designated SEQ ID:2361, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2361 is located at position 217137 relative to the genome of Rat Cytomegalovirus.

[80823] VGAM2375 precursor RNA folds onto itself, forming VGAM2375 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80824] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2375 folded precursor RNA into VGAM2375 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide se-

quence of VGAM2375 RNA is designated SEQ ID:5086, and is provided hereinbelow with reference to the sequence listing part.

[80825] VGAM2375 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2375 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2375 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80826] VGAM2375 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2375 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2375 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2375 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2375 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80827] The complementary binding of VGAM2375 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2375 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2375 host target RNA into VGAM2375 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80828] It is appreciated that VGAM2375 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2375 host target genes. The mRNA of each one of this plurality of VGAM2375 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2375 RNA, herein designated VGAM RNA, and which when bound by VGAM2375 RNA causes inhibition of translation of respective one or more VGAM2375 host target proteins.

[80829] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2375 gene, herein designated VGAM GENE, on one or more VGAM2375 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80830] It is yet further appreciated that a function of VGAM2375

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2375 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2375 correlate with, and may be deduced from, the identity of the host target genes which VGAM2375 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80831] Nucleotide sequences of the VGAM2375 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2375 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2375 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2375 are further described hereinbelow with reference to Table 1.

[80832] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2375 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2375 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80833] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2375 gene, herein designated VGAM is inhibition of expression of VGAM2375 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2375 correlate with, and may be deduced from, the identity of the target genes which VGAM2375 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80834] TIRAP (Accession NM_052887) is a VGAM2375 host target gene. TIRAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIRAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIRAP BINDING SITE, designated SEQ ID:27474, to the nucleotide sequence of VGAM2375 RNA, herein designated VGAM RNA, also designated SEQ ID:5086.

[80835] A function of VGAM2375 is therefore inhibition of TIRAP (Accession NM_052887), a gene which is a adapter involved in theTLR4 signaling pathway in the innate immune response. Accordingly, utilities of VGAM2375 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIRAP. The function of TIRAP

and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM189.Chemokine (C-C motif) Receptor 6 (CCR6, Accession NM_004367) is another VGAM2375 host target gene. CCR6 BINDING SITE1 and CCR6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CCR6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCR6 BINDING SITE1 and CCR6 BINDING SITE2, designated SEQ ID:10575 and SEQ ID:25367 respectively, to the nucleotide sequence of VGAM2375 RNA, herein designated VGAM RNA, also designated SEQ ID:5086.

[80836] Another function of VGAM2375 is therefore inhibition of Chemokine (C-C motif) Receptor 6 (CCR6, Accession NM_004367). Accordingly, utilities of VGAM2375 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCR6. ZIN (Accession NM_013403) is another VGAM2375 host target gene. ZIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZIN, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZIN BINDING SITE, designated SEQ ID:15070, to the nucleotide sequence of VGAM2375 RNA, herein designated VGAM RNA, also designated SEQ ID:5086.

[80837] Another function of VGAM2375 is therefore inhibition of ZIN (Accession NM_013403). Accordingly, utilities of VGAM2375 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZIN. LOC63928 (Accession NM_022097) is another VGAM2375 host target gene. LOC63928 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC63928, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC63928 BINDING SITE, designated SEQ ID:22638, to the nucleotide sequence of VGAM2375 RNA, herein designated VGAM RNA, also designated SEQ ID:5086.

[80838] Another function of VGAM2375 is therefore inhibition of LOC63928 (Accession NM_022097). Accordingly, utilities of VGAM2375 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC63928. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2376 (VGAM2376) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80839] VGAM2376 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2376 was detected is described hereinabove with reference to Figs. 1-8.

[80840] VGAM2376 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2376 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80841] VGAM2376 gene encodes a VGAM2376 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2376 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2376 precursor RNA is desig-

nated SEQ ID:2362, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2362 is located at position 188783 relative to the genome of Rat Cytomegalovirus.

[80842] VGAM2376 precursor RNA folds onto itself, forming VGAM2376 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80843] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2376 folded precursor RNA into VGAM2376 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2376 RNA is designated SEQ ID:5087, and is provided hereinbelow with reference to the sequence

listing part.

[80844] VGAM2376 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2376 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2376 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80845] VGAM2376 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2376 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2376 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2376 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2376 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80846] The complementary binding of VGAM2376 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2376 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2376 host target RNA into VGAM2376 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80847] It is appreciated that VGAM2376 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2376 host target genes. The mRNA of each one of this plurality of VGAM2376 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2376 RNA, herein designated VGAM

RNA, and which when bound by VGAM2376 RNA causes inhibition of translation of respective one or more VGAM2376 host target proteins.

[80848] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2376 gene, herein designated VGAM GENE, on one or more VGAM2376 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80849] It is yet further appreciated that a function of VGAM2376 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2376 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2376 correlate with, and may be deduced from, the identity of the host target genes which VGAM2376 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80850] Nucleotide sequences of the VGAM2376 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2376 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2376 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2376 are further described hereinbelow with reference to Table 1.

[80851] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2376 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2376 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80852] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2376 gene, herein designated VGAM is

inhibition of expression of VGAM2376 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2376 correlate with, and may be deduced from, the identity of the target genes which VGAM2376 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80853] Oligophrenin 1 (OPHN1, Accession NM_002547) is a VGAM2376 host target gene. OPHN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OPHN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OPHN1 BINDING SITE, designated SEQ ID:8404, to the nucleotide sequence of VGAM2376 RNA, herein designated VGAM RNA, also designated SEQ ID:5087.

[80854] A function of VGAM2376 is therefore inhibition of Oligophrenin 1 (OPHN1, Accession NM_002547). Accordingly, utilities of VGAM2376 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OPHN1. X-prolyl Aminopeptidase (aminopeptidase P) 2, Membrane-bound (XPNPEP2, Accession NM_003399) is another VGAM2376 host target gene.

XPNPEP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XPNPEP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XPNPEP2 BINDING SITE, designated SEQ ID:9435, to the nucleotide sequence of VGAM2376 RNA, herein designated VGAM RNA, also designated SEQ ID:5087.

[80855] Another function of VGAM2376 is therefore inhibition of X-prolyl Aminopeptidase (aminopeptidase P) 2, Membrane-bound (XPNPEP2, Accession NM_003399), a gene which is a membrane-associated X-prolyl metallopeptidase . Accordingly, utilities of VGAM2376 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XPNPEP2. The function of XPNPEP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2108.ATIP1 (Accession NM_020749) is another VGAM2376 host target gene. ATIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATIP1, corresponding to a HOST TARGET binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATIP1 BINDING SITE, designated SEQ ID:21859, to the nucleotide sequence of VGAM2376 RNA, herein designated VGAM RNA, also designated SEQ ID:5087.

[80856] Another function of VGAM2376 is therefore inhibition of ATIP1 (Accession NM_020749). Accordingly, utilities of VGAM2376 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATIP1. Cab45 (Accession NM_016547) is another VGAM2376 host target gene. Cab45 BINDING SITE1 and Cab45 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by Cab45, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Cab45 BINDING SITE1 and Cab45 BINDING SITE2, designated SEQ ID:18619 and SEQ ID:18276 respectively, to the nucleotide sequence of VGAM2376 RNA, herein designated VGAM RNA, also designated SEQ ID:5087.

[80857] Another function of VGAM2376 is therefore inhibition of Cab45 (Accession NM_016547). Accordingly, utilities of VGAM2376 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with Cab45. LOC151126 (Accession XM_087103) is another VGAM2376 host target gene. LOC151126 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151126, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151126 BINDING SITE, designated SEQ ID:39056, to the nucleotide sequence of VGAM2376 RNA, herein designated VGAM RNA, also designated SEQ ID:5087.

[80858] Another function of VGAM2376 is therefore inhibition of LOC151126 (Accession XM_087103). Accordingly, utilities of VGAM2376 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151126. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2377 (VGAM2377) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80859] VGAM2377 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2377 was detected is described hereinabove with reference to Figs. 1-8.

[80860] VGAM2377 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2377 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80861] VGAM2377 gene encodes a VGAM2377 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2377 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2377 precursor RNA is designated SEQ ID:2363, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2363 is located at position 197566 relative to the genome of Rat Cytomegalovirus.

[80862] VGAM2377 precursor RNA folds onto itself, forming VGAM2377 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80863] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2377 folded precursor RNA into VGAM2377 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2377 RNA is designated SEQ ID:5088, and is provided hereinbelow with reference to the sequence listing part.

[80864] VGAM2377 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2377 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2377 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80865] VGAM2377 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2377 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2377 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2377 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2377 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80866] The complementary binding of VGAM2377 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2377 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2377 host target RNA into VGAM2377 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80867] It is appreciated that VGAM2377 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2377 host target genes. The mRNA of each one of this plurality of VGAM2377 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2377 RNA, herein designated VGAM RNA, and which when bound by VGAM2377 RNA causes inhibition of translation of respective one or more VGAM2377 host target proteins.

[80868] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2377 gene, herein designated VGAM GENE, on one or more VGAM2377 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80869] It is yet further appreciated that a function of VGAM2377 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2377 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2377 correlate with, and may be deduced from, the identity of the host target genes which VGAM2377 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80870] Nucleotide sequences of the VGAM2377 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2377 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2377 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2377 are further described hereinbelow with reference to Table 1.

[80871] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2377 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2377 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80872] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2377 gene, herein designated VGAM is inhibition of expression of VGAM2377 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2377 correlate with, and may be deduced from, the identity of the target genes which VGAM2377 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80873] LOC151126 (Accession XM_087103) is a VGAM2377 host target gene. LOC151126 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA

encoded by LOC151126, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151126 BINDING SITE, designated SEQ ID:39057, to the nucleotide sequence of VGAM2377 RNA, herein designated VGAM RNA, also designated SEQ ID:5088.

[80874] A function of VGAM2377 is therefore inhibition of LOC151126 (Accession XM_087103). Accordingly, utilities of VGAM2377 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151126. LOC257407 (Accession XM_173078) is another VGAM2377 host target gene. LOC257407 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257407, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257407 BINDING SITE, designated SEQ ID:46334, to the nucleotide sequence of VGAM2377 RNA, herein designated VGAM RNA, also designated SEQ ID:5088.

[80875] Another function of VGAM2377 is therefore inhibition of LOC257407 (Accession XM_173078). Accordingly, utilities

of VGAM2377 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257407. LOC93626 (Accession XM_052635) is another VGAM2377 host target gene. LOC93626 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93626, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93626 BINDING SITE, designated SEQ ID:36043, to the nucleotide sequence of VGAM2377 RNA, herein designated VGAM RNA, also designated SEQ ID:5088.

[80876] Another function of VGAM2377 is therefore inhibition of LOC93626 (Accession XM_052635). Accordingly, utilities of VGAM2377 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93626. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2378 (VGAM2378) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80877] VGAM2378 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2378 was detected is described hereinabove with reference to Figs. 1-8.

[80878] VGAM2378 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2378 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80879] VGAM2378 gene encodes a VGAM2378 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2378 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2378 precursor RNA is designated SEQ ID:2364, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2364 is located at position 219131 relative to the genome of Rat Cytomegalovirus.

[80880] VGAM2378 precursor RNA folds onto itself, forming VGAM2378 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80881] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2378 folded precursor RNA into VGAM2378 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2378 RNA is designated SEQ ID:5089, and is provided hereinbelow with reference to the sequence listing part.

[80882] VGAM2378 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2378 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2378 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[80883] VGAM2378 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2378 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2378 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2378 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2378 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80884] The complementary binding of VGAM2378 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2378 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2378 host target RNA into VGAM2378 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80885] It is appreciated that VGAM2378 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2378 host target genes. The mRNA of each one of this plurality of VGAM2378 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2378 RNA, herein designated VGAM RNA, and which when bound by VGAM2378 RNA causes inhibition of translation of respective one or more VGAM2378 host target proteins.

[80886] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2378 gene, herein designated VGAM GENE, on one or more VGAM2378 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80887] It is yet further appreciated that a function of VGAM2378 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2378 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2378 correlate with, and may be deduced from, the identity of the host target genes which VGAM2378 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80888] Nucleotide sequences of the VGAM2378 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2378 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2378 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2378 are further described hereinbelow with reference to Table 1.

[80889] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2378 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2378 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80890] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2378 gene, herein designated VGAM is inhibition of expression of VGAM2378 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2378 correlate with, and may be deduced from, the identity of the target genes which VGAM2378 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80891] Presenilin 2 (Alzheimer disease 4) (PSEN2, Accession NM_000447) is a VGAM2378 host target gene. PSEN2

BINDING SITE1 and PSEN2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PSEN2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSEN2 BINDING SITE1 and PSEN2 BINDING SITE2, designated SEQ ID:6035 and SEQ ID:14865 respectively, to the nucleotide sequence of VGAM2378 RNA, herein designated VGAM RNA, also designated SEQ ID:5089.

[80892] A function of VGAM2378 is therefore inhibition of Presenilin 2 (Alzheimer disease 4) (PSEN2, Accession NM_000447). Accordingly, utilities of VGAM2378 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSEN2. Wingless-type MMTV Integration Site Family, Member 5B (WNT5B, Accession NM_032642) is another VGAM2378 host target gene. WNT5B BINDING SITE1 and WNT5B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WNT5B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT5B BINDING

SITE1 and WNT5B BINDING SITE2, designated SEQ ID:26358 and SEQ ID:28693 respectively, to the nucleotide sequence of VGAM2378 RNA, herein designated VGAM RNA, also designated SEQ ID:5089.

[80893] Another function of VGAM2378 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 5B (WNT5B, Accession NM_032642), a gene which is the ligand for members of the frizzled family of seven transmembrane receptors and may be a signaling molecule . Accordingly, utilities of VGAM2378 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WNT5B. The function of WNT5B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1928.KIAA0433 (Accession NM_015216) is another VGAM2378 host target gene. KIAA0433 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0433, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0433 BINDING SITE, designated SEQ ID:17549, to the

nucleotide sequence of VGAM2378 RNA, herein designated VGAM RNA, also designated SEQ ID:5089.

[80894] Another function of VGAM2378 is therefore inhibition of KIAA0433 (Accession NM_015216). Accordingly, utilities of VGAM2378 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0433. LOC149606 (Accession XM_086600) is another VGAM2378 host target gene. LOC149606 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149606, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149606 BINDING SITE, designated SEQ ID:38787, to the nucleotide sequence of VGAM2378 RNA, herein designated VGAM RNA, also designated SEQ ID:5089.

[80895] Another function of VGAM2378 is therefore inhibition of LOC149606 (Accession XM_086600). Accordingly, utilities of VGAM2378 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149606. LOC255967 (Accession XM_170737) is another VGAM2378 host target gene. LOC255967 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC255967, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255967 BINDING SITE, designated SEQ ID:45495, to the nucleotide sequence of VGAM2378 RNA, herein designated VGAM RNA, also designated SEQ ID:5089.

[80896] Another function of VGAM2378 is therefore inhibition of LOC255967 (Accession XM_170737). Accordingly, utilities of VGAM2378 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255967. LOC84549 (Accession NM_032509) is another VGAM2378 host target gene. LOC84549 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC84549, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC84549 BINDING SITE, designated SEQ ID:26262, to the nucleotide sequence of VGAM2378 RNA, herein designated VGAM RNA, also designated SEQ ID:5089.

[80897] Another function of VGAM2378 is therefore inhibition of LOC84549 (Accession NM_032509). Accordingly, utilities

of VGAM2378 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC84549. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2379 (VGAM2379) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80898] VGAM2379 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2379 was detected is described hereinabove with reference to Figs. 1-8.

[80899] VGAM2379 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Rat Cytomegalovirus. VGAM2379 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80900] VGAM2379 gene encodes a VGAM2379 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2379 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2379 precursor RNA is designated SEQ ID:2365, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2365 is located at position 212075 relative to the genome of Rat Cytomegalovirus.

[80901] VGAM2379 precursor RNA folds onto itself, forming VGAM2379 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80902] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2379 folded precursor RNA into VGAM2379 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 84%) nucleotide sequence of VGAM2379 RNA is designated SEQ ID:5090, and

is provided hereinbelow with reference to the sequence listing part.

[80903] VGAM2379 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2379 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2379 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80904] VGAM2379 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2379 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2379 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2379 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2379 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80905] The complementary binding of VGAM2379 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2379 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2379 host target RNA into VGAM2379 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80906] It is appreciated that VGAM2379 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2379 host target genes. The mRNA of each one of this plurality of VGAM2379 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2379 RNA, herein designated VGAM RNA, and which when bound by VGAM2379 RNA causes inhibition of translation of respective one or more VGAM2379 host target proteins.

[80907] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2379 gene, herein designated VGAM GENE, on one or more VGAM2379 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80908] It is yet further appreciated that a function of VGAM2379 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of viral infection by Rat Cytomegalovirus. Specific functions, and accordingly utilities, of VGAM2379 correlate with, and may be deduced from, the identity of the host target genes which VGAM2379 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80909] Nucleotide sequences of the VGAM2379 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2379 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2379 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2379 are further described hereinbelow with reference to Table 1.

[80910] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2379 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2379 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80911] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2379 gene, herein designated VGAM is inhibition of expression of VGAM2379 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2379 correlate with, and may be deduced from, the identity of the target genes which VGAM2379 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80912] ATP-binding Cassette, Sub-family B (MDR/TAP), Member 11 (ABCB11, Accession NM_003742) is a VGAM2379 host target gene. ABCB11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCB11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCB11 BINDING SITE, designated SEQ ID:9830, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80913] A function of VGAM2379 is therefore inhibition of ATP-binding Cassette, Sub-family B (MDR/TAP), Member 11 (ABCB11, Accession NM_003742). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

ABCB11. ADP-ribosylation Factor 1 (ARF1, Accession XM_047545) is another VGAM2379 host target gene. ARF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARF1 BINDING SITE, designated SEQ ID:34993, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80914] Another function of VGAM2379 is therefore inhibition of ADP-ribosylation Factor 1 (ARF1, Accession XM_047545). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARF1. Rho Guanine Nucleotide Exchange Factor (GEF) 7 (ARHGEF7, Accession NM_003899) is another VGAM2379 host target gene. ARHGEF7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHGEF7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGEF7 BINDING SITE, designated SEQ ID:9982, to the

nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80915] Another function of VGAM2379 is therefore inhibition of Rho Guanine Nucleotide Exchange Factor (GEF) 7 (ARHGEF7, Accession NM_003899), a gene which acts as a rac1 guanine nucleotide exchange factor (gef) and can induce membrane ruffling. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF7. The function of ARHGEF7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM297.ATPase, Class VI, Type 11A (ATP11A, Accession XM_085028) is another VGAM2379 host target gene. ATP11A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP11A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP11A BINDING SITE, designated SEQ ID:37805, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80916] Another function of VGAM2379 is therefore inhibition of ATPase, Class VI, Type 11A (ATP11A, Accession XM_085028). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP11A. B-cell CLL/lymphoma 2 (BCL2, Accession NM_000633) is another VGAM2379 host target gene. BCL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL2 BINDING SITE, designated SEQ ID:6263, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80917] Another function of VGAM2379 is therefore inhibition of B-cell CLL/lymphoma 2 (BCL2, Accession NM_000633). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL2. Chemokine (C-X-C motif) Ligand 16 (CXCL16, Accession NM_022059) is another VGAM2379 host target gene. CXCL16 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by CXCL16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CXCL16 BINDING SITE, designated SEQ ID:22601, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80918] Another function of VGAM2379 is therefore inhibition of Chemokine (C-X-C motif) Ligand 16 (CXCL16, Accession NM_022059), a gene which induces calcium mobilization. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCL16. The function of CXCL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1845.E2F Transcription Factor 3 (E2F3, Accession NM_001949) is another VGAM2379 host target gene. E2F3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by E2F3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of E2F3 BINDING

SITE, designated SEQ ID:7671, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80919] Another function of VGAM2379 is therefore inhibition of E2F Transcription Factor 3 (E2F3, Accession NM_001949), a gene which binds dna and controls cell-cycle progression from g1 to s phase. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with E2F3. The function of E2F3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM475.Frizzled Homolog 4 (Drosophila) (FZD4, Accession NM_012193) is another VGAM2379 host target gene. FZD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FZD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FZD4 BINDING SITE, designated SEQ ID:14488, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80920] Another function of VGAM2379 is therefore inhibition of

Frizzled Homolog 4 (Drosophila) (FZD4, Accession NM_012193), a gene which may function in cell polarity, cell fate specification and cancer; similar to frizzled receptor family, has seven transmembrane domains. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FZD4. The function of FZD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM309.5-hydroxytryptamine (serotonin) Receptor 4 (HTR4, Accession NM_000870) is another VGAM2379 host target gene. HTR4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HTR4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HTR4 BINDING SITE, designated SEQ ID:6545, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80921] Another function of VGAM2379 is therefore inhibition of 5-hydroxytryptamine (serotonin) Receptor 4 (HTR4, Accession NM_000870), a gene which mediates calcium

channel currents. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTR4. The function of HTR4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM65.Integrin, Alpha 6 (ITGA6, Accession NM_000210) is another VGAM2379 host target gene. ITGA6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA6 BINDING SITE, designated SEQ ID:5704, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80922] Another function of VGAM2379 is therefore inhibition of Integrin, Alpha 6 (ITGA6, Accession NM_000210). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA6. Microtubule-associated Protein 2 (MAP2, Accession NM_031846) is another VGAM2379 host target gene. MAP2 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by MAP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP2 BINDING SITE, designated SEQ ID:25582, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80923] Another function of VGAM2379 is therefore inhibition of Microtubule-associated Protein 2 (MAP2, Accession NM_031846), a gene which may act in stabilizing microtubules against depolymerization.also seems to have a stiffening effect on microtubules. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP2. The function of MAP2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.C-myc Binding Protein (MYCBP, Accession NM_012333) is another VGAM2379 host target gene. MYCBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYCBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of MYCBP BINDING SITE, designated SEQ ID:14727, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80924] Another function of VGAM2379 is therefore inhibition of C-myc Binding Protein (MYCBP, Accession NM_012333), a gene which binds c-Myc stimulating the activation of E-box-dependent transcription. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYCBP. The function of MYCBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM435.RNA Guanylyltransferase and 5'-phosphatase (RNGTT, Accession NM_003800) is another VGAM2379 host target gene. RNGTT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNGTT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNGTT BINDING SITE, designated SEQ ID:9897, to the nucleotide sequence of

VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80925] Another function of VGAM2379 is therefore inhibition of RNA Guanylyltransferase and 5'-phosphatase (RNGTT, Accession NM_003800), a gene which is an MRNA capping enzyme; bifunctional enzyme containing both 5'-triphosphatase and mRNA guanylyltransferase activity. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNGTT. The function of RNGTT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM292.Splicing Factor, Arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1, Accession NM_006924) is another VGAM2379 host target gene. SFRS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFRS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRS1 BINDING SITE, designated SEQ ID:13802, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5090.

[80926] Another function of VGAM2379 is therefore inhibition of Splicing Factor, Arginine/serine-rich 1 (splicing factor 2, alternate splicing factor) (SFRS1, Accession NM_006924), a gene which plays an essential role in pre-mRNA splicing. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRS1. The function of SFRS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM323.Solute Carrier Family 17 (sodium phosphate), Member 4 (SLC17A4, Accession NM_005495) is another VGAM2379 host target gene. SLC17A4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC17A4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC17A4 BINDING SITE, designated SEQ ID:12000, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80927] Another function of VGAM2379 is therefore inhibition of

Solute Carrier Family 17 (sodium phosphate), Member 4 (SLC17A4, Accession NM_005495). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC17A4. Solute Carrier Family 21 (organic anion transporter), Member 3 (SLC21A3, Accession NM_134431) is another VGAM2379 host target gene. SLC21A3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC21A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC21A3 BINDING SITE, designated SEQ ID:28674, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80928] Another function of VGAM2379 is therefore inhibition of Solute Carrier Family 21 (organic anion transporter), Member 3 (SLC21A3, Accession NM_134431), a gene which mediates the na(+)-independent transport of organic anions such as bsp and conjugated (taurocholate) and unconjugated (cholate) bile acids. Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with SLC21A3. The function of SLC21A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1965.SRY (sex determining region Y)-box 13 (SOX13, Accession NM_005686) is another VGAM2379 host target gene. SOX13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX13 BINDING SITE, designated SEQ ID:12245, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80929] Another function of VGAM2379 is therefore inhibition of SRY (sex determining region Y)-box 13 (SOX13, Accession NM_005686). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX13. Adaptor-related Protein Complex 4, Sigma 1 Subunit (AP4S1, Accession NM_007077) is another VGAM2379 host target gene. AP4S1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AP4S1,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AP4S1 BINDING SITE, designated SEQ ID:13943, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80930] Another function of VGAM2379 is therefore inhibition of Adaptor-related Protein Complex 4, Sigma 1 Subunit (AP4S1, Accession NM_007077). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AP4S1. Chromosome 5 Open Reading Frame 5 (C5orf5, Accession NM_016603) is another VGAM2379 host target gene. C5orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C5orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5orf5 BINDING SITE, designated SEQ ID:18697, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80931] Another function of VGAM2379 is therefore inhibition of Chromosome 5 Open Reading Frame 5 (C5orf5, Accession NM_016603). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf5. CGG Triplet Repeat Binding Protein 1 (CGGBP1, Accession NM_003663) is another VGAM2379 host target gene. CGGBP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CGGBP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CGGBP1 BINDING SITE, designated SEQ ID:9741, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80932] Another function of VGAM2379 is therefore inhibition of CGG Triplet Repeat Binding Protein 1 (CGGBP1, Accession NM_003663). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CGGBP1. CMG2 (Accession NM_058172) is another VGAM2379 host target gene. CMG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CMG2,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CMG2 BINDING SITE, designated SEQ ID:27718, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80933] Another function of VGAM2379 is therefore inhibition of CMG2 (Accession NM_058172). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CMG2. DKFZP727C091 (Accession XM_038689) is another VGAM2379 host target gene. DKFZP727C091 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP727C091, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP727C091 BINDING SITE, designated SEQ ID:32904, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80934] Another function of VGAM2379 is therefore inhibition of

DKFZP727C091 (Accession XM_038689). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP727C091. ELKS (Accession NM_015064) is another VGAM2379 host target gene. ELKS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ELKS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ELKS BINDING SITE, designated SEQ ID:17420, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80935] Another function of VGAM2379 is therefore inhibition of ELKS (Accession NM_015064). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ELKS. KIAA0179 (Accession XM_035973) is another VGAM2379 host target gene. KIAA0179 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0179, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of KIAA0179 BINDING SITE, designated SEQ ID:32367, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80936] Another function of VGAM2379 is therefore inhibition of KIAA0179 (Accession XM_035973). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0179. KIAA0265 (Accession XM_045954) is another VGAM2379 host target gene. KIAA0265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0265 BINDING SITE, designated SEQ ID:34629, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80937] Another function of VGAM2379 is therefore inhibition of KIAA0265 (Accession XM_045954). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0265. KIAA0323 (Accession XM_032634) is another

VGAM2379 host target gene. KIAA0323 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0323 BINDING SITE, designated SEQ ID:31697, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80938] Another function of VGAM2379 is therefore inhibition of KIAA0323 (Accession XM_032634). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0323. KIAA0352 (Accession NM_014830) is another VGAM2379 host target gene. KIAA0352 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0352, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0352 BINDING SITE, designated SEQ ID:16824, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80939] Another function of VGAM2379 is therefore inhibition of KIAA0352 (Accession NM_014830). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0352. KIAA1163 (Accession XM_086231) is another VGAM2379 host target gene. KIAA1163 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1163, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1163 BINDING SITE, designated SEQ ID:38557, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80940] Another function of VGAM2379 is therefore inhibition of KIAA1163 (Accession XM_086231). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1163. MGC20235 (Accession NM_145041) is another VGAM2379 host target gene. MGC20235 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC20235, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC20235 BINDING SITE, designated SEQ ID:29670, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80941] Another function of VGAM2379 is therefore inhibition of MGC20235 (Accession NM_145041). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC20235. MGC4677 (Accession NM_052871) is another VGAM2379 host target gene. MGC4677 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC4677, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4677 BINDING SITE, designated SEQ ID:27451, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80942] Another function of VGAM2379 is therefore inhibition of MGC4677 (Accession NM_052871). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC4677. NECL1 (Accession NM_021189) is another VGAM2379 host target gene. NECL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NECL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NECL1 BINDING SITE, designated SEQ ID:22166, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80943] Another function of VGAM2379 is therefore inhibition of NECL1 (Accession NM_021189). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NECL1. Placenta-specific 3 (PLAC3, Accession XM_045115) is another VGAM2379 host target gene. PLAC3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PLAC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLAC3 BINDING SITE, designated SEQ ID:34368, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA,

also designated SEQ ID:5090.

[80944] Another function of VGAM2379 is therefore inhibition of Placenta-specific 3 (PLAC3, Accession XM_045115). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLAC3. LOC149603 (Accession XM_047499) is another VGAM2379 host target gene. LOC149603 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149603, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149603 BINDING SITE, designated SEQ ID:34972, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80945] Another function of VGAM2379 is therefore inhibition of LOC149603 (Accession XM_047499). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149603. LOC152445 (Accession XM_098231) is another VGAM2379 host target gene. LOC152445 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC152445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152445 BINDING SITE, designated SEQ ID:41511, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80946] Another function of VGAM2379 is therefore inhibition of LOC152445 (Accession XM_098231). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152445. LOC199992 (Accession XM_114082) is another VGAM2379 host target gene. LOC199992 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC199992, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199992 BINDING SITE, designated SEQ ID:42678, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80947] Another function of VGAM2379 is therefore inhibition of LOC199992 (Accession XM_114082). Accordingly, utilities

of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199992. LOC90462 (Accession XM_031852) is another VGAM2379 host target gene. LOC90462 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90462, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90462 BINDING SITE, designated SEQ ID:31504, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80948] Another function of VGAM2379 is therefore inhibition of LOC90462 (Accession XM_031852). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90462. LOC91496 (Accession XM_038788) is another VGAM2379 host target gene. LOC91496 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91496, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC91496 BINDING SITE, designated SEQ ID:32916, to the nucleotide sequence of VGAM2379 RNA, herein designated VGAM RNA, also designated SEQ ID:5090.

[80949] Another function of VGAM2379 is therefore inhibition of LOC91496 (Accession XM_038788). Accordingly, utilities of VGAM2379 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91496. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2380 (VGAM2380) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80950] VGAM2380 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2380 was detected is described hereinabove with reference to Figs. 1-8.

[80951] VGAM2380 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 4. VGAM2380 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80952] VGAM2380 gene encodes a VGAM2380 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2380 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2380 precursor RNA is designated SEQ ID:2366, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2366 is located at position 7588 relative to the genome of Human Herpesvirus 4.

[80953] VGAM2380 precursor RNA folds onto itself, forming VGAM2380 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80954] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2380 folded precursor RNA into VGAM2380 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 91%) nucleotide sequence of VGAM2380 RNA is designated SEQ ID:5091, and is provided hereinbelow with reference to the sequence listing part.

[80955] VGAM2380 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2380 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2380 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80956] VGAM2380 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2380 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2380 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2380 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2380 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80957] The complementary binding of VGAM2380 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2380 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2380 host target RNA into VGAM2380 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80958] It is appreciated that VGAM2380 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2380 host target genes. The mRNA of each one of this plurality of VGAM2380 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2380 RNA, herein designated VGAM RNA, and which when bound by VGAM2380 RNA causes inhibition of translation of respective one or more VGAM2380 host target proteins.

[80959] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2380 gene, herein designated VGAM GENE, on one or more VGAM2380 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80960] It is yet further appreciated that a function of VGAM2380 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2380 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2380 correlate with, and may be deduced from, the identity of the host target genes which VGAM2380 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80961] Nucleotide sequences of the VGAM2380 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2380 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2380 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2380 are further described hereinbelow with reference to Table 1.

[80962] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2380 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2380 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80963] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2380 gene, herein designated VGAM is inhibition of expression of VGAM2380 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2380 correlate with, and may be deduced from, the identity of the target genes which VGAM2380 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80964] Dual-specificity tyrosine-(Y)-phosphorylation Regulated Kinase 2 (DYRK2, Accession NM_003583) is a VGAM2380 host target gene. DYRK2 BINDING SITE1 and DYRK2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DYRK2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DYRK2 BINDING SITE1 and DYRK2 BINDING SITE2, designated SEQ ID:9630 and SEQ ID:13206 respectively, to the nucleotide sequence of VGAM2380 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5091.

[80965] A function of VGAM2380 is therefore inhibition of Dual-specificity tyrosine-(Y)-phosphorylation Regulated Kinase 2 (DYRK2, Accession NM_003583). Accordingly, utilities of VGAM2380 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DYRK2. MGC29891 (Accession NM_144618) is another VGAM2380 host target gene. MGC29891 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC29891, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC29891 BINDING SITE, designated SEQ ID:29439, to the nucleotide sequence of VGAM2380 RNA, herein designated VGAM RNA, also designated SEQ ID:5091.

[80966] Another function of VGAM2380 is therefore inhibition of MGC29891 (Accession NM_144618). Accordingly, utilities of VGAM2380 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29891. PRO1163 (Accession NM_018576) is another VGAM2380 host target gene. PRO1163 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by PRO1163, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1163 BINDING SITE, designated SEQ ID:20654, to the nucleotide sequence of VGAM2380 RNA, herein designated VGAM RNA, also designated SEQ ID:5091.

[80967] Another function of VGAM2380 is therefore inhibition of PRO1163 (Accession NM_018576). Accordingly, utilities of VGAM2380 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1163. Zinc Finger Protein 294 (ZNF294, Accession XM_047829) is another VGAM2380 host target gene. ZNF294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF294 BINDING SITE, designated SEQ ID:35056, to the nucleotide sequence of VGAM2380 RNA, herein designated VGAM RNA, also designated SEQ ID:5091.

[80968] Another function of VGAM2380 is therefore inhibition of

Zinc Finger Protein 294 (ZNF294, Accession XM_047829). Accordingly, utilities of VGAM2380 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF294. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2381 (VGAM2381) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80969] VGAM2381 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2381 was detected is described hereinabove with reference to Figs. 1-8.

[80970] VGAM2381 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 4. VGAM2381 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80971] VGAM2381 gene encodes a VGAM2381 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2381 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2381 precursor RNA is designated SEQ ID:2367, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2367 is located at position 48597 relative to the genome of Human Herpesvirus 4.

[80972] VGAM2381 precursor RNA folds onto itself, forming VGAM2381 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80973] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2381 folded precursor RNA into VGAM2381 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 69%) nucleotide se-

quence of VGAM2381 RNA is designated SEQ ID:5092, and is provided hereinbelow with reference to the sequence listing part.

[80974] VGAM2381 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2381 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2381 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80975] VGAM2381 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2381 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2381 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2381 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2381 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80976] The complementary binding of VGAM2381 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2381 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2381 host target RNA into VGAM2381 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80977] It is appreciated that VGAM2381 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2381 host target genes. The mRNA of each one of this plurality of VGAM2381 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2381 RNA, herein designated VGAM RNA, and which when bound by VGAM2381 RNA causes inhibition of translation of respective one or more VGAM2381 host target proteins.

[80978] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2381 gene, herein designated VGAM GENE, on one or more VGAM2381 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80979] It is yet further appreciated that a function of VGAM2381

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2381 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2381 correlate with, and may be deduced from, the identity of the host target genes which VGAM2381 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80980] Nucleotide sequences of the VGAM2381 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2381 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2381 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2381 are further described hereinbelow with reference to Table 1.

[80981] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2381 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2381 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[80982] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2381 gene, herein designated VGAM is inhibition of expression of VGAM2381 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2381 correlate with, and may be deduced from, the identity of the target genes which VGAM2381 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[80983] Cadherin, EGF LAG Seven-pass G-type Receptor 1 (flamingo homolog, Drosophila) (CELSR1, Accession NM_014246) is a VGAM2381 host target gene. CELSR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CELSR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CELSR1 BINDING SITE, designated SEQ ID:15520, to the nucleotide sequence of VGAM2381 RNA, herein designated VGAM RNA, also designated SEQ ID:5092.

[80984] A function of VGAM2381 is therefore inhibition of Cadherin, EGF LAG Seven-pass G-type Receptor 1 (flamingo homolog, Drosophila) (CELSR1, Accession NM_014246), a gene which is involved in contact-mediated communica-

tion. Accordingly, utilities of VGAM2381 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CELSR1. The function of CELSR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM459.FLJ10815 (Accession NM_018231) is another VGAM2381 host target gene. FLJ10815 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10815, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10815 BINDING SITE, designated SEQ ID:20170, to the nucleotide sequence of VGAM2381 RNA, herein designated VGAM RNA, also designated SEQ ID:5092.

[80985] Another function of VGAM2381 is therefore inhibition of FLJ10815 (Accession NM_018231). Accordingly, utilities of VGAM2381 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10815. FLJ21290 (Accession NM_025034) is another VGAM2381 host target gene. FLJ21290 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ21290, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21290 BINDING SITE, designated SEQ ID:24632, to the nucleotide sequence of VGAM2381 RNA, herein designated VGAM RNA, also designated SEQ ID:5092.

[80986] Another function of VGAM2381 is therefore inhibition of FLJ21290 (Accession NM_025034). Accordingly, utilities of VGAM2381 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21290. LOC122830 (Accession XM_058661) is another VGAM2381 host target gene. LOC122830 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC122830, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122830 BINDING SITE, designated SEQ ID:36702, to the nucleotide sequence of VGAM2381 RNA, herein designated VGAM RNA, also designated SEQ ID:5092.

[80987] Another function of VGAM2381 is therefore inhibition of LOC122830 (Accession XM_058661). Accordingly, utilities

of VGAM2381 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122830. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2382 (VGAM2382) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[80988] VGAM2382 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2382 was detected is described hereinabove with reference to Figs. 1-8.

[80989] VGAM2382 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 4. VGAM2382 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[80990] VGAM2382 gene encodes a VGAM2382 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2382 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2382 precursor RNA is designated SEQ ID:2368, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2368 is located at position 54739 relative to the genome of Human Herpesvirus 4.

[80991] VGAM2382 precursor RNA folds onto itself, forming VGAM2382 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[80992] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2382 folded precursor RNA into VGAM2382 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2382 RNA is designated SEQ ID:5093, and

is provided hereinbelow with reference to the sequence listing part.

[80993] VGAM2382 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2382 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2382 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[80994] VGAM2382 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2382 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2382 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2382 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2382 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[80995] The complementary binding of VGAM2382 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2382 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2382 host target RNA into VGAM2382 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[80996] It is appreciated that VGAM2382 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2382 host target genes. The mRNA of each one of this plurality of VGAM2382 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2382 RNA, herein designated VGAM RNA, and which when bound by VGAM2382 RNA causes inhibition of translation of respective one or more VGAM2382 host target proteins.

[80997] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2382 gene, herein designated VGAM GENE, on one or more VGAM2382 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[80998] It is yet further appreciated that a function of VGAM2382 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2382 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2382 correlate with, and may be deduced from, the identity of the host target genes which VGAM2382 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[80999] Nucleotide sequences of the VGAM2382 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2382 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2382 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2382 are further described hereinbelow with reference to Table 1.

[81000] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2382 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2382 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81001] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2382 gene, herein designated VGAM is inhibition of expression of VGAM2382 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2382 correlate with, and may be deduced from, the identity of the target genes which VGAM2382 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81002] Paired Mesoderm Homeo Box 1 (PMX1, Accession NM_006902) is a VGAM2382 host target gene. PMX1 BINDING SITE1 and PMX1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PMX1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMX1 BINDING SITE1 and PMX1 BINDING SITE2, designated SEQ ID:13780 and SEQ ID:22915 respectively, to the nucleotide sequence of VGAM2382 RNA, herein designated VGAM RNA, also designated SEQ ID:5093.

[81003] A function of VGAM2382 is therefore inhibition of Paired Mesoderm Homeo Box 1 (PMX1, Accession NM_006902), a gene which acts as a transcriptional regulator of muscle creatine kinase. Accordingly, utilities of VGAM2382 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with PMX1. The function of PMX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2383 (VGAM2383) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81004] VGAM2383 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2383 was detected is described hereinabove with reference to Figs. 1-8.

[81005] VGAM2383 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 4. VGAM2383 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81006] VGAM2383 gene encodes a VGAM2383 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2383 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2383 precursor RNA is designated SEQ ID:2369, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2369 is located at position 53736 relative to the genome of Human Herpesvirus 4.

[81007] VGAM2383 precursor RNA folds onto itself, forming VGAM2383 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81008] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2383 folded precursor RNA into VGAM2383 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2383 RNA is designated SEQ ID:5094, and is provided hereinbelow with reference to the sequence listing part.

[81009] VGAM2383 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2383 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2383 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81010] VGAM2383 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2383 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2383 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2383 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2383 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81011] The complementary binding of VGAM2383 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2383 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2383 host target RNA into VGAM2383 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81012] It is appreciated that VGAM2383 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2383 host target genes. The mRNA of each one of this plurality of VGAM2383 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2383 RNA, herein designated VGAM RNA, and which when bound by VGAM2383 RNA causes inhibition of translation of respective one or more VGAM2383 host target proteins.

[81013] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2383 gene, herein designated VGAM GENE, on one or more VGAM2383 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81014] It is yet further appreciated that a function of VGAM2383 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2383 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2383 correlate with, and may be deduced from, the identity of the host target genes which VGAM2383 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81015] Nucleotide sequences of the VGAM2383 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2383 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2383 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2383 are further described hereinbelow with reference to Table 1.

[81016] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2383 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2383 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[81017] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2383 gene, herein designated VGAM is inhibition of expression of VGAM2383 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2383 correlate with, and may be deduced from, the identity of the target genes which VGAM2383 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81018] Fucosyltransferase 8 (alpha (1,6) Fucosyltransferase) (FUT8, Accession NM_004480) is a VGAM2383 host target gene. FUT8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FUT8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FUT8 BINDING SITE, designated SEQ ID:10794, to the nucleotide sequence of VGAM2383 RNA, herein designated VGAM RNA, also designated SEQ ID:5094.

[81019] A function of VGAM2383 is therefore inhibition of Fucosyltransferase 8 (alpha (1,6) Fucosyltransferase) (FUT8, Accession NM_004480), a gene which transfers fucose to N-linked type complex glycopeptides from GDP-Fuc;

functions in asparagine-linked glycoprotein oligosaccharide synthesis. Accordingly, utilities of VGAM2383 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FUT8. The function of FUT8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM64.Leucine-zipper-like Transcriptional Regulator, 1 (LZTR1, Accession NM_006767) is another VGAM2383 host target gene. LZTR1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LZTR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LZTR1 BINDING SITE, designated SEQ ID:13634, to the nucleotide sequence of VGAM2383 RNA, herein designated VGAM RNA, also designated SEQ ID:5094.

[81020] Another function of VGAM2383 is therefore inhibition of Leucine-zipper-like Transcriptional Regulator, 1 (LZTR1, Accession NM_006767). Accordingly, utilities of VGAM2383 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LZTR1.

DKFZP434L187 (Accession XM_044070) is another VGAM2383 host target gene. DKFZP434L187 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434L187, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434L187 BINDING SITE, designated SEQ ID:34116, to the nucleotide sequence of VGAM2383 RNA, herein designated VGAM RNA, also designated SEQ ID:5094.

[81021] Another function of VGAM2383 is therefore inhibition of DKFZP434L187 (Accession XM_044070). Accordingly, utilities of VGAM2383 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434L187. FLJ13881 (Accession NM_024729) is another VGAM2383 host target gene. FLJ13881 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13881, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13881 BINDING SITE, designated SEQ ID:24069, to the

nucleotide sequence of VGAM2383 RNA, herein designated VGAM RNA, also designated SEQ ID:5094.

[81022] Another function of VGAM2383 is therefore inhibition of FLJ13881 (Accession NM_024729). Accordingly, utilities of VGAM2383 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13881. KIAA0971 (Accession NM_014929) is another VGAM2383 host target gene. KIAA0971 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0971, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0971 BINDING SITE, designated SEQ ID:17223, to the nucleotide sequence of VGAM2383 RNA, herein designated VGAM RNA, also designated SEQ ID:5094.

[81023] Another function of VGAM2383 is therefore inhibition of KIAA0971 (Accession NM_014929). Accordingly, utilities of VGAM2383 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0971. RNA Binding Motif Protein 7 (RBM7, Accession NM_016090) is another VGAM2383 host target gene. RBM7 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by RBM7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBM7 BINDING SITE, designated SEQ ID:18177, to the nucleotide sequence of VGAM2383 RNA, herein designated VGAM RNA, also designated SEQ ID:5094.

[81024] Another function of VGAM2383 is therefore inhibition of RNA Binding Motif Protein 7 (RBM7, Accession NM_016090). Accordingly, utilities of VGAM2383 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBM7. LOC151277 (Accession XM_087155) is another VGAM2383 host target gene. LOC151277 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151277, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151277 BINDING SITE, designated SEQ ID:39093, to the nucleotide sequence of VGAM2383 RNA, herein designated VGAM RNA, also designated SEQ ID:5094.

[81025] Another function of VGAM2383 is therefore inhibition of

LOC151277 (Accession XM_087155). Accordingly, utilities of VGAM2383 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151277. LOC159199 (Accession XM_089441) is another VGAM2383 host target gene. LOC159199 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC159199, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159199 BINDING SITE, designated SEQ ID:39977, to the nucleotide sequence of VGAM2383 RNA, herein designated VGAM RNA, also designated SEQ ID:5094.

[81026] Another function of VGAM2383 is therefore inhibition of LOC159199 (Accession XM_089441). Accordingly, utilities of VGAM2383 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159199. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2384 (VGAM2384) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[81027] VGAM2384 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2384 was detected is described hereinabove with reference to Figs. 1-8.

[81028] VGAM2384 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 4. VGAM2384 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81029] VGAM2384 gene encodes a VGAM2384 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2384 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2384 precursor RNA is designated SEQ ID:2370, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2370 is located at position 5198 relative to the genome of Human Herpesvirus 4.

[81030] VGAM2384 precursor RNA folds onto itself, forming VGAM2384 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81031] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2384 folded precursor RNA into VGAM2384 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2384 RNA is designated SEQ ID:5095, and is provided hereinbelow with reference to the sequence listing part.

[81032] VGAM2384 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2384 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2384 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81033] VGAM2384 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2384 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2384 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2384 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2384 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[81034] The complementary binding of VGAM2384 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2384 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2384 host target RNA into VGAM2384 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81035] It is appreciated that VGAM2384 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2384 host target genes. The mRNA of each one of this plurality of VGAM2384 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2384 RNA, herein designated VGAM RNA, and which when bound by VGAM2384 RNA causes inhibition of translation of respective one or more VGAM2384 host target proteins.

[81036] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2384 gene, herein designated VGAM GENE, on one

or more VGAM2384 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81037] It is yet further appreciated that a function of VGAM2384 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2384 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2384 correlate with, and may be deduced from, the identity of the host target genes which VGAM2384 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81038] Nucleotide sequences of the VGAM2384 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2384 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2384 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2384 are further described hereinbelow with reference to Table 1.

[81039] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2384 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2384 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81040] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2384 gene, herein designated VGAM is inhibition of expression of VGAM2384 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2384 correlate with, and may be deduced from, the identity of the target genes which VGAM2384 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81041] WNT1 Inducible Signaling Pathway Protein 1 (WISP1, Ac-

cession NM_003882) is a VGAM2384 host target gene. WISP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WISP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WISP1 BINDING SITE, designated SEQ ID:9963, to the nucleotide sequence of VGAM2384 RNA, herein designated VGAM RNA, also designated SEQ ID:5095.

[81042] A function of VGAM2384 is therefore inhibition of WNT1 Inducible Signaling Pathway Protein 1 (WISP1, Accession NM_003882), a gene which is a member of connective tissue growth factor family. Accordingly, utilities of VGAM2384 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WISP1. The function of WISP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1656.Chromosome 20 Open Reading Frame 121 (C20orf121, Accession NM_024331) is another VGAM2384 host target gene. C20orf121 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C20orf121, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf121 BINDING SITE, designated SEQ ID:23633, to the nucleotide sequence of VGAM2384 RNA, herein designated VGAM RNA, also designated SEQ ID:5095.

[81043] Another function of VGAM2384 is therefore inhibition of Chromosome 20 Open Reading Frame 121 (C20orf121, Accession NM_024331). Accordingly, utilities of VGAM2384 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf121. KIAA0763 (Accession NM_014869) is another VGAM2384 host target gene. KIAA0763 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0763, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0763 BINDING SITE, designated SEQ ID:16969, to the nucleotide sequence of VGAM2384 RNA, herein designated VGAM RNA, also designated SEQ ID:5095.

[81044] Another function of VGAM2384 is therefore inhibition of KIAA0763 (Accession NM_014869). Accordingly, utilities

of VGAM2384 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0763. KIAA0820 (Accession XM_044463) is another VGAM2384 host target gene. KIAA0820 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0820, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0820 BINDING SITE, designated SEQ ID:34222, to the nucleotide sequence of VGAM2384 RNA, herein designated VGAM RNA, also designated SEQ ID:5095.

[81045] Another function of VGAM2384 is therefore inhibition of KIAA0820 (Accession XM_044463). Accordingly, utilities of VGAM2384 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0820. Seizure Related 6 Homolog (mouse) (SEZ6, Accession XM_058869) is another VGAM2384 host target gene. SEZ6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SEZ6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of SEZ6 BINDING SITE, designated SEQ ID:36775, to the nucleotide sequence of VGAM2384 RNA, herein designated VGAM RNA, also designated SEQ ID:5095.

[81046] Another function of VGAM2384 is therefore inhibition of Seizure Related 6 Homolog (mouse) (SEZ6, Accession XM_058869). Accordingly, utilities of VGAM2384 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEZ6. LOC152359 (Accession XM_098213) is another VGAM2384 host target gene. LOC152359 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152359, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152359 BINDING SITE, designated SEQ ID:41494, to the nucleotide sequence of VGAM2384 RNA, herein designated VGAM RNA, also designated SEQ ID:5095.

[81047] Another function of VGAM2384 is therefore inhibition of LOC152359 (Accession XM_098213). Accordingly, utilities of VGAM2384 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152359. LOC161829 (Accession XM_091161) is an-

other VGAM2384 host target gene. LOC161829 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC161829, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161829 BINDING SITE, designated SEQ ID:40038, to the nucleotide sequence of VGAM2384 RNA, herein designated VGAM RNA, also designated SEQ ID:5095.

[81048] Another function of VGAM2384 is therefore inhibition of LOC161829 (Accession XM_091161). Accordingly, utilities of VGAM2384 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161829. LOC220739 (Accession XM_167548) is another VGAM2384 host target gene. LOC220739 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220739, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220739 BINDING SITE, designated SEQ ID:44658, to the nucleotide sequence of VGAM2384 RNA, herein designated VGAM RNA, also designated SEQ ID:5095.

[81049] Another function of VGAM2384 is therefore inhibition of LOC220739 (Accession XM_167548). Accordingly, utilities of VGAM2384 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220739. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2385 (VGAM2385) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81050] VGAM2385 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2385 was detected is described hereinabove with reference to Figs. 1-8.

[81051] VGAM2385 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 4. VGAM2385 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81052] VGAM2385 gene encodes a VGAM2385 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2385 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2385 precursor RNA is designated SEQ ID:2371, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2371 is located at position 7899 relative to the genome of Human Herpesvirus 4.

[81053] VGAM2385 precursor RNA folds onto itself, forming VGAM2385 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81054] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2385 folded precursor RNA into VGAM2385 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 90%) nucleotide sequence of VGAM2385 RNA is designated SEQ ID:5096, and is provided hereinbelow with reference to the sequence listing part.

[81055] VGAM2385 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2385 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2385 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81056] VGAM2385 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2385 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2385 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2385 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2385 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81057] The complementary binding of VGAM2385 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2385 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2385 host target RNA into VGAM2385 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81058] It is appreciated that VGAM2385 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2385 host target genes. The mRNA of each one of this plurality of VGAM2385 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2385 RNA, herein designated VGAM RNA, and which when bound by VGAM2385 RNA causes inhibition of translation of respective one or more VGAM2385 host target proteins.

[81059] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2385 gene, herein designated VGAM GENE, on one or more VGAM2385 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81060] It is yet further appreciated that a function of VGAM2385 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2385 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2385 correlate with, and may be deduced from, the identity of the host target genes which VGAM2385 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81061] Nucleotide sequences of the VGAM2385 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2385 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2385 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2385 are further described hereinbelow with reference to Table 1.

[81062] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2385 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2385 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[81063] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2385 gene, herein designated VGAM is inhibition of expression of VGAM2385 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2385 correlate with, and may be deduced from, the identity of the target genes which VGAM2385 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81064] Dual-specificity tyrosine-(Y)-phosphorylation Regulated Kinase 2 (DYRK2, Accession NM_003583) is a VGAM2385 host target gene. DYRK2 BINDING SITE1 and DYRK2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DYRK2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DYRK2 BINDING SITE1 and DYRK2 BINDING SITE2, designated SEQ ID:9630 and SEQ ID:13206 respectively, to the nucleotide sequence of VGAM2385 RNA, herein designated VGAM RNA, also designated SEQ ID:5096.

[81065] A function of VGAM2385 is therefore inhibition of Dual-specificity tyrosine-(Y)-phosphorylation Regulated Kinase

2 (DYRK2, Accession NM_003583). Accordingly, utilities of VGAM2385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DYRK2. MGC29891 (Accession NM_144618) is another VGAM2385 host target gene. MGC29891 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC29891, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC29891 BINDING SITE, designated SEQ ID:29439, to the nucleotide sequence of VGAM2385 RNA, herein designated VGAM RNA, also designated SEQ ID:5096.

[81066] Another function of VGAM2385 is therefore inhibition of MGC29891 (Accession NM_144618). Accordingly, utilities of VGAM2385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC29891. PRO1163 (Accession NM_018576) is another VGAM2385 host target gene. PRO1163 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1163, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PRO1163 BINDING SITE, designated SEQ ID:20654, to the nucleotide sequence of VGAM2385 RNA, herein designated VGAM RNA, also designated SEQ ID:5096.

[81067] Another function of VGAM2385 is therefore inhibition of PRO1163 (Accession NM_018576). Accordingly, utilities of VGAM2385 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1163. Zinc Finger Protein 294 (ZNF294, Accession XM_047829) is another VGAM2385 host target gene. ZNF294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF294 BINDING SITE, designated SEQ ID:35056, to the nucleotide sequence of VGAM2385 RNA, herein designated VGAM RNA, also designated SEQ ID:5096.

[81068] Another function of VGAM2385 is therefore inhibition of Zinc Finger Protein 294 (ZNF294, Accession XM_047829). Accordingly, utilities of VGAM2385 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with ZNF294. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2386 (VGAM2386) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81069] VGAM2386 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2386 was detected is described hereinabove with reference to Figs. 1-8.

[81070] VGAM2386 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 4. VGAM2386 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81071] VGAM2386 gene encodes a VGAM2386 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2386 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2386 precursor RNA is designated SEQ ID:2372, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2372 is located at position 6848 relative to the genome of Human Herpesvirus 4.

[81072] VGAM2386 precursor RNA folds onto itself, forming VGAM2386 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81073] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2386 folded precursor RNA into VGAM2386 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2386 RNA is designated SEQ ID:5097, and is provided hereinbelow with reference to the sequence listing part.

[81074] VGAM2386 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2386 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2386 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81075] VGAM2386 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2386 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2386 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2386 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2386 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81076] The complementary binding of VGAM2386 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2386 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2386 host target RNA into VGAM2386 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81077] It is appreciated that VGAM2386 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2386 host target genes. The mRNA of each one of this plurality of VGAM2386 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2386 RNA, herein designated VGAM RNA, and which when bound by VGAM2386 RNA causes

inhibition of translation of respective one or more VGAM2386 host target proteins.

[81078] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2386 gene, herein designated VGAM GENE, on one or more VGAM2386 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81079] It is yet further appreciated that a function of VGAM2386 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2386 include diagnosis, prevention and

treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2386 correlate with, and may be deduced from, the identity of the host target genes which VGAM2386 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81080] Nucleotide sequences of the VGAM2386 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2386 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2386 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2386 are further described hereinbelow with reference to Table 1.

[81081] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2386 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2386 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81082] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2386 gene, herein designated VGAM is inhibition of expression of VGAM2386 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2386 correlate with, and may be deduced from, the identity of the target genes which VGAM2386 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81083] ARGBP2 (Accession NM_003603) is a VGAM2386 host target gene. ARGBP2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARGBP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARGBP2 BINDING SITE, designated SEQ ID:9657, to the nucleotide sequence of VGAM2386 RNA, herein designated VGAM RNA, also designated SEQ ID:5097.

[81084] A function of VGAM2386 is therefore inhibition of ARGBP2 (Accession NM_003603). Accordingly, utilities of VGAM2386 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARGBP2. FLJ00058 (Accession XM_086123) is another VGAM2386 host target gene. FLJ00058 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ00058, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00058 BINDING SITE, designated SEQ ID:38511, to the nucleotide sequence of VGAM2386 RNA, herein designated VGAM RNA, also designated SEQ ID:5097.

[81085] Another function of VGAM2386 is therefore inhibition of FLJ00058 (Accession XM_086123). Accordingly, utilities of VGAM2386 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00058. IL22R (Accession NM_021258) is another VGAM2386 host target gene. IL22R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL22R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL22R BINDING SITE, designated SEQ ID:22234, to the nucleotide sequence of VGAM2386 RNA, herein designated VGAM RNA, also designated SEQ ID:5097.

[81086] Another function of VGAM2386 is therefore inhibition of IL22R (Accession NM_021258). Accordingly, utilities of VGAM2386 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with IL22R. KIAA0748 (Accession NM_014796) is another VGAM2386 host target gene. KIAA0748 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0748, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0748 BINDING SITE, designated SEQ ID:16704, to the nucleotide sequence of VGAM2386 RNA, herein designated VGAM RNA, also designated SEQ ID:5097.

[81087] Another function of VGAM2386 is therefore inhibition of KIAA0748 (Accession NM_014796). Accordingly, utilities of VGAM2386 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0748. LOC147184 (Accession NM_145274) is another VGAM2386 host target gene. LOC147184 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147184, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147184 BINDING SITE, designated SEQ ID:29788, to

the nucleotide sequence of VGAM2386 RNA, herein designated VGAM RNA, also designated SEQ ID:5097.

[81088] Another function of VGAM2386 is therefore inhibition of LOC147184 (Accession NM_145274). Accordingly, utilities of VGAM2386 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147184. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2387 (VGAM2387) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81089] VGAM2387 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2387 was detected is described hereinabove with reference to Figs. 1-8.

[81090] VGAM2387 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 4. VGAM2387 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81091] VGAM2387 gene encodes a VGAM2387 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2387 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2387 precursor RNA is designated SEQ ID:2373, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2373 is located at position 7029 relative to the genome of Human Herpesvirus 4.

[81092] VGAM2387 precursor RNA folds onto itself, forming VGAM2387 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81093] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2387 folded precursor RNA into VGAM2387 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2387 RNA is designated SEQ ID:5098, and is provided hereinbelow with reference to the sequence listing part.

[81094] VGAM2387 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2387 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2387 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81095] VGAM2387 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2387 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2387 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2387 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2387 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81096] The complementary binding of VGAM2387 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2387 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2387 host target RNA into VGAM2387 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81097] It is appreciated that VGAM2387 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2387 host target genes. The mRNA of each one of this plurality of VGAM2387 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2387 RNA, herein designated VGAM RNA, and which when bound by VGAM2387 RNA causes inhibition of translation of respective one or more VGAM2387 host target proteins.

[81098] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2387 gene, herein designated VGAM GENE, on one or more VGAM2387 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81099] It is yet further appreciated that a function of VGAM2387 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2387 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2387 correlate with, and may be deduced from, the identity of the host target genes which VGAM2387 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81100] Nucleotide sequences of the VGAM2387 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2387 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2387 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2387 are further described hereinbelow with reference to Table 1.

[81101] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2387 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2387 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81102] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2387 gene, herein designated VGAM is inhibition of expression of VGAM2387 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2387 correlate with, and may be deduced from, the identity of the target genes which VGAM2387 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81103] ATPase, Ca++ Transporting, Ubiquitous (ATP2A3, Accession NM_005173) is a VGAM2387 host target gene. ATP2A3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP2A3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP2A3 BINDING SITE, designated SEQ ID:11673, to the nucleotide sequence of VGAM2387 RNA, herein designated VGAM RNA, also designated SEQ ID:5098.

[81104] A function of VGAM2387 is therefore inhibition of ATPase,

Ca++ Transporting, Ubiquitous (ATP2A3, Accession NM_005173). Accordingly, utilities of VGAM2387 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP2A3. Oculocerebrorenal Syndrome of Lowe (OCRL, Accession NM_000276) is another VGAM2387 host target gene. OCRL BINDING SITE1 and OCRL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by OCRL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OCRL BINDING SITE1 and OCRL BINDING SITE2, designated SEQ ID:5817 and SEQ ID:7304 respectively, to the nucleotide sequence of VGAM2387 RNA, herein designated VGAM RNA, also designated SEQ ID:5098.

[81105] Another function of VGAM2387 is therefore inhibition of Oculocerebrorenal Syndrome of Lowe (OCRL, Accession NM_000276). Accordingly, utilities of VGAM2387 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OCRL. Cdc42 Guanine Nucleotide Exchange Factor (GEF) 9 (ARHGEF9, Accession NM_015185) is another VGAM2387 host target gene. ARHGEF9 BINDING SITE is HOST TARGET binding site

found in the 5` untranslated region of mRNA encoded by ARHGEF9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGEF9 BINDING SITE, designated SEQ ID:17538, to the nucleotide sequence of VGAM2387 RNA, herein designated VGAM RNA, also designated SEQ ID:5098.

[81106] Another function of VGAM2387 is therefore inhibition of Cdc42 Guanine Nucleotide Exchange Factor (GEF) 9 (ARHGEF9, Accession NM_015185). Accordingly, utilities of VGAM2387 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF9. Nudix (nucleoside diphosphate linked moiety X)-type Motif 12 (NUDT12, Accession NM_031438) is another VGAM2387 host target gene. NUDT12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUDT12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUDT12 BINDING SITE, designated SEQ ID:25447, to the nucleotide sequence of VGAM2387 RNA, herein designated VGAM

RNA, also designated SEQ ID:5098.

[81107] Another function of VGAM2387 is therefore inhibition of Nudix (nucleoside diphosphate linked moiety X)-type Motif 12 (NUDT12, Accession NM_031438). Accordingly, utilities of VGAM2387 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUDT12. UBE3B (Accession XM_084941) is another VGAM2387 host target gene. UBE3B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UBE3B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UBE3B BINDING SITE, designated SEQ ID:37772, to the nucleotide sequence of VGAM2387 RNA, herein designated VGAM RNA, also designated SEQ ID:5098.

[81108] Another function of VGAM2387 is therefore inhibition of UBE3B (Accession XM_084941). Accordingly, utilities of VGAM2387 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UBE3B. LOC149506 (Accession XM_097661) is another VGAM2387 host target gene. LOC149506 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC149506, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149506 BINDING SITE, designated SEQ ID:41002, to the nucleotide sequence of VGAM2387 RNA, herein designated VGAM RNA, also designated SEQ ID:5098.

[81109] Another function of VGAM2387 is therefore inhibition of LOC149506 (Accession XM_097661). Accordingly, utilities of VGAM2387 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149506. LOC153711 (Accession XM_098419) is another VGAM2387 host target gene. LOC153711 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153711, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153711 BINDING SITE, designated SEQ ID:41666, to the nucleotide sequence of VGAM2387 RNA, herein designated VGAM RNA, also designated SEQ ID:5098.

[81110] Another function of VGAM2387 is therefore inhibition of LOC153711 (Accession XM_098419). Accordingly, utilities

of VGAM2387 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153711. LOC253912 (Accession XM_173222) is another VGAM2387 host target gene. LOC253912 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253912, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253912 BINDING SITE, designated SEQ ID:46483, to the nucleotide sequence of VGAM2387 RNA, herein designated VGAM RNA, also designated SEQ ID:5098.

[81111] Another function of VGAM2387 is therefore inhibition of LOC253912 (Accession XM_173222). Accordingly, utilities of VGAM2387 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253912. LOC255106 (Accession XM_170805) is another VGAM2387 host target gene. LOC255106 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255106, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC255106 BINDING SITE, designated SEQ ID:45570, to the nucleotide sequence of VGAM2387 RNA, herein designated VGAM RNA, also designated SEQ ID:5098.

[81112] Another function of VGAM2387 is therefore inhibition of LOC255106 (Accession XM_170805). Accordingly, utilities of VGAM2387 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255106. LOC90917 (Accession XM_034861) is another VGAM2387 host target gene. LOC90917 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90917, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90917 BINDING SITE, designated SEQ ID:32163, to the nucleotide sequence of VGAM2387 RNA, herein designated VGAM RNA, also designated SEQ ID:5098.

[81113] Another function of VGAM2387 is therefore inhibition of LOC90917 (Accession XM_034861). Accordingly, utilities of VGAM2387 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90917. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2388 (VGAM2388) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81114] VGAM2388 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2388 was detected is described hereinabove with reference to Figs. 1-8.

[81115] VGAM2388 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Human Herpesvirus 4. VGAM2388 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81116] VGAM2388 gene encodes a VGAM2388 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2388 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2388 precursor RNA is designated SEQ ID:2374, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2374 is located at position 55246 relative to the

genome of Human Herpesvirus 4.

[81117] VGAM2388 precursor RNA folds onto itself, forming VGAM2388 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81118] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2388 folded precursor RNA into VGAM2388 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2388 RNA is designated SEQ ID:5099, and is provided hereinbelow with reference to the sequence listing part.

[81119] VGAM2388 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2388 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2388 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81120] VGAM2388 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2388 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2388 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2388 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2388 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81121] The complementary binding of VGAM2388 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2388 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2388 host target RNA into VGAM2388 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81122] It is appreciated that VGAM2388 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2388 host target genes. The mRNA of each one of this plurality of VGAM2388 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2388 RNA, herein designated VGAM RNA, and which when bound by VGAM2388 RNA causes inhibition of translation of respective one or more VGAM2388 host target proteins.

[81123] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2388 gene, herein designated VGAM GENE, on one or more VGAM2388 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81124] It is yet further appreciated that a function of VGAM2388 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2388 include diagnosis, prevention and treatment of viral infection by Human Herpesvirus 4. Specific functions, and accordingly utilities, of VGAM2388

correlate with, and may be deduced from, the identity of the host target genes which VGAM2388 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81125] Nucleotide sequences of the VGAM2388 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2388 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2388 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2388 are further described hereinbelow with reference to Table 1.

[81126] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2388 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2388 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81127] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2388 gene, herein designated VGAM is inhibition of expression of VGAM2388 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2388 correlate with, and may be deduced

from, the identity of the target genes which VGAM2388 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81128] Stearoyl-CoA Desaturase (delta-9-desaturase) (SCD, Accession NM_005063) is a VGAM2388 host target gene. SCD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCD BINDING SITE, designated SEQ ID:11492, to the nucleotide sequence of VGAM2388 RNA, herein designated VGAM RNA, also designated SEQ ID:5099.

[81129] A function of VGAM2388 is therefore inhibition of Stearoyl-CoA Desaturase (delta-9-desaturase) (SCD, Accession NM_005063), a gene which functions in the synthesis of unsaturated fatty acids. Accordingly, utilities of VGAM2388 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCD. The function of SCD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM314.Tripartite Motif-containing 9 (TRIM9, Acces-

sion NM_052978) is another VGAM2388 host target gene. TRIM9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM9 BINDING SITE, designated SEQ ID:27552, to the nucleotide sequence of VGAM2388 RNA, herein designated VGAM RNA, also designated SEQ ID:5099.

[81130] Another function of VGAM2388 is therefore inhibition of Tripartite Motif-containing 9 (TRIM9, Accession NM_052978), a gene which may function as a positive regulator for mannosylphosphate transferase and is required to mediate mannosylphosphate transfer in both the core and outer chain portions of n-linked. oligosaccharides. Accordingly, utilities of VGAM2388 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM9. The function of TRIM9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.FLJ12604 (Accession XM_035022) is another VGAM2388 host target

gene. FLJ12604 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12604, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12604 BINDING SITE, designated SEQ ID:32192, to the nucleotide sequence of VGAM2388 RNA, herein designated VGAM RNA, also designated SEQ ID:5099.

[81131] Another function of VGAM2388 is therefore inhibition of FLJ12604 (Accession XM_035022). Accordingly, utilities of VGAM2388 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12604. FLJ13162 (Accession NM_025002) is another VGAM2388 host target gene. FLJ13162 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13162 BINDING SITE, designated SEQ ID:24574, to the nucleotide sequence of VGAM2388 RNA, herein designated VGAM RNA, also designated SEQ ID:5099.

[81132] Another function of VGAM2388 is therefore inhibition of FLJ13162 (Accession NM_025002). Accordingly, utilities of VGAM2388 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13162. LOC145474 (Accession XM_085147) is another VGAM2388 host target gene. LOC145474 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145474, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145474 BINDING SITE, designated SEQ ID:37869, to the nucleotide sequence of VGAM2388 RNA, herein designated VGAM RNA, also designated SEQ ID:5099.

[81133] Another function of VGAM2388 is therefore inhibition of LOC145474 (Accession XM_085147). Accordingly, utilities of VGAM2388 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145474. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2389 (VGAM2389) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[81134] VGAM2389 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2389 was detected is described hereinabove with reference to Figs. 1-8.

[81135] VGAM2389 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2389 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81136] VGAM2389 gene encodes a VGAM2389 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2389 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2389 precursor RNA is designated SEQ ID:2375, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2375 is located at position 19516 relative to the genome of Goatpox Virus.

[81137] VGAM2389 precursor RNA folds onto itself, forming VGAM2389 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81138] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2389 folded precursor RNA into VGAM2389 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2389 RNA is designated SEQ ID:5100, and is provided hereinbelow with reference to the sequence listing part.

[81139] VGAM2389 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2389 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2389 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81140] VGAM2389 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2389 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2389 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2389 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2389 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81141] The complementary binding of VGAM2389 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2389 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2389 host target RNA into VGAM2389 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81142] It is appreciated that VGAM2389 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2389 host target genes. The mRNA of each one of this plurality of VGAM2389 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2389 RNA, herein designated VGAM RNA, and which when bound by VGAM2389 RNA causes inhibition of translation of respective one or more VGAM2389 host target proteins.

[81143] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2389 gene, herein designated VGAM GENE, on one or more VGAM2389 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81144] It is yet further appreciated that a function of VGAM2389 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2389 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2389 correlate with, and may be deduced from, the identity of the host target genes which VGAM2389 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[81145] Nucleotide sequences of the VGAM2389 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2389 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2389 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2389 are further described hereinbelow with reference to Table 1.

[81146] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2389 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2389 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81147] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2389 gene, herein designated VGAM is inhibition of expression of VGAM2389 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2389 correlate with, and may be deduced from, the identity of the target genes which VGAM2389 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81148] Chloride Channel 4 (CLCN4, Accession NM_001830) is a VGAM2389 host target gene. CLCN4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CLCN4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLCN4 BINDING SITE, designated SEQ ID:7572, to the nucleotide sequence of VGAM2389 RNA, herein designated VGAM RNA, also designated SEQ ID:5100.

[81149] A function of VGAM2389 is therefore inhibition of Chloride Channel 4 (CLCN4, Accession NM_001830), a gene which is regulation of cell volume; membrane potential stabilization, signal transduction and transepithelial transport. Accordingly, utilities of VGAM2389 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLCN4. The function of CLCN4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM558.Cannabinoid Receptor 1 (brain) (CNR1, Accession NM_016083) is another VGAM2389 host target gene. CNR1 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by CNR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNR1 BINDING SITE, designated SEQ ID:18161, to the nucleotide sequence of VGAM2389 RNA, herein designated VGAM RNA, also designated SEQ ID:5100.

[81150] Another function of VGAM2389 is therefore inhibition of Cannabinoid Receptor 1 (brain) (CNR1, Accession NM_016083), a gene which is involved in the cannabinoid-induced CNS effects. Accordingly, utilities of VGAM2389 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNR1. The function of CNR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM533.Male-specific Lethal 3-like 1 (Drosophila) (MSL3L1, Accession NM_078628) is another VGAM2389 host target gene. MSL3L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MSL3L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of MSL3L1 BINDING SITE, designated SEQ ID:27810, to the nucleotide sequence of VGAM2389 RNA, herein designated VGAM RNA, also designated SEQ ID:5100.

[81151] Another function of VGAM2389 is therefore inhibition of Male-specific Lethal 3-like 1 (Drosophila) (MSL3L1, Accession NM_078628). Accordingly, utilities of VGAM2389 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSL3L1. S100 Calcium Binding Protein, Beta (neural) (S100B, Accession NM_006272) is another VGAM2389 host target gene. S100B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by S100B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of S100B BINDING SITE, designated SEQ ID:12954, to the nucleotide sequence of VGAM2389 RNA, herein designated VGAM RNA, also designated SEQ ID:5100.

[81152] Another function of VGAM2389 is therefore inhibition of S100 Calcium Binding Protein, Beta (neural) (S100B, Accession NM_006272), a gene which weakly binds calcium

but binds zinc very tightly- distinct binding sites with different affinities exist for both ions on each monomer. Accordingly, utilities of VGAM2389 include diagnosis, prevention and treatment of diseases and clinical conditions associated with S100B. The function of S100B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1078.Cyclin M1 (CNNM1, Accession NM_020348) is another VGAM2389 host target gene. CNNM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNNM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNNM1 BINDING SITE, designated SEQ ID:21602, to the nucleotide sequence of VGAM2389 RNA, herein designated VGAM RNA, also designated SEQ ID:5100.

[81153] Another function of VGAM2389 is therefore inhibition of Cyclin M1 (CNNM1, Accession NM_020348). Accordingly, utilities of VGAM2389 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNNM1. MGC16309 (Accession NM_033413) is an-

other VGAM2389 host target gene. MGC16309 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC16309, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16309 BINDING SITE, designated SEQ ID:27238, to the nucleotide sequence of VGAM2389 RNA, herein designated VGAM RNA, also designated SEQ ID:5100.

[81154] Another function of VGAM2389 is therefore inhibition of MGC16309 (Accession NM_033413). Accordingly, utilities of VGAM2389 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16309. PURG (Accession NM_013357) is another VGAM2389 host target gene. PURG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PURG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PURG BINDING SITE, designated SEQ ID:15005, to the nucleotide sequence of VGAM2389 RNA, herein designated VGAM RNA, also designated SEQ ID:5100.

[81155] Another function of VGAM2389 is therefore inhibition of PURG (Accession NM_013357). Accordingly, utilities of VGAM2389 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PURG. LOC137362 (Accession XM_059905) is another VGAM2389 host target gene. LOC137362 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC137362, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC137362 BINDING SITE, designated SEQ ID:37104, to the nucleotide sequence of VGAM2389 RNA, herein designated VGAM RNA, also designated SEQ ID:5100.

[81156] Another function of VGAM2389 is therefore inhibition of LOC137362 (Accession XM_059905). Accordingly, utilities of VGAM2389 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137362. LOC203025 (Accession XM_114610) is another VGAM2389 host target gene. LOC203025 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203025, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203025 BINDING SITE, designated SEQ ID:42999, to the nucleotide sequence of VGAM2389 RNA, herein designated VGAM RNA, also designated SEQ ID:5100.

[81157] Another function of VGAM2389 is therefore inhibition of LOC203025 (Accession XM_114610). Accordingly, utilities of VGAM2389 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203025. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2390 (VGAM2390) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81158] VGAM2390 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2390 was detected is described hereinabove with reference to Figs. 1-8.

[81159] VGAM2390 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus.

VGAM2390 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[81160] VGAM2390 gene encodes a VGAM2390 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2390 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2390 precursor RNA is designated SEQ ID:2376, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2376 is located at position 85371 relative to the genome of Goatpox Virus.

[81161] VGAM2390 precursor RNA folds onto itself, forming VGAM2390 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81162] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2390 folded precursor RNA into VGAM2390

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2390 RNA is designated SEQ ID:5101, and is provided hereinbelow with reference to the sequence listing part.

[81163] VGAM2390 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2390 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2390 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81164] VGAM2390 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2390 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2390 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2390 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2390 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81165] The complementary binding of VGAM2390 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2390 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2390 host target RNA into VGAM2390 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[81166] It is appreciated that VGAM2390 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2390 host target genes. The mRNA of each one of this plurality of VGAM2390 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2390 RNA, herein designated VGAM RNA, and which when bound by VGAM2390 RNA causes inhibition of translation of respective one or more VGAM2390 host target proteins.

[81167] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2390 gene, herein designated VGAM GENE, on one or more VGAM2390 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81168] It is yet further appreciated that a function of VGAM2390 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2390 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2390 correlate with, and may be deduced from, the identity of the host target genes which VGAM2390 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81169] Nucleotide sequences of the VGAM2390 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2390 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2390 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2390 are further described hereinbelow with reference to Table 1.

[81170] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2390 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2390 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81171] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2390 gene, herein designated VGAM is inhibition of expression of VGAM2390 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2390 correlate with, and may be deduced from, the identity of the target genes which VGAM2390 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81172] Glutamate Decarboxylase 1 (brain, 67kDa) (GAD1, Accession NM_000817) is a VGAM2390 host target gene. GAD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GAD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAD1 BINDING SITE, designated SEQ ID:6478, to the nucleotide sequence of VGAM2390 RNA, herein designated

VGAM RNA, also designated SEQ ID:5101.

[81173] A function of VGAM2390 is therefore inhibition of Glutamate Decarboxylase 1 (brain, 67kDa) (GAD1, Accession NM_000817), a gene which catalyzes the conversion of glutamic acid to gamma-aminobutyric acid. Accordingly, utilities of VGAM2390 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAD1. The function of GAD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM691.UDP-N-acetyl-alpha-D-galactosamine:(N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase (GalNAc-T) (GALGT, Accession NM_001478) is another VGAM2390 host target gene. GALGT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GALGT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALGT BINDING SITE, designated SEQ ID:7211, to the nucleotide sequence of VGAM2390 RNA, herein designated VGAM RNA, also designated SEQ

ID:5101.

[81174] Another function of VGAM2390 is therefore inhibition of UDP-N-acetyl-alpha-D-galactosamine:(N-acetylneuraminyl)-galactosylglucosylceramide N-acetylgalactosaminyltransferase (GalNAc-T) (GALGT, Accession NM_001478), a gene which is involved in the biosynthesis of gangliosides gm2, gd2 and ga2. Accordingly, utilities of VGAM2390 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALGT. The function of GALGT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM179.DKFZp761H2121 (Accession NM_138339) is another VGAM2390 host target gene. DKFZp761H2121 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp761H2121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of DKFZp761H2121 BINDING SITE, designated SEQ ID:28737, to the nucleotide sequence of VGAM2390 RNA, herein designated VGAM RNA, also designated SEQ ID:5101.

[81175] Another function of VGAM2390 is therefore inhibition of DKFZp761H2121 (Accession NM_138339). Accordingly, utilities of VGAM2390 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761H2121. EphA7 (EPHA7, Accession NM_004440) is another VGAM2390 host target gene. EPHA7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPHA7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPHA7 BINDING SITE, designated SEQ ID:10723, to the nucleotide sequence of VGAM2390 RNA, herein designated VGAM RNA, also designated SEQ ID:5101.

[81176] Another function of VGAM2390 is therefore inhibition of EphA7 (EPHA7, Accession NM_004440). Accordingly, utilities of VGAM2390 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with EPHA7. KIAA1655 (Accession XM_039442) is another VGAM2390 host target gene. KIAA1655 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1655, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1655 BINDING SITE, designated SEQ ID:33089, to the nucleotide sequence of VGAM2390 RNA, herein designated VGAM RNA, also designated SEQ ID:5101.

[81177] Another function of VGAM2390 is therefore inhibition of KIAA1655 (Accession XM_039442). Accordingly, utilities of VGAM2390 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1655. MGC2541 (Accession NM_080670) is another VGAM2390 host target gene. MGC2541 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2541, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2541 BINDING SITE, designated SEQ ID:27964, to the nucleotide sequence of VGAM2390 RNA, herein designated VGAM

RNA, also designated SEQ ID:5101.

[81178] Another function of VGAM2390 is therefore inhibition of MGC2541 (Accession NM_080670). Accordingly, utilities of VGAM2390 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2541. Ring Finger Protein 2 (RNF2, Accession NM_007212) is another VGAM2390 host target gene. RNF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF2 BINDING SITE, designated SEQ ID:14076, to the nucleotide sequence of VGAM2390 RNA, herein designated VGAM RNA, also designated SEQ ID:5101.

[81179] Another function of VGAM2390 is therefore inhibition of Ring Finger Protein 2 (RNF2, Accession NM_007212). Accordingly, utilities of VGAM2390 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF2. LOC139770 (Accession XM_060053) is another VGAM2390 host target gene. LOC139770 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

LOC139770, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC139770 BINDING SITE, designated SEQ ID:37145, to the nucleotide sequence of VGAM2390 RNA, herein designated VGAM RNA, also designated SEQ ID:5101.

[81180] Another function of VGAM2390 is therefore inhibition of LOC139770 (Accession XM_060053). Accordingly, utilities of VGAM2390 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139770. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2391 (VGAM2391) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81181] VGAM2391 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2391 was detected is described hereinabove with reference to Figs. 1-8.

[81182] VGAM2391 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Goatpox Virus. VGAM2391 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81183] VGAM2391 gene encodes a VGAM2391 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2391 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2391 precursor RNA is designated SEQ ID:2377, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2377 is located at position 22657 relative to the genome of Goatpox Virus.

[81184] VGAM2391 precursor RNA folds onto itself, forming VGAM2391 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81185] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2391 folded precursor RNA into VGAM2391 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 71%) nucleotide sequence of VGAM2391 RNA is designated SEQ ID:5102, and is provided hereinbelow with reference to the sequence listing part.

[81186] VGAM2391 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2391 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2391 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81187] VGAM2391 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2391 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2391 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2391 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2391 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81188] The complementary binding of VGAM2391 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2391 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2391

host target RNA into VGAM2391 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81189] It is appreciated that VGAM2391 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2391 host target genes. The mRNA of each one of this plurality of VGAM2391 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2391 RNA, herein designated VGAM RNA, and which when bound by VGAM2391 RNA causes inhibition of translation of respective one or more VGAM2391 host target proteins.

[81190] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2391 gene, herein designated VGAM GENE, on one or more VGAM2391 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81191] It is yet further appreciated that a function of VGAM2391 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2391 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2391 correlate with, and may be deduced from, the identity of the host target genes which VGAM2391 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81192] Nucleotide sequences of the VGAM2391 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2391 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2391 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2391 are further

described hereinbelow with reference to Table 1.

[81193] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2391 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2391 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81194] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2391 gene, herein designated VGAM is inhibition of expression of VGAM2391 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2391 correlate with, and may be deduced from, the identity of the target genes which VGAM2391 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81195] LOC91408 (Accession XM_038290) is a VGAM2391 host target gene. LOC91408 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91408, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91408 BINDING SITE,

designated SEQ ID:32790, to the nucleotide sequence of VGAM2391 RNA, herein designated VGAM RNA, also designated SEQ ID:5102.

[81196] A function of VGAM2391 is therefore inhibition of LOC91408 (Accession XM_038290). Accordingly, utilities of VGAM2391 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91408. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2392 (VGAM2392) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81197] VGAM2392 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2392 was detected is described hereinabove with reference to Figs. 1-8.

[81198] VGAM2392 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2392 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81199] VGAM2392 gene encodes a VGAM2392 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2392 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2392 precursor RNA is designated SEQ ID:2378, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2378 is located at position 9075 relative to the genome of Goatpox Virus.

[81200] VGAM2392 precursor RNA folds onto itself, forming VGAM2392 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81201] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2392 folded precursor RNA into VGAM2392 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 63%) nucleotide sequence of VGAM2392 RNA is designated SEQ ID:5103, and is provided hereinbelow with reference to the sequence listing part.

[81202] VGAM2392 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2392 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2392 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81203] VGAM2392 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2392 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2392 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2392 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2392 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81204] The complementary binding of VGAM2392 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2392 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2392 host target RNA into VGAM2392 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81205] It is appreciated that VGAM2392 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2392 host target genes. The mRNA of each one of this plurality of VGAM2392 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2392 RNA, herein designated VGAM RNA, and which when bound by VGAM2392 RNA causes inhibition of translation of respective one or more VGAM2392 host target proteins.

[81206] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2392 gene, herein designated VGAM GENE, on one or more VGAM2392 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81207] It is yet further appreciated that a function of VGAM2392 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2392 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2392 correlate with, and may be deduced from, the identity of the host target genes which VGAM2392 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81208] Nucleotide sequences of the VGAM2392 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2392 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2392 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2392 are further described hereinbelow with reference to Table 1.

[81209] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2392 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2392 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81210] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2392 gene, herein designated VGAM is inhibition of expression of VGAM2392 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2392 correlate with, and may be deduced from, the identity of the target genes which VGAM2392 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81211] Gap Junction Protein, Alpha 1, 43kDa (connexin 43) (GJA1, Accession NM_000165) is a VGAM2392 host target gene. GJA1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GJA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GJA1 BINDING SITE, designated SEQ ID:5675, to the nucleotide sequence of VGAM2392 RNA, herein designated VGAM RNA, also designated SEQ ID:5103.

[81212] A function of VGAM2392 is therefore inhibition of Gap

Junction Protein, Alpha 1, 43kDa (connexin 43) (GJA1, Accession NM_000165), a gene which may act in synchronizing heart contraction and embryonic development. Accordingly, utilities of VGAM2392 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GJA1. The function of GJA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM341.Retinoblastoma 1 (including osteosarcoma) (RB1, Accession XM_165641) is another VGAM2392 host target gene. RB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RB1 BINDING SITE, designated SEQ ID:43703, to the nucleotide sequence of VGAM2392 RNA, herein designated VGAM RNA, also designated SEQ ID:5103.

[81213] Another function of VGAM2392 is therefore inhibition of Retinoblastoma 1 (including osteosarcoma) (RB1, Accession XM_165641), a gene which probably acts as a regulator of other genes. Accordingly, utilities of VGAM2392 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with RB1. The function of RB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM795.Ribulose-5-phosphate-3-epimerase (RPE, Accession XM_030834) is another VGAM2392 host target gene. RPE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RPE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPE BINDING SITE, designated SEQ ID:31155, to the nucleotide sequence of VGAM2392 RNA, herein designated VGAM RNA, also designated SEQ ID:5103.

[81214] Another function of VGAM2392 is therefore inhibition of Ribulose-5-phosphate-3-epimerase (RPE, Accession XM_030834). Accordingly, utilities of VGAM2392 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPE. KIAA1078 (Accession XM_036589) is another VGAM2392 host target gene. KIAA1078 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

KIAA1078, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1078 BINDING SITE, designated SEQ ID:32469, to the nucleotide sequence of VGAM2392 RNA, herein designated VGAM RNA, also designated SEQ ID:5103.

[81215] Another function of VGAM2392 is therefore inhibition of KIAA1078 (Accession XM_036589). Accordingly, utilities of VGAM2392 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1078. RYK Receptor-like Tyrosine Kinase (RYK, Accession XM_093692) is another VGAM2392 host target gene. RYK BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RYK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RYK BINDING SITE, designated SEQ ID:40205, to the nucleotide sequence of VGAM2392 RNA, herein designated VGAM RNA, also designated SEQ ID:5103.

[81216] Another function of VGAM2392 is therefore inhibition of RYK Receptor-like Tyrosine Kinase (RYK, Accession

XM_093692). Accordingly, utilities of VGAM2392 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RYK. TBDN100 (Accession NM_025085) is another VGAM2392 host target gene. TBDN100 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBDN100, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBDN100 BINDING SITE, designated SEQ ID:24694, to the nucleotide sequence of VGAM2392 RNA, herein designated VGAM RNA, also designated SEQ ID:5103.

[81217] Another function of VGAM2392 is therefore inhibition of TBDN100 (Accession NM_025085). Accordingly, utilities of VGAM2392 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBDN100. LOC157627 (Accession XM_088347) is another VGAM2392 host target gene. LOC157627 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157627, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC157627 BINDING SITE, designated SEQ ID:39620, to the nucleotide sequence of VGAM2392 RNA, herein designated VGAM RNA, also designated SEQ ID:5103.

[81218] Another function of VGAM2392 is therefore inhibition of LOC157627 (Accession XM_088347). Accordingly, utilities of VGAM2392 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157627. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2393 (VGAM2393) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81219] VGAM2393 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2393 was detected is described hereinabove with reference to Figs. 1-8.

[81220] VGAM2393 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2393 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[81221] VGAM2393 gene encodes a VGAM2393 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2393 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2393 precursor RNA is designated SEQ ID:2379, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2379 is located at position 35069 relative to the genome of Goatpox Virus.

[81222] VGAM2393 precursor RNA folds onto itself, forming VGAM2393 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81223] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2393 folded precursor RNA into VGAM2393 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2393 RNA is designated SEQ ID:5104, and is provided hereinbelow with reference to the sequence listing part.

[81224] VGAM2393 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2393 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2393 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81225] VGAM2393 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2393 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2393 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2393 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2393 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81226] The complementary binding of VGAM2393 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2393 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2393 host target RNA into VGAM2393 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81227] It is appreciated that VGAM2393 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2393 host target genes. The mRNA of each one of this plurality of VGAM2393 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2393 RNA, herein designated VGAM RNA, and which when bound by VGAM2393 RNA causes inhibition of translation of respective one or more VGAM2393 host target proteins.

[81228] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2393 gene, herein designated VGAM GENE, on one or more VGAM2393 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81229] It is yet further appreciated that a function of VGAM2393 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2393 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2393 correlate with, and may be deduced from, the identity of the host target genes which VGAM2393 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81230] Nucleotide sequences of the VGAM2393 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2393 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2393 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2393 are further described hereinbelow with reference to Table 1.

[81231] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2393 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2393 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81232] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2393 gene, herein designated VGAM is inhibition of expression of VGAM2393 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2393 correlate with, and may be deduced from, the identity of the target genes which VGAM2393 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81233] A Disintegrin-like and Metalloprotease (reprolysin type) with Thrombospondin Type 1 Motif, 5 (aggrecanase-2) (ADAMTS5, Accession NM_007038) is a VGAM2393 host target gene. ADAMTS5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADAMTS5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAMTS5 BINDING SITE, designated SEQ ID:13917, to the nucleotide sequence of

VGAM2393 RNA, herein designated VGAM RNA, also designated SEQ ID:5104.

[81234] A function of VGAM2393 is therefore inhibition of A Disintegrin-like and Metalloprotease (reprolysin type) with Thrombospondin Type 1 Motif, 5 (aggrecanase-2) (ADAMTS5, Accession NM_007038), a gene which cleaves aggrecan, a cartilage proteoglycan, and may be involved in its turnover. Accordingly, utilities of VGAM2393 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAMTS5. The function of ADAMTS5 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM35.Synovial Sarcoma, X Breakpoint 3 (SSX3, Accession NM_021014) is another VGAM2393 host target gene. SSX3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SSX3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SSX3 BINDING SITE, designated SEQ ID:22002, to the nucleotide sequence of VGAM2393 RNA, herein designated VGAM RNA, also designated SEQ ID:5104.

[81235] Another function of VGAM2393 is therefore inhibition of Synovial Sarcoma, X Breakpoint 3 (SSX3, Accession NM_021014), a gene which could act as a modulator of transcription. Accordingly, utilities of VGAM2393 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSX3. The function of SSX3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM835.LOC144486 (Accession XM_096608) is another VGAM2393 host target gene. LOC144486 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144486, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144486 BINDING SITE, designated SEQ ID:40416, to the nucleotide sequence of VGAM2393 RNA, herein designated VGAM RNA, also designated SEQ ID:5104.

[81236] Another function of VGAM2393 is therefore inhibition of LOC144486 (Accession XM_096608). Accordingly, utilities of VGAM2393 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC144486. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2394 (VGAM2394) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81237] VGAM2394 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2394 was detected is described hereinabove with reference to Figs. 1-8.

[81238] VGAM2394 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2394 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81239] VGAM2394 gene encodes a VGAM2394 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2394 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2394 precursor RNA is designated SEQ ID:2380, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2380 is located at position 149142 relative to the genome of Goatpox Virus.

[81240] VGAM2394 precursor RNA folds onto itself, forming VGAM2394 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81241] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2394 folded precursor RNA into VGAM2394 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2394 RNA is designated SEQ ID:5105, and is provided hereinbelow with reference to the sequence listing part.

[81242] VGAM2394 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2394 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2394 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81243] VGAM2394 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2394 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2394 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2394 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2394 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81244] The complementary binding of VGAM2394 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2394 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2394 host target RNA into VGAM2394 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81245] It is appreciated that VGAM2394 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2394 host target genes. The mRNA of each one of this plurality of VGAM2394 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2394 RNA, herein designated VGAM RNA, and which when bound by VGAM2394 RNA causes

inhibition of translation of respective one or more VGAM2394 host target proteins.

[81246] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2394 gene, herein designated VGAM GENE, on one or more VGAM2394 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81247] It is yet further appreciated that a function of VGAM2394 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2394 include diagnosis, prevention and

treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2394 correlate with, and may be deduced from, the identity of the host target genes which VGAM2394 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81248] Nucleotide sequences of the VGAM2394 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2394 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2394 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2394 are further described hereinbelow with reference to Table 1.

[81249] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2394 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2394 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81250] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2394 gene, herein designated VGAM is inhibition of expression of VGAM2394 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2394 correlate with, and may be deduced from, the identity of the target genes which VGAM2394 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81251] Ankyrin 1, Erythrocytic (ANK1, Accession NM_020481) is a VGAM2394 host target gene. ANK1 BINDING SITE1 through ANK1 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ANK1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANK1 BINDING SITE1 through ANK1 BINDING SITE3, designated SEQ ID:21734, SEQ ID:21732 and SEQ ID:21733 respectively, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81252] A function of VGAM2394 is therefore inhibition of Ankyrin 1, Erythrocytic (ANK1, Accession NM_020481). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANK1. Doublesex and Mab-3 Related Transcription Factor 1 (DMRT1, Accession NM_021951) is another

VGAM2394 host target gene. DMRT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DMRT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DMRT1 BINDING SITE, designated SEQ ID:22479, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81253] Another function of VGAM2394 is therefore inhibition of Doublesex and Mab-3 Related Transcription Factor 1 (DMRT1, Accession NM_021951), a gene which May be involved in male sexual development. Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DMRT1. The function of DMRT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM59.Exostoses (multiple)-like 3 (EXTL3, Accession NM_001440) is another VGAM2394 host target gene. EXTL3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EXTL3, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EXTL3 BINDING SITE, designated SEQ ID:7165, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81254] Another function of VGAM2394 is therefore inhibition of Exostoses (multiple)-like 3 (EXTL3, Accession NM_001440), a gene which a member of the multiple exostoses gene family. Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EXTL3. The function of EXTL3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM95.Integrin, Alpha 6 (ITGA6, Accession NM_000210) is another VGAM2394 host target gene. ITGA6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA6 BINDING SITE, designated SEQ ID:5700, to the nu-

cleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81255] Another function of VGAM2394 is therefore inhibition of Integrin, Alpha 6 (ITGA6, Accession NM_000210). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA6. NEBL (Accession NM_006393) is another VGAM2394 host target gene. NEBL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NEBL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NEBL BINDING SITE, designated SEQ ID:13096, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81256] Another function of VGAM2394 is therefore inhibition of NEBL (Accession NM_006393). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NEBL. Tumor Necrosis Factor (ligand) Superfamily, Member 10 (TNFSF10, Accession NM_003810) is another VGAM2394 host target gene. TNFSF10 BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by TNFSF10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFSF10 BINDING SITE, designated SEQ ID:9900, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81257] Another function of VGAM2394 is therefore inhibition of Tumor Necrosis Factor (ligand) Superfamily, Member 10 (TNFSF10, Accession NM_003810), a gene which mediates cell death. Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFSF10. The function of TNFSF10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM637.WAS Protein Family, Member 3 (WASF3, Accession NM_006646) is another VGAM2394 host target gene. WASF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WASF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of WASF3 BINDING SITE, designated SEQ ID:13439, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81258] Another function of VGAM2394 is therefore inhibition of WAS Protein Family, Member 3 (WASF3, Accession NM_006646), a gene which stimulates actin polymerization. Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WASF3. The function of WASF3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1692.Chromosome 15 Open Reading Frame 5 (C15orf5, Accession NM_030944) is another VGAM2394 host target gene. C15orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C15orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C15orf5 BINDING SITE, designated SEQ ID:25212, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5105.

[81259] Another function of VGAM2394 is therefore inhibition of Chromosome 15 Open Reading Frame 5 (C15orf5, Accession NM_030944). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C15orf5. Centaurin, Alpha 2 (CENTA2, Accession NM_018404) is another VGAM2394 host target gene. CENTA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CENTA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CENTA2 BINDING SITE, designated SEQ ID:20441, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81260] Another function of VGAM2394 is therefore inhibition of Centaurin, Alpha 2 (CENTA2, Accession NM_018404). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CENTA2. Fatty Acid Desaturase 1 (FADS1, Accession NM_013402) is another VGAM2394 host target gene. FADS1 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by FADS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FADS1 BINDING SITE, designated SEQ ID:15066, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81261] Another function of VGAM2394 is therefore inhibition of Fatty Acid Desaturase 1 (FADS1, Accession NM_013402). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FADS1. FLJ11088 (Accession NM_018318) is another VGAM2394 host target gene. FLJ11088 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11088, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11088 BINDING SITE, designated SEQ ID:20311, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81262] Another function of VGAM2394 is therefore inhibition of FLJ11088 (Accession NM_018318). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11088. HSNOV1 (Accession NM_017515) is another VGAM2394 host target gene. HSNOV1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HSNOV1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HSNOV1 BINDING SITE, designated SEQ ID:18963, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81263] Another function of VGAM2394 is therefore inhibition of HSNOV1 (Accession NM_017515). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HSNOV1. Potassium Voltage-gated Channel, Subfamily H (eag-related), Member 8 (KCNH8, Accession NM_144633) is another VGAM2394 host target gene. KCNH8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNH8, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNH8 BINDING SITE, designated SEQ ID:29453, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81264] Another function of VGAM2394 is therefore inhibition of Potassium Voltage-gated Channel, Subfamily H (eag-related), Member 8 (KCNH8, Accession NM_144633). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNH8. KIAA0087 (Accession NM_014769) is another VGAM2394 host target gene. KIAA0087 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0087, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0087 BINDING SITE, designated SEQ ID:16555, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81265] Another function of VGAM2394 is therefore inhibition of

KIAA0087 (Accession NM_014769). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0087. KIAA0217 (Accession XM_040265) is another VGAM2394 host target gene. KIAA0217 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0217, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0217 BINDING SITE, designated SEQ ID:33278, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81266] Another function of VGAM2394 is therefore inhibition of KIAA0217 (Accession XM_040265). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0217. KIAA0350 (Accession XM_028332) is another VGAM2394 host target gene. KIAA0350 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0350, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0350 BINDING SITE, designated SEQ ID:30657, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81267] Another function of VGAM2394 is therefore inhibition of KIAA0350 (Accession XM_028332). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0350. KIAA1128 (Accession XM_043596) is another VGAM2394 host target gene. KIAA1128 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1128, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1128 BINDING SITE, designated SEQ ID:33966, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81268] Another function of VGAM2394 is therefore inhibition of KIAA1128 (Accession XM_043596). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1128. Kallikrein 7 (chymotryptic, stratum corneum)

(KLK7, Accession NM_005046) is another VGAM2394 host target gene. KLK7 BINDING SITE1 and KLK7 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KLK7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLK7 BINDING SITE1 and KLK7 BINDING SITE2, designated SEQ ID:11475 and SEQ ID:29272 respectively, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81269] Another function of VGAM2394 is therefore inhibition of Kallikrein 7 (chymotryptic, stratum corneum) (KLK7, Accession NM_005046). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLK7. MGC4827 (Accession NM_024114) is another VGAM2394 host target gene. MGC4827 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4827, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4827 BINDING SITE, designated

SEQ ID:23566, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81270] Another function of VGAM2394 is therefore inhibition of MGC4827 (Accession NM_024114). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4827. MGC4832 (Accession NM_145061) is another VGAM2394 host target gene. MGC4832 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4832, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4832 BINDING SITE, designated SEQ ID:29698, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81271] Another function of VGAM2394 is therefore inhibition of MGC4832 (Accession NM_145061). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4832. SNRK (Accession NM_017719) is another VGAM2394 host target gene. SNRK BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by SNRK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNRK BINDING SITE, designated SEQ ID:19308, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81272] Another function of VGAM2394 is therefore inhibition of SNRK (Accession NM_017719). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNRK. LOC145842 (Accession XM_085254) is another VGAM2394 host target gene. LOC145842 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145842, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145842 BINDING SITE, designated SEQ ID:37995, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81273] Another function of VGAM2394 is therefore inhibition of

LOC145842 (Accession XM_085254). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145842. LOC149111 (Accession XM_086429) is another VGAM2394 host target gene. LOC149111 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149111, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149111 BINDING SITE, designated SEQ ID:38647, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81274] Another function of VGAM2394 is therefore inhibition of LOC149111 (Accession XM_086429). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149111. LOC155435 (Accession XM_088257) is another VGAM2394 host target gene. LOC155435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC155435 BINDING SITE, designated SEQ ID:39566, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81275] Another function of VGAM2394 is therefore inhibition of LOC155435 (Accession XM_088257). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155435. LOC201562 (Accession XM_114343) is another VGAM2394 host target gene. LOC201562 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201562, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201562 BINDING SITE, designated SEQ ID:42882, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81276] Another function of VGAM2394 is therefore inhibition of LOC201562 (Accession XM_114343). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201562. LOC219401 (Accession XM_166706) is an-

other VGAM2394 host target gene. LOC219401 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219401, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219401 BINDING SITE, designated SEQ ID:44585, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81277] Another function of VGAM2394 is therefore inhibition of LOC219401 (Accession XM_166706). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219401. LOC220766 (Accession XM_165471) is another VGAM2394 host target gene. LOC220766 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220766, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220766 BINDING SITE, designated SEQ ID:43646, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81278] Another function of VGAM2394 is therefore inhibition of LOC220766 (Accession XM_165471). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220766. LOC221495 (Accession XM_168136) is another VGAM2394 host target gene. LOC221495 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221495, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221495 BINDING SITE, designated SEQ ID:45056, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81279] Another function of VGAM2394 is therefore inhibition of LOC221495 (Accession XM_168136). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221495. LOC256112 (Accession XM_172829) is another VGAM2394 host target gene. LOC256112 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256112, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256112 BINDING SITE, designated SEQ ID:46102, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81280] Another function of VGAM2394 is therefore inhibition of LOC256112 (Accession XM_172829). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256112. LOC256846 (Accession XM_170921) is another VGAM2394 host target gene. LOC256846 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256846, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256846 BINDING SITE, designated SEQ ID:45696, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81281] Another function of VGAM2394 is therefore inhibition of LOC256846 (Accession XM_170921). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC256846. LOC86651 (Accession XM_044052) is another VGAM2394 host target gene. LOC86651 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC86651, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC86651 BINDING SITE, designated SEQ ID:34096, to the nucleotide sequence of VGAM2394 RNA, herein designated VGAM RNA, also designated SEQ ID:5105.

[81282] Another function of VGAM2394 is therefore inhibition of LOC86651 (Accession XM_044052). Accordingly, utilities of VGAM2394 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC86651. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2395 (VGAM2395) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81283] VGAM2395 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2395 was detected is described hereinabove with reference to Figs. 1-8.

[81284] VGAM2395 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2395 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81285] VGAM2395 gene encodes a VGAM2395 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2395 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2395 precursor RNA is designated SEQ ID:2381, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2381 is located at position 120551 relative to the genome of Goatpox Virus.

[81286] VGAM2395 precursor RNA folds onto itself, forming VGAM2395 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81287] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2395 folded precursor RNA into VGAM2395 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2395 RNA is designated SEQ ID:5106, and is provided hereinbelow with reference to the sequence listing part.

[81288] VGAM2395 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2395 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2395 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81289] VGAM2395 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2395 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2395 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2395 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2395 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81290] The complementary binding of VGAM2395 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2395 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2395 host target RNA into VGAM2395 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81291] It is appreciated that VGAM2395 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2395 host target genes. The mRNA of each one of this plurality of VGAM2395 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2395 RNA, herein designated VGAM RNA, and which when bound by VGAM2395 RNA causes inhibition of translation of respective one or more VGAM2395 host target proteins.

[81292] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2395 gene, herein designated VGAM GENE, on one or more VGAM2395 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81293] It is yet further appreciated that a function of VGAM2395 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2395 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2395 correlate with, and may be deduced from, the identity of the host target genes which VGAM2395 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81294] Nucleotide sequences of the VGAM2395 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2395 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2395 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2395 are further described hereinbelow with reference to Table 1.

[81295] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2395 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2395 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81296] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2395 gene, herein designated VGAM is inhibition of expression of VGAM2395 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2395 correlate with, and may be deduced from, the identity of the target genes which VGAM2395 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81297] MGC4832 (Accession NM_145061) is a VGAM2395 host target gene. MGC4832 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4832, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4832 BINDING SITE, designated SEQ ID:29702, to the nucleotide sequence of VGAM2395 RNA, herein designated VGAM RNA, also designated SEQ ID:5106.

[81298] A function of VGAM2395 is therefore inhibition of MGC4832 (Accession NM_145061). Accordingly, utilities of VGAM2395 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4832. Palmdelphin (PALMD, Accession NM_017734) is another VGAM2395 host target gene. PALMD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PALMD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PALMD BINDING SITE, designated SEQ ID:19320, to the nucleotide sequence of VGAM2395 RNA, herein designated VGAM RNA, also designated SEQ ID:5106.

[81299] Another function of VGAM2395 is therefore inhibition of Palmdelphin (PALMD, Accession NM_017734). Accordingly, utilities of VGAM2395 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with PALMD. LOC151647 (Accession XM_087261) is another VGAM2395 host target gene. LOC151647 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151647, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151647 BINDING SITE, designated SEQ ID:39160, to the nucleotide sequence of VGAM2395 RNA, herein designated VGAM RNA, also designated SEQ ID:5106.

[81300] Another function of VGAM2395 is therefore inhibition of LOC151647 (Accession XM_087261). Accordingly, utilities of VGAM2395 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151647. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2396 (VGAM2396) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81301] VGAM2396 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2396 was detected is described hereinabove with reference to Figs. 1-8.

[81302] VGAM2396 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2396 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81303] VGAM2396 gene encodes a VGAM2396 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2396 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2396 precursor RNA is designated SEQ ID:2382, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2382 is located at position 93517 relative to the genome of Goatpox Virus.

[81304] VGAM2396 precursor RNA folds onto itself, forming VGAM2396 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81305] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2396 folded precursor RNA into VGAM2396 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2396 RNA is designated SEQ ID:5107, and is provided hereinbelow with reference to the sequence listing part.

[81306] VGAM2396 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2396 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2396 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81307] VGAM2396 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2396 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2396 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2396 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2396 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81308] The complementary binding of VGAM2396 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2396 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2396 host target RNA into VGAM2396 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81309] It is appreciated that VGAM2396 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2396 host target genes. The mRNA of each one of this plurality of VGAM2396 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2396 RNA, herein designated VGAM RNA, and which when bound by VGAM2396 RNA causes inhibition of translation of respective one or more VGAM2396 host target proteins.

[81310] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2396 gene, herein designated VGAM GENE, on one or more VGAM2396 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81311] It is yet further appreciated that a function of VGAM2396 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2396 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2396 correlate with, and may be deduced from, the identity of the host target genes which VGAM2396 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81312] Nucleotide sequences of the VGAM2396 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2396 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2396 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2396 are further described hereinbelow with reference to Table 1.

[81313] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2396 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2396 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81314] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2396 gene, herein designated VGAM is inhibition of expression of VGAM2396 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2396 correlate with, and may be deduced from, the identity of the target genes which VGAM2396 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81315] A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, alpha, converting enzyme) (ADAM17, Accession NM_003183) is a VGAM2396 host target gene.

ADAM17 BINDING SITE1 and ADAM17 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ADAM17, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAM17 BINDING SITE1 and ADAM17 BINDING SITE2, designated SEQ ID:9157 and SEQ ID:22410 respectively, to the nucleotide sequence of VGAM2396 RNA, herein designated VGAM RNA, also designated SEQ ID:5107.

[81316] A function of VGAM2396 is therefore inhibition of A Disintegrin and Metalloproteinase Domain 17 (tumor necrosis factor, alpha, converting enzyme) (ADAM17, Accession NM_003183), a gene which member of ADAM family of zinc metalloproteases. Accordingly, utilities of VGAM2396 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAM17. The function of ADAM17 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM264.DKFZP586D2223 (Accession NM_018561) is another VGAM2396 host target gene. DKFZP586D2223 BINDING SITE is HOST TARGET binding site found in the

5` untranslated region of mRNA encoded by DKFZP586D2223, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586D2223 BINDING SITE, designated SEQ ID:20643, to the nucleotide sequence of VGAM2396 RNA, herein designated VGAM RNA, also designated SEQ ID:5107.

[81317] Another function of VGAM2396 is therefore inhibition of DKFZP586D2223 (Accession NM_018561). Accordingly, utilities of VGAM2396 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586D2223. FLJ20276 (Accession NM_017738) is another VGAM2396 host target gene. FLJ20276 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20276, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20276 BINDING SITE, designated SEQ ID:19325, to the nucleotide sequence of VGAM2396 RNA, herein designated VGAM RNA, also designated SEQ ID:5107.

[81318] Another function of VGAM2396 is therefore inhibition of

FLJ20276 (Accession NM_017738). Accordingly, utilities of VGAM2396 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20276. LOC150848 (Accession XM_097959) is another VGAM2396 host target gene. LOC150848 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150848, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150848 BINDING SITE, designated SEQ ID:41255, to the nucleotide sequence of VGAM2396 RNA, herein designated VGAM RNA, also designated SEQ ID:5107.

[81319] Another function of VGAM2396 is therefore inhibition of LOC150848 (Accession XM_097959). Accordingly, utilities of VGAM2396 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150848. LOC93206 (Accession XM_049838) is another VGAM2396 host target gene. LOC93206 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93206, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of LOC93206 BINDING SITE, designated SEQ ID:35516, to the nucleotide sequence of VGAM2396 RNA, herein designated VGAM RNA, also designated SEQ ID:5107.

[81320] Another function of VGAM2396 is therefore inhibition of LOC93206 (Accession XM_049838). Accordingly, utilities of VGAM2396 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93206. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2397 (VGAM2397) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81321] VGAM2397 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2397 was detected is described hereinabove with reference to Figs. 1-8.

[81322] VGAM2397 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2397 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[81323] VGAM2397 gene encodes a VGAM2397 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2397 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2397 precursor RNA is designated SEQ ID:2383, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2383 is located at position 149485 relative to the genome of Goatpox Virus.

[81324] VGAM2397 precursor RNA folds onto itself, forming VGAM2397 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81325] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2397 folded precursor RNA into VGAM2397 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2397 RNA is designated SEQ ID:5108, and is provided hereinbelow with reference to the sequence listing part.

[81326] VGAM2397 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2397 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2397 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81327] VGAM2397 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2397 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2397 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2397 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2397 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81328] The complementary binding of VGAM2397 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2397 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2397 host target RNA into VGAM2397 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81329] It is appreciated that VGAM2397 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2397 host target genes. The mRNA of each one of this plurality of VGAM2397 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2397 RNA, herein designated VGAM RNA, and which when bound by VGAM2397 RNA causes inhibition of translation of respective one or more VGAM2397 host target proteins.

[81330] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2397 gene, herein designated VGAM GENE, on one or more VGAM2397 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81331] It is yet further appreciated that a function of VGAM2397 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2397 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2397 correlate with, and may be deduced from, the identity of the host target genes which VGAM2397 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81332] Nucleotide sequences of the VGAM2397 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2397 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2397 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2397 are further described hereinbelow with reference to Table 1.

[81333] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2397 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2397 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81334] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2397 gene, herein designated VGAM is inhibition of expression of VGAM2397 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2397 correlate with, and may be deduced from, the identity of the target genes which VGAM2397 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81335] Component of Oligomeric Golgi Complex 3 (COG3, Accession NM_031431) is a VGAM2397 host target gene. COG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COG3 BINDING SITE, designated SEQ ID:25426, to the nucleotide sequence of VGAM2397 RNA, herein designated VGAM RNA, also designated SEQ ID:5108.

[81336] A function of VGAM2397 is therefore inhibition of Component of Oligomeric Golgi Complex 3 (COG3, Accession NM_031431), a gene which is critical for the structure and function of the Golgi apparatus. Accordingly, utilities of VGAM2397 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COG3. The function of COG3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2069.Chromobox Homolog 3 (HP1 gamma homolog, Drosophila) (CBX3, Accession NM_016587) is another VGAM2397 host target gene. CBX3 BINDING SITE1 and CBX3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CBX3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBX3 BINDING SITE1 and CBX3 BINDING SITE2, designated SEQ ID:18659 and SEQ ID:14139 respectively, to the nucleotide sequence of VGAM2397 RNA, herein designated VGAM RNA, also designated SEQ ID:5108.

[81337] Another function of VGAM2397 is therefore inhibition of Chromobox Homolog 3 (HP1 gamma homolog,

Drosophila) (CBX3, Accession NM_016587). Accordingly, utilities of VGAM2397 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBX3. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2398 (VGAM2398) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81338] VGAM2398 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2398 was detected is described hereinabove with reference to Figs. 1-8.

[81339] VGAM2398 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2398 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81340] VGAM2398 gene encodes a VGAM2398 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2398 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2398 precursor RNA is designated SEQ ID:2384, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2384 is located at position 101040 relative to the genome of Goatpox Virus.

[81341] VGAM2398 precursor RNA folds onto itself, forming VGAM2398 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81342] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2398 folded precursor RNA into VGAM2398 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2398 RNA is designated SEQ ID:5109, and is provided hereinbelow with reference to the sequence listing part.

[81343] VGAM2398 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2398 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2398 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81344] VGAM2398 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2398 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2398 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2398 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2398 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81345] The complementary binding of VGAM2398 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2398 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2398 host target RNA into VGAM2398 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81346] It is appreciated that VGAM2398 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2398 host target genes. The mRNA of each one of this plurality of VGAM2398 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2398 RNA, herein designated VGAM RNA, and which when bound by VGAM2398 RNA causes inhibition of translation of respective one or more VGAM2398 host target proteins.

[81347] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2398 gene, herein designated VGAM GENE, on one or more VGAM2398 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81348] It is yet further appreciated that a function of VGAM2398

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2398 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2398 correlate with, and may be deduced from, the identity of the host target genes which VGAM2398 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81349] Nucleotide sequences of the VGAM2398 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2398 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2398 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2398 are further described hereinbelow with reference to Table 1.

[81350] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2398 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2398 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81351] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2398 gene, herein designated VGAM is inhibition of expression of VGAM2398 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2398 correlate with, and may be deduced from, the identity of the target genes which VGAM2398 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81352] Frizzled Homolog 7 (Drosophila) (FZD7, Accession NM_003507) is a VGAM2398 host target gene. FZD7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FZD7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FZD7 BINDING SITE, designated SEQ ID:9598, to the nucleotide sequence of VGAM2398 RNA, herein designated VGAM RNA, also designated SEQ ID:5109.

[81353] A function of VGAM2398 is therefore inhibition of Frizzled Homolog 7 (Drosophila) (FZD7, Accession NM_003507), a gene which enhances beta-catenin mediated signaling. Accordingly, utilities of VGAM2398 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with FZD7. The function of FZD7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1063.LEC3 (Accession NM_015236) is another VGAM2398 host target gene. LEC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LEC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LEC3 BINDING SITE, designated SEQ ID:17567, to the nucleotide sequence of VGAM2398 RNA, herein designated VGAM RNA, also designated SEQ ID:5109.

[81354] Another function of VGAM2398 is therefore inhibition of LEC3 (Accession NM_015236). Accordingly, utilities of VGAM2398 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LEC3. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2399 (VGAM2399) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81355] VGAM2399 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2399 was detected is described hereinabove with reference to Figs. 1-8.

[81356] VGAM2399 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2399 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81357] VGAM2399 gene encodes a VGAM2399 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2399 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2399 precursor RNA is designated SEQ ID:2385, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2385 is located at position 23504 relative to the genome of Goatpox Virus.

[81358] VGAM2399 precursor RNA folds onto itself, forming VGAM2399 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81359] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2399 folded precursor RNA into VGAM2399 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2399 RNA is designated SEQ ID:5110, and is provided hereinbelow with reference to the sequence listing part.

[81360] VGAM2399 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2399 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2399 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[81361] VGAM2399 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2399 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2399 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2399 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2399 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81362] The complementary binding of VGAM2399 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2399 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2399 host target RNA into VGAM2399 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81363] It is appreciated that VGAM2399 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2399 host target genes. The mRNA of each one of this plurality of VGAM2399 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2399 RNA, herein designated VGAM RNA, and which when bound by VGAM2399 RNA causes inhibition of translation of respective one or more VGAM2399 host target proteins.

[81364] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2399 gene, herein designated VGAM GENE, on one or more VGAM2399 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81365] It is yet further appreciated that a function of VGAM2399 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2399 correlate with, and may be deduced from, the identity of the host target genes which VGAM2399 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81366] Nucleotide sequences of the VGAM2399 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2399 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2399 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2399 are further described hereinbelow with reference to Table 1.

[81367] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2399 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2399 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81368] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2399 gene, herein designated VGAM is inhibition of expression of VGAM2399 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2399 correlate with, and may be deduced from, the identity of the target genes which VGAM2399 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81369] ATPase, Cu++ Transporting, Alpha Polypeptide (Menkes syndrome) (ATP7A, Accession NM_000052) is a

VGAM2399 host target gene. ATP7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:5495, to the nucleotide sequence of VGAM2399 RNA, herein designated VGAM RNA, also designated SEQ ID:5110.

[81370] A function of VGAM2399 is therefore inhibition of ATPase, Cu++ Transporting, Alpha Polypeptide (Menkes syndrome) (ATP7A, Accession NM_000052). Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7A. Forkhead Box F2 (FOXF2, Accession NM_001452) is another VGAM2399 host target gene. FOXF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FOXF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FOXF2 BINDING SITE, designated SEQ ID:7187, to the nucleotide sequence of VGAM2399 RNA, herein

designated VGAM RNA, also designated SEQ ID:5110.

[81371] Another function of VGAM2399 is therefore inhibition of Forkhead Box F2 (FOXF2, Accession NM_001452), a gene which is a probable transcription activator for a number of lung- specific genes. Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FOXF2. The function of FOXF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM217.FLJ12085 (Accession NM_022771) is another VGAM2399 host target gene. FLJ12085 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12085, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12085 BINDING SITE, designated SEQ ID:23033, to the nucleotide sequence of VGAM2399 RNA, herein designated VGAM RNA, also designated SEQ ID:5110.

[81372] Another function of VGAM2399 is therefore inhibition of FLJ12085 (Accession NM_022771). Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12085. FLJ20502 (Accession NM_017845) is another VGAM2399 host target gene. FLJ20502 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20502, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20502 BINDING SITE, designated SEQ ID:19508, to the nucleotide sequence of VGAM2399 RNA, herein designated VGAM RNA, also designated SEQ ID:5110.

[81373] Another function of VGAM2399 is therefore inhibition of FLJ20502 (Accession NM_017845). Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20502. KIAA0826 (Accession XM_093839) is another VGAM2399 host target gene. KIAA0826 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0826, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0826 BINDING SITE, designated SEQ ID:40215, to the

nucleotide sequence of VGAM2399 RNA, herein designated VGAM RNA, also designated SEQ ID:5110.

[81374] Another function of VGAM2399 is therefore inhibition of KIAA0826 (Accession XM_093839). Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0826. KIAA0903 (Accession XM_049251) is another VGAM2399 host target gene. KIAA0903 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0903, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0903 BINDING SITE, designated SEQ ID:35369, to the nucleotide sequence of VGAM2399 RNA, herein designated VGAM RNA, also designated SEQ ID:5110.

[81375] Another function of VGAM2399 is therefore inhibition of KIAA0903 (Accession XM_049251). Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0903. KIAA1729 (Accession XM_114418) is another VGAM2399 host target gene. KIAA1729 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by KIAA1729, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1729 BINDING SITE, designated SEQ ID:42945, to the nucleotide sequence of VGAM2399 RNA, herein designated VGAM RNA, also designated SEQ ID:5110.

[81376] Another function of VGAM2399 is therefore inhibition of KIAA1729 (Accession XM_114418). Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1729. Ligand of Numb-protein X (LNX, Accession NM_032622) is another VGAM2399 host target gene. LNX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LNX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LNX BINDING SITE, designated SEQ ID:26338, to the nucleotide sequence of VGAM2399 RNA, herein designated VGAM RNA, also designated SEQ ID:5110.

[81377] Another function of VGAM2399 is therefore inhibition of Ligand of Numb-protein X (LNX, Accession NM_032622).

Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LNX. PRO1866 (Accession NM_018510) is another VGAM2399 host target gene. PRO1866 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1866, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1866 BINDING SITE, designated SEQ ID:20582, to the nucleotide sequence of VGAM2399 RNA, herein designated VGAM RNA, also designated SEQ ID:5110.

[81378] Another function of VGAM2399 is therefore inhibition of PRO1866 (Accession NM_018510). Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1866. LOC122830 (Accession XM_058661) is another VGAM2399 host target gene. LOC122830 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC122830, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC122830 BINDING SITE, designated SEQ ID:36703, to the nucleotide sequence of VGAM2399 RNA, herein designated VGAM RNA, also designated SEQ ID:5110.

[81379] Another function of VGAM2399 is therefore inhibition of LOC122830 (Accession XM_058661). Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122830. LOC170372 (Accession XM_084317) is another VGAM2399 host target gene. LOC170372 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC170372, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC170372 BINDING SITE, designated SEQ ID:37538, to the nucleotide sequence of VGAM2399 RNA, herein designated VGAM RNA, also designated SEQ ID:5110.

[81380] Another function of VGAM2399 is therefore inhibition of LOC170372 (Accession XM_084317). Accordingly, utilities of VGAM2399 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC170372. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2400 (VGAM2400) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81381] VGAM2400 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2400 was detected is described hereinabove with reference to Figs. 1-8.

[81382] VGAM2400 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2400 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81383] VGAM2400 gene encodes a VGAM2400 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2400 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2400 precursor RNA is designated SEQ ID:2386, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2386 is located at position 89837 relative to the genome of Goatpox Virus.

[81384] VGAM2400 precursor RNA folds onto itself, forming VGAM2400 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81385] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2400 folded precursor RNA into VGAM2400 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2400 RNA is designated SEQ ID:5111, and is provided hereinbelow with reference to the sequence listing part.

[81386] VGAM2400 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2400 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2400 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81387] VGAM2400 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2400 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2400 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2400 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2400 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81388] The complementary binding of VGAM2400 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2400 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2400 host target RNA into VGAM2400 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81389] It is appreciated that VGAM2400 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2400 host target genes. The mRNA of each one of this plurality of VGAM2400 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2400 RNA, herein designated VGAM RNA, and which when bound by VGAM2400 RNA causes inhibition of translation of respective one or more

VGAM2400 host target proteins.

[81390] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2400 gene, herein designated VGAM GENE, on one or more VGAM2400 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81391] It is yet further appreciated that a function of VGAM2400 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2400 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific

functions, and accordingly utilities, of VGAM2400 correlate with, and may be deduced from, the identity of the host target genes which VGAM2400 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81392] Nucleotide sequences of the VGAM2400 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2400 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2400 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2400 are further described hereinbelow with reference to Table 1.

[81393] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2400 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2400 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81394] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2400 gene, herein designated VGAM is inhibition of expression of VGAM2400 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2400 correlate with, and may be deduced from, the identity of the target genes which VGAM2400 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81395] Phosphodiesterase 4D, CAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D, Accession XM_056815) is a VGAM2400 host target gene. PDE4D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE4D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE4D BINDING SITE, designated SEQ ID:36429, to the nucleotide sequence of VGAM2400 RNA, herein designated VGAM RNA, also designated SEQ ID:5111.

[81396] A function of VGAM2400 is therefore inhibition of Phosphodiesterase 4D, CAMP-specific (phosphodiesterase E3 dunce homolog, Drosophila) (PDE4D, Accession XM_056815), a gene which has similarity to Drosophila dnc, which is the affected protein in learning and memory mutant dunce. Accordingly, utilities of VGAM2400 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE4D. The function of

PDE4D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM180.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2401 (VGAM2401) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81397] VGAM2401 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2401 was detected is described hereinabove with reference to Figs. 1-8.

[81398] VGAM2401 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2401 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81399] VGAM2401 gene encodes a VGAM2401 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2401 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2401 precursor RNA is designated SEQ ID:2387, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2387 is located at position 109414 relative to the genome of Goatpox Virus.

[81400] VGAM2401 precursor RNA folds onto itself, forming VGAM2401 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81401] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2401 folded precursor RNA into VGAM2401 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 53%) nucleotide sequence of VGAM2401 RNA is designated SEQ ID:5112, and

is provided hereinbelow with reference to the sequence listing part.

[81402] VGAM2401 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2401 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2401 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81403] VGAM2401 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2401 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2401 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2401 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2401 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81404] The complementary binding of VGAM2401 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2401 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2401 host target RNA into VGAM2401 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81405] It is appreciated that VGAM2401 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2401 host target genes. The mRNA of each one of this plurality of VGAM2401 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2401 RNA, herein designated VGAM RNA, and which when bound by VGAM2401 RNA causes inhibition of translation of respective one or more VGAM2401 host target proteins.

[81406] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2401 gene, herein designated VGAM GENE, on one or more VGAM2401 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81407] It is yet further appreciated that a function of VGAM2401 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2401 correlate with, and may be deduced from, the identity of the host target genes which VGAM2401 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81408] Nucleotide sequences of the VGAM2401 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2401 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2401 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2401 are further described hereinbelow with reference to Table 1.

[81409] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2401 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2401 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81410] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2401 gene, herein designated VGAM is inhibition of expression of VGAM2401 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2401 correlate with, and may be deduced from, the identity of the target genes which VGAM2401 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81411] ATP Synthase, H+ Transporting, Mitochondrial F1 Complex, Beta Polypeptide (ATP5B, Accession XM_006710) is a VGAM2401 host target gene. ATP5B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ATP5B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP5B BINDING SITE, designated SEQ ID:30006, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81412] A function of VGAM2401 is therefore inhibition of ATP Synthase, H+ Transporting, Mitochondrial F1 Complex, Beta Polypeptide (ATP5B, Accession XM_006710). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associ-

ated with ATP5B. Cadherin, EGF LAG Seven-pass G-type Receptor 3 (flamingo homolog, Drosophila) (CELSR3, Accession NM_001407) is another VGAM2401 host target gene. CELSR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CELSR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CELSR3 BINDING SITE, designated SEQ ID:7102, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81413] Another function of VGAM2401 is therefore inhibition of Cadherin, EGF LAG Seven-pass G-type Receptor 3 (flamingo homolog, Drosophila) (CELSR3, Accession NM_001407), a gene which interacts in a homophilic manner in connecting cells. Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CELSR3. The function of CELSR3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM893.Epidermal Growth Factor Receptor

Pathway Substrate 15 (EPS15, Accession NM_001981) is another VGAM2401 host target gene. EPS15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPS15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPS15 BINDING SITE, designated SEQ ID:7711, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81414] Another function of VGAM2401 is therefore inhibition of Epidermal Growth Factor Receptor Pathway Substrate 15 (EPS15, Accession NM_001981), a gene which involved in cell growth regulation. Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPS15. The function of EPS15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.Interleukin 4 Receptor (IL4R, Accession NM_000418) is another VGAM2401 host target gene. IL4R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL4R, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL4R BINDING SITE, designated SEQ ID:6000, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81415] Another function of VGAM2401 is therefore inhibition of Interleukin 4 Receptor (IL4R, Accession NM_000418), a gene which may represent a regulatory molecule specific for il-4-dependent immune responses. Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL4R. The function of IL4R has been established by previous studies. Interleukin-4 (IL4; 147780) plays a major role in immunoglobulin E (IgE) production. Its signal is conferred to effector cells through binding to the alpha chain of the IL4 receptor (IL4RA). Caggana et al. (1999) examined the frequency of the IL4R sequence variants gly551 to arg and ile50 to val in 4 anonymous New York state populations defined by ethnic origin. These variants were studied because they are associated with atopy or atopic asthma, the prevalence of which varies in different populations. Methods were developed to detect both

polymorphisms in 855 newborn screening specimens. The arg551 allele was found most frequently in blacks (allele frequency of 68%), whereas the ile50 allele was most common in whites (allele frequency of 87%). Significantly more blacks had chromosomes bearing both of the 'enhanced-signaling' variants (ile50/arg551). Since enhanced IL4R signaling is associated with increased IgE production (atopy), Caggana et al. (1999) interpreted their data as suggesting that African-American populations may be at increased risk for diseases, including asthma, that are associated with atopy. The data pointed to the importance of determining the frequencies of single-nucleotide polymorphisms in different populations before drawing conclusions from allele association studies, since the background allele frequencies may be disparate. A genomewide screen for atopy susceptibility alleles in the Hutterites, a founder population of European origin living mainly in Canada, provided evidence for linkage to 16p (Ober et al., 1999). Ober et al. (2000) examined the IL4RA gene as the 16p-linked susceptibility locus. The Hutterites and outbred white, black, and Hispanic families all showed evidence of association between variants in the IL4RA gene and atopy or asthma; however, the alleles or haplo-

types showing the strongest evidence differed between the groups.

[81416] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[81417] Caggana, M.; Walker, K.; Reilly, A. A.; Conroy, J. M.; Duva, S.; Walsh, A. C. : Population-based studies reveal differences in the allelic frequencies of two functionally significant human interleukin-4 receptor polymorphisms in several ethnic groups. Genet. Med. 1: 267-271, 1999. ; and

[81418] Ober, C.; Leavitt, S. A.; Tsalenko, A.; Howard, T. D.; Hoki, D. M.; Daniel, R.; Newman, D. L.; Wu, X.; Parry, R.; Lester, L. A.; Solway, J.; Blumenthal, M.; King, R. A.; Xu, J.; Meyers.

[81419] Further studies establishing the function and utilities of IL4R are found in John Hopkins OMIM database record ID 147781, and in sited publications numbered 11337-11338, 11595-11596, 688, 11597, 11598, 11599-1160 and 11592 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Integrin, Alpha M (complement component receptor 3, alpha; also known as CD11b (p170), Macrophage Antigen Alpha Polypeptide) (ITGAM, Accession NM_000632) is another VGAM2401 host target gene. ITGAM BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGAM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGAM BINDING SITE, designated SEQ ID:6248, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81420] Another function of VGAM2401 is therefore inhibition of Integrin, Alpha M (complement component receptor 3, alpha; also known as CD11b (p170), Macrophage Antigen Alpha Polypeptide) (ITGAM, Accession NM_000632), a gene which is invovled in various adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles. Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAM. The function of ITGAM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1386.SPS2 (Accession NM_012248) is another VGAM2401 host target gene. SPS2 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by SPS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPS2 BINDING SITE, designated SEQ ID:14554, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81421] Another function of VGAM2401 is therefore inhibition of SPS2 (Accession NM_012248), a gene which synthesizes selenophosphate from selenide and ATP. Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPS2. The function of SPS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1754.Stanniocalcin 1 (STC1, Accession NM_003155) is another VGAM2401 host target gene. STC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STC1 BINDING SITE, designated SEQ ID:9135,

to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81422] Another function of VGAM2401 is therefore inhibition of Stanniocalcin 1 (STC1, Accession NM_003155), a gene which stimulates renal phosphate reabsorption, and could therefore prevent hypercalcemia. Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STC1. The function of STC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM623.T-cell Leukemia Translocation Altered Gene (TCTA, Accession NM_022171) is another VGAM2401 host target gene. TCTA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCTA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCTA BINDING SITE, designated SEQ ID:22729, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81423] Another function of VGAM2401 is therefore inhibition of

T-cell Leukemia Translocation Altered Gene (TCTA, Accession NM_022171). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCTA. Triadin (TRDN, Accession NM_006073) is another VGAM2401 host target gene. TRDN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRDN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRDN BINDING SITE, designated SEQ ID:12717, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81424] Another function of VGAM2401 is therefore inhibition of Triadin (TRDN, Accession NM_006073). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRDN. Activin A Receptor, Type II (ACVR2, Accession NM_001616) is another VGAM2401 host target gene. ACVR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ACVR2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACVR2 BINDING SITE, designated SEQ ID:7320, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81425] Another function of VGAM2401 is therefore inhibition of Activin A Receptor, Type II (ACVR2, Accession NM_001616). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACVR2. A Kinase (PRKA) Anchor Protein (gravin) 12 (AKAP12, Accession NM_005100) is another VGAM2401 host target gene. AKAP12 BINDING SITE1 and AKAP12 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AKAP12, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP12 BINDING SITE1 and AKAP12 BINDING SITE2, designated SEQ ID:11573 and SEQ ID:29314 respectively, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81426] Another function of VGAM2401 is therefore inhibition of A Kinase (PRKA) Anchor Protein (gravin) 12 (AKAP12, Accession NM_005100). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP12. FLJ20154 (Accession XM_053688) is another VGAM2401 host target gene. FLJ20154 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20154, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20154 BINDING SITE, designated SEQ ID:36105, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81427] Another function of VGAM2401 is therefore inhibition of FLJ20154 (Accession XM_053688). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20154. FLJ21616 (Accession NM_024567) is another VGAM2401 host target gene. FLJ21616 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21616, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21616 BINDING SITE, designated SEQ ID:23794, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81428] Another function of VGAM2401 is therefore inhibition of FLJ21616 (Accession NM_024567). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21616. FLJ22009 (Accession XM_015700) is another VGAM2401 host target gene. FLJ22009 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22009, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22009 BINDING SITE, designated SEQ ID:30242, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81429] Another function of VGAM2401 is therefore inhibition of FLJ22009 (Accession XM_015700). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ22009. GNB4 (Accession NM_021629) is another VGAM2401 host target gene. GNB4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNB4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNB4 BINDING SITE, designated SEQ ID:22271, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81430] Another function of VGAM2401 is therefore inhibition of GNB4 (Accession NM_021629). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNB4. KIAA0630 (Accession XM_114729) is another VGAM2401 host target gene. KIAA0630 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0630, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0630 BINDING SITE, designated SEQ ID:43066, to the nucleotide sequence of

VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81431] Another function of VGAM2401 is therefore inhibition of KIAA0630 (Accession XM_114729). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0630. KIAA0680 (Accession NM_014721) is another VGAM2401 host target gene. KIAA0680 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0680, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0680 BINDING SITE, designated SEQ ID:16283, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81432] Another function of VGAM2401 is therefore inhibition of KIAA0680 (Accession NM_014721). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0680. KIAA0716 (Accession NM_014705) is another VGAM2401 host target gene. KIAA0716 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA0716, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0716 BINDING SITE, designated SEQ ID:16246, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81433] Another function of VGAM2401 is therefore inhibition of KIAA0716 (Accession NM_014705). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0716. KIAA0953 (Accession XM_039733) is another VGAM2401 host target gene. KIAA0953 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0953, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0953 BINDING SITE, designated SEQ ID:33171, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81434] Another function of VGAM2401 is therefore inhibition of KIAA0953 (Accession XM_039733). Accordingly, utilities

of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0953. KIAA1319 (Accession NM_020770) is another VGAM2401 host target gene. KIAA1319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1319, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1319 BINDING SITE, designated SEQ ID:21866, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81435] Another function of VGAM2401 is therefore inhibition of KIAA1319 (Accession NM_020770). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1319. KIAA1361 (Accession XM_030845) is another VGAM2401 host target gene. KIAA1361 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1361, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1361 BINDING SITE, designated SEQ ID:31172, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81436] Another function of VGAM2401 is therefore inhibition of KIAA1361 (Accession XM_030845). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1361. KIAA1719 (Accession XM_042936) is another VGAM2401 host target gene. KIAA1719 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1719, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1719 BINDING SITE, designated SEQ ID:33825, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81437] Another function of VGAM2401 is therefore inhibition of KIAA1719 (Accession XM_042936). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1719. NCK Adaptor Protein 1 (NCK1, Accession NM_006153) is another VGAM2401 host target gene.

NCK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NCK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCK1 BINDING SITE, designated SEQ ID:12808, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81438] Another function of VGAM2401 is therefore inhibition of NCK Adaptor Protein 1 (NCK1, Accession NM_006153). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCK1. PRO1866 (Accession NM_018510) is another VGAM2401 host target gene. PRO1866 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1866, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1866 BINDING SITE, designated SEQ ID:20579, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81439] Another function of VGAM2401 is therefore inhibition of PRO1866 (Accession NM_018510). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1866. LOC148697 (Accession XM_086276) is another VGAM2401 host target gene. LOC148697 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148697, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148697 BINDING SITE, designated SEQ ID:38575, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81440] Another function of VGAM2401 is therefore inhibition of LOC148697 (Accession XM_086276). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148697. LOC154215 (Accession XM_087875) is another VGAM2401 host target gene. LOC154215 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154215, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154215 BINDING SITE, designated SEQ ID:39465, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81441] Another function of VGAM2401 is therefore inhibition of LOC154215 (Accession XM_087875). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154215. LOC205418 (Accession XM_119792) is another VGAM2401 host target gene. LOC205418 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC205418, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC205418 BINDING SITE, designated SEQ ID:43597, to the nucleotide sequence of VGAM2401 RNA, herein designated VGAM RNA, also designated SEQ ID:5112.

[81442] Another function of VGAM2401 is therefore inhibition of LOC205418 (Accession XM_119792). Accordingly, utilities of VGAM2401 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC205418. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2402 (VGAM2402) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81443] VGAM2402 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2402 was detected is described hereinabove with reference to Figs. 1-8.

[81444] VGAM2402 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2402 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81445] VGAM2402 gene encodes a VGAM2402 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2402 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2402 precursor RNA is designated SEQ ID:2388, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2388 is located at position 702 relative to the genome of Goatpox Virus.

[81446] VGAM2402 precursor RNA folds onto itself, forming VGAM2402 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81447] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2402 folded precursor RNA into VGAM2402 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2402 RNA is designated SEQ ID:5113, and is provided hereinbelow with reference to the sequence listing part.

[81448] VGAM2402 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2402 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2402 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81449] VGAM2402 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2402 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2402 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2402 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2402 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81450] The complementary binding of VGAM2402 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2402 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2402 host target RNA into VGAM2402 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81451] It is appreciated that VGAM2402 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2402 host target genes. The mRNA of each one of this plurality of VGAM2402 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2402 RNA, herein designated VGAM RNA, and which when bound by VGAM2402 RNA causes

inhibition of translation of respective one or more VGAM2402 host target proteins.

[81452] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2402 gene, herein designated VGAM GENE, on one or more VGAM2402 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81453] It is yet further appreciated that a function of VGAM2402 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2402 include diagnosis, prevention and

treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2402 correlate with, and may be deduced from, the identity of the host target genes which VGAM2402 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81454] Nucleotide sequences of the VGAM2402 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2402 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2402 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2402 are further described hereinbelow with reference to Table 1.

[81455] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2402 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2402 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81456] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2402 gene, herein designated VGAM is inhibition of expression of VGAM2402 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2402 correlate with, and may be deduced from, the identity of the target genes which VGAM2402 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81457] Protocadherin 11 X-linked (PCDH11X, Accession NM_032968) is a VGAM2402 host target gene. PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDH11X, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2, designated SEQ ID:26787 and SEQ ID:26802 respectively, to the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81458] A function of VGAM2402 is therefore inhibition of Protocadherin 11 X-linked (PCDH11X, Accession NM_032968), a gene which is thought to play a fundamental role in cell-cell recognition essential for the segmental development and function of the central nervous system. Accordingly, utilities of VGAM2402 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with PCDH11X. The function of PCDH11X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Solute Carrier Family 25 (mitochondrial carrier; ornithine transporter) Member 15 (SLC25A15, Accession NM_014252) is another VGAM2402 host target gene. SLC25A15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC25A15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC25A15 BINDING SITE, designated SEQ ID:15525, to the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81459] Another function of VGAM2402 is therefore inhibition of Solute Carrier Family 25 (mitochondrial carrier; ornithine transporter) Member 15 (SLC25A15, Accession NM_014252), a gene which participates theornithine transport across inner mitochondrial membrane, from the cytoplasm to the matrix. Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with SLC25A15. The function of SLC25A15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM172.Baculoviral IAP Repeat-containing 5 (survivin) (BIRC5, Accession NM_001168) is another VGAM2402 host target gene. BIRC5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BIRC5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BIRC5 BINDING SITE, designated SEQ ID:6835, to the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81460] Another function of VGAM2402 is therefore inhibition of Baculoviral IAP Repeat-containing 5 (survivin) (BIRC5, Accession NM_001168). Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BIRC5. Carbohydrate (chondroitin) Synthase 1 (CHSY1, Accession NM_014918) is another VGAM2402 host target gene. CHSY1 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by CHSY1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHSY1 BINDING SITE, designated SEQ ID:17170, to the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81461] Another function of VGAM2402 is therefore inhibition of Carbohydrate (chondroitin) Synthase 1 (CHSY1, Accession NM_014918). Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHSY1. DKFZP434P0721 (Accession XM_033181) is another VGAM2402 host target gene. DKFZP434P0721 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434P0721, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434P0721 BINDING SITE, designated SEQ ID:31868, to the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81462] Another function of VGAM2402 is therefore inhibition of DKFZP434P0721 (Accession XM_033181). Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434P0721. KIAA1336 (Accession XM_051306) is another VGAM2402 host target gene. KIAA1336 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1336, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1336 BINDING SITE, designated SEQ ID:35800, to the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81463] Another function of VGAM2402 is therefore inhibition of KIAA1336 (Accession XM_051306). Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1336. Period Homolog 3 (Drosophila) (PER3, Accession NM_016831) is another VGAM2402 host target gene. PER3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PER3, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PER3 BINDING SITE, designated SEQ ID:18821, to the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81464] Another function of VGAM2402 is therefore inhibition of Period Homolog 3 (Drosophila) (PER3, Accession NM_016831). Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PER3. SS-56 (Accession XM_006063) is another VGAM2402 host target gene. SS-56 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SS-56, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SS-56 BINDING SITE, designated SEQ ID:29987, to the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81465] Another function of VGAM2402 is therefore inhibition of SS-56 (Accession XM_006063). Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with SS-56. LOC148195 (Accession XM_097419) is another VGAM2402 host target gene. LOC148195 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148195 BINDING SITE, designated SEQ ID:40871, to the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81466] Another function of VGAM2402 is therefore inhibition of LOC148195 (Accession XM_097419). Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148195. LOC152503 (Accession XM_098238) is another VGAM2402 host target gene. LOC152503 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152503, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152503 BINDING SITE, designated SEQ ID:41515, to

the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81467] Another function of VGAM2402 is therefore inhibition of LOC152503 (Accession XM_098238). Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152503. LOC51580 (Accession NM_015874) is another VGAM2402 host target gene. LOC51580 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51580, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51580 BINDING SITE, designated SEQ ID:18015, to the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81468] Another function of VGAM2402 is therefore inhibition of LOC51580 (Accession NM_015874). Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51580. LOC90906 (Accession XM_034809) is another VGAM2402 host target gene. LOC90906 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC90906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90906 BINDING SITE, designated SEQ ID:32146, to the nucleotide sequence of VGAM2402 RNA, herein designated VGAM RNA, also designated SEQ ID:5113.

[81469] Another function of VGAM2402 is therefore inhibition of LOC90906 (Accession XM_034809). Accordingly, utilities of VGAM2402 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90906. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2403 (VGAM2403) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81470] VGAM2403 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2403 was detected is described hereinabove with reference to Figs. 1-8.

[81471] VGAM2403 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Goatpox Virus. VGAM2403 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81472] VGAM2403 gene encodes a VGAM2403 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2403 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2403 precursor RNA is designated SEQ ID:2389, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2389 is located at position 52365 relative to the genome of Goatpox Virus.

[81473] VGAM2403 precursor RNA folds onto itself, forming VGAM2403 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81474] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2403 folded precursor RNA into VGAM2403 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 85%) nucleotide sequence of VGAM2403 RNA is designated SEQ ID:5114, and is provided hereinbelow with reference to the sequence listing part.

[81475] VGAM2403 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2403 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2403 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81476] VGAM2403 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2403 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2403 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2403 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2403 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81477] The complementary binding of VGAM2403 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2403 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2403

host target RNA into VGAM2403 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81478] It is appreciated that VGAM2403 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2403 host target genes. The mRNA of each one of this plurality of VGAM2403 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2403 RNA, herein designated VGAM RNA, and which when bound by VGAM2403 RNA causes inhibition of translation of respective one or more VGAM2403 host target proteins.

[81479] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2403 gene, herein designated VGAM GENE, on one or more VGAM2403 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81480] It is yet further appreciated that a function of VGAM2403 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2403 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2403 correlate with, and may be deduced from, the identity of the host target genes which VGAM2403 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81481] Nucleotide sequences of the VGAM2403 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2403 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2403 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2403 are further

described hereinbelow with reference to Table 1.

[81482] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2403 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2403 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81483] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2403 gene, herein designated VGAM is inhibition of expression of VGAM2403 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2403 correlate with, and may be deduced from, the identity of the target genes which VGAM2403 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81484] Solute Carrier Family 6 (neurotransmitter transporter, creatine), Member 8 (SLC6A8, Accession NM_005629) is a VGAM2403 host target gene. SLC6A8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC6A8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of SLC6A8 BINDING SITE, designated SEQ ID:12145, to the nucleotide sequence of VGAM2403 RNA, herein designated VGAM RNA, also designated SEQ ID:5114.

[81485] A function of VGAM2403 is therefore inhibition of Solute Carrier Family 6 (neurotransmitter transporter, creatine), Member 8 (SLC6A8, Accession NM_005629). Accordingly, utilities of VGAM2403 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A8. FLJ20291 (Accession NM_017748) is another VGAM2403 host target gene. FLJ20291 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20291, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20291 BINDING SITE, designated SEQ ID:19341, to the nucleotide sequence of VGAM2403 RNA, herein designated VGAM RNA, also designated SEQ ID:5114.

[81486] Another function of VGAM2403 is therefore inhibition of FLJ20291 (Accession NM_017748). Accordingly, utilities of VGAM2403 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20291. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2404 (VGAM2404) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81487] VGAM2404 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2404 was detected is described hereinabove with reference to Figs. 1-8.

[81488] VGAM2404 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2404 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81489] VGAM2404 gene encodes a VGAM2404 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2404 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2404 precursor RNA is designated SEQ ID:2390, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2390 is located at position 65726 relative to the genome of Goatpox Virus.

[81490] VGAM2404 precursor RNA folds onto itself, forming VGAM2404 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81491] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2404 folded precursor RNA into VGAM2404 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2404 RNA is designated SEQ ID:5115, and is provided hereinbelow with reference to the sequence listing part.

[81492] VGAM2404 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2404 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2404 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81493] VGAM2404 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2404 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2404 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2404 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2404 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81494] The complementary binding of VGAM2404 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2404 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2404 host target RNA into VGAM2404 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81495] It is appreciated that VGAM2404 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2404 host target genes. The mRNA of each one of this plurality of VGAM2404 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2404 RNA, herein designated VGAM RNA, and which when bound by VGAM2404 RNA causes

inhibition of translation of respective one or more VGAM2404 host target proteins.

[81496] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2404 gene, herein designated VGAM GENE, on one or more VGAM2404 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81497] It is yet further appreciated that a function of VGAM2404 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2404 include diagnosis, prevention and

treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2404 correlate with, and may be deduced from, the identity of the host target genes which VGAM2404 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81498] Nucleotide sequences of the VGAM2404 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2404 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2404 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2404 are further described hereinbelow with reference to Table 1.

[81499] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2404 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2404 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81500] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2404 gene, herein designated VGAM is inhibition of expression of VGAM2404 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2404 correlate with, and may be deduced from, the identity of the target genes which VGAM2404 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81501] DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 20, 103kDa (DDX20, Accession NM_007204) is a VGAM2404 host target gene. DDX20 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DDX20, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDX20 BINDING SITE, designated SEQ ID:14066, to the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81502] A function of VGAM2404 is therefore inhibition of DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 20, 103kDa (DDX20, Accession NM_007204), a gene which interacts with SMN and is required for pre-mRNA splicing in the nucleus. Accordingly, utilities of VGAM2404 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX20. The function of DDX20

and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1929.Transforming, Acidic Coiled-coil Containing Protein 1 (TACC1, Accession NM_006283) is another VGAM2404 host target gene. TACC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TACC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TACC1 BINDING SITE, designated SEQ ID:12965, to the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81503] Another function of VGAM2404 is therefore inhibition of Transforming, Acidic Coiled-coil Containing Protein 1 (TACC1, Accession NM_006283). Accordingly, utilities of VGAM2404 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TACC1. DnaJ (Hsp40) Homolog, Subfamily A, Member 2 (DNAJA2, Accession XM_007963) is another VGAM2404 host target gene. DNAJA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

DNAJA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DNAJA2 BINDING SITE, designated SEQ ID:30068, to the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81504] Another function of VGAM2404 is therefore inhibition of DnaJ (Hsp40) Homolog, Subfamily A, Member 2 (DNAJA2, Accession XM_007963). Accordingly, utilities of VGAM2404 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DNAJA2. FLJ12888 (Accession NM_024945) is another VGAM2404 host target gene. FLJ12888 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12888, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12888 BINDING SITE, designated SEQ ID:24496, to the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81505] Another function of VGAM2404 is therefore inhibition of

FLJ12888 (Accession NM_024945). Accordingly, utilities of VGAM2404 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12888. KIAA0205 (Accession NM_014873) is another VGAM2404 host target gene. KIAA0205 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0205, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0205 BINDING SITE, designated SEQ ID:17007, to the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81506] Another function of VGAM2404 is therefore inhibition of KIAA0205 (Accession NM_014873). Accordingly, utilities of VGAM2404 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0205. KIAA0332 (Accession XM_031553) is another VGAM2404 host target gene. KIAA0332 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0332, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0332 BINDING SITE, designated SEQ ID:31415, to the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81507] Another function of VGAM2404 is therefore inhibition of KIAA0332 (Accession XM_031553). Accordingly, utilities of VGAM2404 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0332. Nudix (nucleoside diphosphate linked moiety X)-type Motif 11 (NUDT11, Accession XM_010230) is another VGAM2404 host target gene. NUDT11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUDT11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUDT11 BINDING SITE, designated SEQ ID:30142, to the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81508] Another function of VGAM2404 is therefore inhibition of Nudix (nucleoside diphosphate linked moiety X)-type Motif 11 (NUDT11, Accession XM_010230). Accordingly, utilities of VGAM2404 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with NUDT11. PI4KII (Accession NM_018425) is another VGAM2404 host target gene. PI4KII BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PI4KII, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PI4KII BINDING SITE, designated SEQ ID:20483, to the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81509] Another function of VGAM2404 is therefore inhibition of PI4KII (Accession NM_018425). Accordingly, utilities of VGAM2404 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PI4KII. LOC152316 (Accession XM_098185) is another VGAM2404 host target gene. LOC152316 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152316, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152316 BINDING SITE, designated SEQ ID:41456, to

the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81510] Another function of VGAM2404 is therefore inhibition of LOC152316 (Accession XM_098185). Accordingly, utilities of VGAM2404 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152316. LOC153259 (Accession XM_098342) is another VGAM2404 host target gene. LOC153259 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153259 BINDING SITE, designated SEQ ID:41602, to the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81511] Another function of VGAM2404 is therefore inhibition of LOC153259 (Accession XM_098342). Accordingly, utilities of VGAM2404 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153259. LOC90488 (Accession XM_032129) is another VGAM2404 host target gene. LOC90488 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC90488, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90488 BINDING SITE, designated SEQ ID:31558, to the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81512] Another function of VGAM2404 is therefore inhibition of LOC90488 (Accession XM_032129). Accordingly, utilities of VGAM2404 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90488. LOC90750 (Accession XM_033868) is another VGAM2404 host target gene. LOC90750 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90750, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90750 BINDING SITE, designated SEQ ID:31968, to the nucleotide sequence of VGAM2404 RNA, herein designated VGAM RNA, also designated SEQ ID:5115.

[81513] Another function of VGAM2404 is therefore inhibition of LOC90750 (Accession XM_033868). Accordingly, utilities

of VGAM2404 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90750. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2405 (VGAM2405) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81514] VGAM2405 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2405 was detected is described hereinabove with reference to Figs. 1-8.

[81515] VGAM2405 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2405 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81516] VGAM2405 gene encodes a VGAM2405 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2405 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2405 precursor RNA is designated SEQ ID:2391, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2391 is located at position 127713 relative to the genome of Goatpox Virus.

[81517] VGAM2405 precursor RNA folds onto itself, forming VGAM2405 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81518] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2405 folded precursor RNA into VGAM2405 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2405 RNA is designated SEQ ID:5116, and

is provided hereinbelow with reference to the sequence listing part.

[81519] VGAM2405 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2405 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2405 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81520] VGAM2405 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2405 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2405 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2405 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2405 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81521] The complementary binding of VGAM2405 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2405 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2405 host target RNA into VGAM2405 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81522] It is appreciated that VGAM2405 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2405 host target genes. The mRNA of each one of this plurality of VGAM2405 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2405 RNA, herein designated VGAM RNA, and which when bound by VGAM2405 RNA causes inhibition of translation of respective one or more VGAM2405 host target proteins.

[81523] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2405 gene, herein designated VGAM GENE, on one or more VGAM2405 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81524] It is yet further appreciated that a function of VGAM2405 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2405 correlate with, and may be deduced from, the identity of the host target genes which VGAM2405 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81525] Nucleotide sequences of the VGAM2405 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2405 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2405 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2405 are further described hereinbelow with reference to Table 1.

[81526] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2405 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2405 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81527] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2405 gene, herein designated VGAM is inhibition of expression of VGAM2405 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2405 correlate with, and may be deduced from, the identity of the target genes which VGAM2405 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81528] Carbohydrate Kinase-like (CARKL, Accession NM_013276) is a VGAM2405 host target gene. CARKL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CARKL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CARKL BINDING SITE, designated SEQ ID:14939, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81529] A function of VGAM2405 is therefore inhibition of Carbohydrate Kinase-like (CARKL, Accession NM_013276), a gene which is a putative carbohydrate kinase and may be a modifier for the cystinosis phenotype. Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with CARKL. The function of CARKL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM419.Cell Division Cycle 25B (CDC25B, Accession NM_021873) is another VGAM2405 host target gene. CDC25B BINDING SITE1 and CDC25B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CDC25B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDC25B BINDING SITE1 and CDC25B BINDING SITE2, designated SEQ ID:22414 and SEQ ID:22418 respectively, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81530] Another function of VGAM2405 is therefore inhibition of Cell Division Cycle 25B (CDC25B, Accession NM_021873), a gene which is positively activated by dephosphorylation. Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC25B. The function of CDC25B and its association with various diseases and clinical conditions, has been established by previous studies, as de-

scribed hereinabove with reference to VGAM165.Cytochrome P450, Subfamily XIX (aromatization of androgens) (CYP19, Accession NM_000103) is another VGAM2405 host target gene. CYP19 BINDING SITE1 and CYP19 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CYP19, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP19 BINDING SITE1 and CYP19 BINDING SITE2, designated SEQ ID:5562 and SEQ ID:13531 respectively, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81531] Another function of VGAM2405 is therefore inhibition of Cytochrome P450, Subfamily XIX (aromatization of androgens) (CYP19, Accession NM_000103), a gene which catalyzes the last steps of estrogen biosynthesis. Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP19. The function of CYP19 and its association with various diseases and clinical conditions, has been established by previous studies, as described here-

inabove with reference to VGAM508.Membrane-spanning 4-domains, Subfamily A, Member 4 (MS4A4A, Accession NM_024021) is another VGAM2405 host target gene. MS4A4A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MS4A4A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MS4A4A BINDING SITE, designated SEQ ID:23449, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81532] Another function of VGAM2405 is therefore inhibition of Membrane-spanning 4-domains, Subfamily A, Member 4 (MS4A4A, Accession NM_024021), a gene which binds to the fc region of immunoglobulins epsilon. high affinity receptor. initiating the allergic response. Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MS4A4A. The function of MS4A4A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM329.C-myc Binding Protein

(MYCBP, Accession NM_012333) is another VGAM2405 host target gene. MYCBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYCBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYCBP BINDING SITE, designated SEQ ID:14726, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81533] Another function of VGAM2405 is therefore inhibition of C-myc Binding Protein (MYCBP, Accession NM_012333), a gene which binds c-Myc stimulating the activation of E-box-dependent transcription. Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYCBP. The function of MYCBP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM435.Phosphoribosylaminoimidazole Carboxylase, Phosphoribosylaminoimidazole Succinocarboxamide Synthetase (PAICS, Accession NM_006452) is another VGAM2405 host target gene. PAICS BINDING SITE is HOST

TARGET binding site found in the 3` untranslated region of mRNA encoded by PAICS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAICS BINDING SITE, designated SEQ ID:13167, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81534] Another function of VGAM2405 is therefore inhibition of Phosphoribosylaminoimidazole Carboxylase, Phosphoribosylaminoimidazole Succinocarboxamide Synthetase (PAICS, Accession NM_006452), a gene which is required for purine biosynthesis. Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAICS. The function of PAICS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM894.PRV1 (Accession XM_056490) is another VGAM2405 host target gene. PRV1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRV1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRV1 BINDING SITE, designated SEQ ID:36397, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81535] Another function of VGAM2405 is therefore inhibition of PRV1 (Accession XM_056490), a gene which may function as a hematopoietic receptor. Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRV1. The function of PRV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM778.Visinin-like 1 (VSNL1, Accession NM_003385) is another VGAM2405 host target gene. VSNL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VSNL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VSNL1 BINDING SITE, designated SEQ ID:9415, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81536] Another function of VGAM2405 is therefore inhibition of Visinin-like 1 (VSNL1, Accession NM_003385). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VSNL1. Kell Blood Group Precursor (McLeod phenotype) (XK, Accession NM_021083) is another VGAM2405 host target gene. XK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XK BINDING SITE, designated SEQ ID:22055, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81537] Another function of VGAM2405 is therefore inhibition of Kell Blood Group Precursor (McLeod phenotype) (XK, Accession NM_021083). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XK. Zinc Finger Protein 202 (ZNF202, Accession NM_003455) is another VGAM2405 host target gene. ZNF202 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by ZNF202, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF202 BINDING SITE, designated SEQ ID:9511, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81538] Another function of VGAM2405 is therefore inhibition of Zinc Finger Protein 202 (ZNF202, Accession NM_003455). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF202. Chromosome 21 Open Reading Frame 42 (C21orf42, Accession NM_058184) is another VGAM2405 host target gene. C21orf42 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C21orf42, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C21orf42 BINDING SITE, designated SEQ ID:27751, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81539] Another function of VGAM2405 is therefore inhibition of

Chromosome 21 Open Reading Frame 42 (C21orf42, Accession NM_058184). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C21orf42. Cyclin M4 (CNNM4, Accession NM_020184) is another VGAM2405 host target gene. CNNM4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNNM4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNNM4 BINDING SITE, designated SEQ ID:21423, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81540] Another function of VGAM2405 is therefore inhibition of Cyclin M4 (CNNM4, Accession NM_020184). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNNM4. CPEB1 (Accession NM_030594) is another VGAM2405 host target gene. CPEB1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CPEB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPEB1 BINDING SITE, designated SEQ ID:24960, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81541] Another function of VGAM2405 is therefore inhibition of CPEB1 (Accession NM_030594). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPEB1. DKFZP434G1415 (Accession NM_031292) is another VGAM2405 host target gene. DKFZP434G1415 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434G1415, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434G1415 BINDING SITE, designated SEQ ID:25316, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81542] Another function of VGAM2405 is therefore inhibition of DKFZP434G1415 (Accession NM_031292). Accordingly, utilities of VGAM2405 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZP434G1415. DKFZP564D0462 (Accession XM_047080) is another VGAM2405 host target gene. DKFZP564D0462 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564D0462, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564D0462 BINDING SITE, designated SEQ ID:34896, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81543] Another function of VGAM2405 is therefore inhibition of DKFZP564D0462 (Accession XM_047080). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564D0462. DKFZp761F2014 (Accession NM_020215) is another VGAM2405 host target gene. DKFZp761F2014 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp761F2014, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the

nucleotide sequences of DKFZp761F2014 BINDING SITE, designated SEQ ID:21461, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81544] Another function of VGAM2405 is therefore inhibition of DKFZp761F2014 (Accession NM_020215). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp761F2014. FLJ10830 (Accession NM_018235) is another VGAM2405 host target gene. FLJ10830 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10830, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10830 BINDING SITE, designated SEQ ID:20183, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81545] Another function of VGAM2405 is therefore inhibition of FLJ10830 (Accession NM_018235). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10830. FLJ14753 (Accession NM_032558) is another

VGAM2405 host target gene. FLJ14753 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14753, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14753 BINDING SITE, designated SEQ ID:26286, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81546] Another function of VGAM2405 is therefore inhibition of FLJ14753 (Accession NM_032558). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14753. FLJ20195 (Accession NM_017706) is another VGAM2405 host target gene. FLJ20195 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20195, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20195 BINDING SITE, designated SEQ ID:19282, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81547] Another function of VGAM2405 is therefore inhibition of FLJ20195 (Accession NM_017706). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20195. Gamma-aminobutyric Acid (GABA) B Receptor, 1 (GABBR1, Accession NM_001470) is another VGAM2405 host target gene. GABBR1 BINDING SITE1 and GABBR1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GABBR1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABBR1 BINDING SITE1 and GABBR1 BINDING SITE2, designated SEQ ID:7207 and SEQ ID:22425 respectively, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81548] Another function of VGAM2405 is therefore inhibition of Gamma-aminobutyric Acid (GABA) B Receptor, 1 (GABBR1, Accession NM_001470). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABBR1. Syndecan 3 (N-syndecan) (SDC3, Accession NM_014654) is another VGAM2405 host target gene.

SDC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SDC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDC3 BINDING SITE, designated SEQ ID:16092, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81549] Another function of VGAM2405 is therefore inhibition of Syndecan 3 (N-syndecan) (SDC3, Accession NM_014654). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SDC3. Zinc Finger Protein 297B (ZNF297B, Accession NM_014007) is another VGAM2405 host target gene. ZNF297B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF297B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF297B BINDING SITE, designated SEQ ID:15219, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81550] Another function of VGAM2405 is therefore inhibition of Zinc Finger Protein 297B (ZNF297B, Accession NM_014007). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF297B. LOC133418 (Accession XM_059649) is another VGAM2405 host target gene. LOC133418 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC133418, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133418 BINDING SITE, designated SEQ ID:37042, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81551] Another function of VGAM2405 is therefore inhibition of LOC133418 (Accession XM_059649). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133418. LOC143173 (Accession XM_016685) is another VGAM2405 host target gene. LOC143173 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143173, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143173 BINDING SITE, designated SEQ ID:30274, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81552] Another function of VGAM2405 is therefore inhibition of LOC143173 (Accession XM_016685). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143173. LOC148811 (Accession XM_086326) is another VGAM2405 host target gene. LOC148811 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148811, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148811 BINDING SITE, designated SEQ ID:38601, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81553] Another function of VGAM2405 is therefore inhibition of LOC148811 (Accession XM_086326). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC148811. LOC152018 (Accession XM_098156) is another VGAM2405 host target gene. LOC152018 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152018, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152018 BINDING SITE, designated SEQ ID:41422, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81554] Another function of VGAM2405 is therefore inhibition of LOC152018 (Accession XM_098156). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152018. LOC253639 (Accession XM_171060) is another VGAM2405 host target gene. LOC253639 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253639, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253639 BINDING SITE, designated SEQ ID:45855, to

the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81555] Another function of VGAM2405 is therefore inhibition of LOC253639 (Accession XM_171060). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253639. LOC91689 (Accession NM_033318) is another VGAM2405 host target gene. LOC91689 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91689, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91689 BINDING SITE, designated SEQ ID:27158, to the nucleotide sequence of VGAM2405 RNA, herein designated VGAM RNA, also designated SEQ ID:5116.

[81556] Another function of VGAM2405 is therefore inhibition of LOC91689 (Accession NM_033318). Accordingly, utilities of VGAM2405 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91689. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2406 (VGAM2406) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81557] VGAM2406 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2406 was detected is described hereinabove with reference to Figs. 1-8.

[81558] VGAM2406 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2406 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81559] VGAM2406 gene encodes a VGAM2406 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2406 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2406 precursor RNA is designated SEQ ID:2392, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2392 is located at position 118549 relative to the genome of Goatpox Virus.

[81560] VGAM2406 precursor RNA folds onto itself, forming VGAM2406 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81561] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2406 folded precursor RNA into VGAM2406 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2406 RNA is designated SEQ ID:5117, and is provided hereinbelow with reference to the sequence listing part.

[81562] VGAM2406 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2406 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2406 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81563] VGAM2406 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2406 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2406 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2406 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2406 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81564] The complementary binding of VGAM2406 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2406 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2406 host target RNA into VGAM2406 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81565] It is appreciated that VGAM2406 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2406 host target genes. The mRNA of each one of this plurality of VGAM2406 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2406 RNA, herein designated VGAM RNA, and which when bound by VGAM2406 RNA causes inhibition of translation of respective one or more VGAM2406 host target proteins.

[81566] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2406 gene, herein designated VGAM GENE, on one or more VGAM2406 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81567] It is yet further appreciated that a function of VGAM2406 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2406 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2406 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2406 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81568] Nucleotide sequences of the VGAM2406 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2406 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2406 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2406 are further described hereinbelow with reference to Table 1.

[81569] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2406 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2406 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81570] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2406 gene, herein designated VGAM is inhibition of expression of VGAM2406 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2406 correlate with, and may be deduced from, the identity of the target genes which VGAM2406

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81571] Dishevelled Associated Activator of Morphogenesis 2 (DAAM2, Accession XM_166434) is a VGAM2406 host target gene. DAAM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DAAM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DAAM2 BINDING SITE, designated SEQ ID:44333, to the nucleotide sequence of VGAM2406 RNA, herein designated VGAM RNA, also designated SEQ ID:5117.

[81572] A function of VGAM2406 is therefore inhibition of Dishevelled Associated Activator of Morphogenesis 2 (DAAM2, Accession XM_166434), a gene which controls cell polarity and movement during development. Accordingly, utilities of VGAM2406 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DAAM2. The function of DAAM2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM247.LOC153711 (Accession

XM_098419) is another VGAM2406 host target gene. LOC153711 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153711, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153711 BINDING SITE, designated SEQ ID:41667, to the nucleotide sequence of VGAM2406 RNA, herein designated VGAM RNA, also designated SEQ ID:5117.

[81573] Another function of VGAM2406 is therefore inhibition of LOC153711 (Accession XM_098419). Accordingly, utilities of VGAM2406 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153711. LOC154442 (Accession XM_098536) is another VGAM2406 host target gene. LOC154442 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154442, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154442 BINDING SITE, designated SEQ ID:41704, to the nucleotide sequence of VGAM2406 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5117.

[81574] Another function of VGAM2406 is therefore inhibition of LOC154442 (Accession XM_098536). Accordingly, utilities of VGAM2406 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154442. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2407 (VGAM2407) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81575] VGAM2407 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2407 was detected is described hereinabove with reference to Figs. 1-8.

[81576] VGAM2407 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2407 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81577] VGAM2407 gene encodes a VGAM2407 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2407 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2407 precursor RNA is designated SEQ ID:2393, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2393 is located at position 111620 relative to the genome of Goatpox Virus.

[81578] VGAM2407 precursor RNA folds onto itself, forming VGAM2407 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81579] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2407 folded precursor RNA into VGAM2407 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2407 RNA is designated SEQ ID:5118, and is provided hereinbelow with reference to the sequence listing part.

[81580] VGAM2407 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2407 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2407 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81581] VGAM2407 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2407 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2407 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2407 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2407 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81582] The complementary binding of VGAM2407 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2407 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2407 host target RNA into VGAM2407 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81583] It is appreciated that VGAM2407 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2407 host target genes. The mRNA of

each one of this plurality of VGAM2407 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2407 RNA, herein designated VGAM RNA, and which when bound by VGAM2407 RNA causes inhibition of translation of respective one or more VGAM2407 host target proteins.

[81584] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2407 gene, herein designated VGAM GENE, on one or more VGAM2407 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[81585] It is yet further appreciated that a function of VGAM2407 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2407 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2407 correlate with, and may be deduced from, the identity of the host target genes which VGAM2407 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81586] Nucleotide sequences of the VGAM2407 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2407 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2407 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2407 are further described hereinbelow with reference to Table 1.

[81587] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2407 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2407 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81588] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2407 gene, herein designated VGAM is inhibition of expression of VGAM2407 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2407 correlate with, and may be deduced from, the identity of the target genes which VGAM2407 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81589] DEAD/H (Asp-Glu-Ala-Asp/His) Box Polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (DDX11, Accession NM_030655) is a VGAM2407 host target gene. DDX11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DDX11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDX11 BINDING SITE, designated SEQ ID:24985, to the nucleotide sequence of VGAM2407 RNA, herein designated VGAM RNA, also designated SEQ ID:5118.

[81590] A function of VGAM2407 is therefore inhibition of DEAD/

H (Asp-Glu-Ala-Asp/His) Box Polypeptide 11 (CHL1-like helicase homolog, S. cerevisiae) (DDX11, Accession NM_030655), a gene which could be an ATP-dependent DNA-binding helicase and may intervene in cell cycle regulation. Accordingly, utilities of VGAM2407 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDX11. The function of DDX11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1533.KIAA0836 (Accession XM_035390) is another VGAM2407 host target gene. KIAA0836 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0836, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0836 BINDING SITE, designated SEQ ID:32243, to the nucleotide sequence of VGAM2407 RNA, herein designated VGAM RNA, also designated SEQ ID:5118.

[81591] Another function of VGAM2407 is therefore inhibition of KIAA0836 (Accession XM_035390). Accordingly, utilities of VGAM2407 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0836. MGC2574 (Accession NM_024098) is another VGAM2407 host target gene. MGC2574 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2574, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2574 BINDING SITE, designated SEQ ID:23537, to the nucleotide sequence of VGAM2407 RNA, herein designated VGAM RNA, also designated SEQ ID:5118.

[81592] Another function of VGAM2407 is therefore inhibition of MGC2574 (Accession NM_024098). Accordingly, utilities of VGAM2407 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2574. LOC133362 (Accession XM_068305) is another VGAM2407 host target gene. LOC133362 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC133362, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133362 BINDING SITE, designated SEQ ID:37379, to

the nucleotide sequence of VGAM2407 RNA, herein designated VGAM RNA, also designated SEQ ID:5118.

[81593] Another function of VGAM2407 is therefore inhibition of LOC133362 (Accession XM_068305). Accordingly, utilities of VGAM2407 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133362. LOC145078 (Accession XM_015840) is another VGAM2407 host target gene. LOC145078 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145078, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145078 BINDING SITE, designated SEQ ID:30247, to the nucleotide sequence of VGAM2407 RNA, herein designated VGAM RNA, also designated SEQ ID:5118.

[81594] Another function of VGAM2407 is therefore inhibition of LOC145078 (Accession XM_015840). Accordingly, utilities of VGAM2407 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145078. LOC145676 (Accession XM_085202) is another VGAM2407 host target gene. LOC145676 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC145676, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145676 BINDING SITE, designated SEQ ID:37920, to the nucleotide sequence of VGAM2407 RNA, herein designated VGAM RNA, also designated SEQ ID:5118.

[81595] Another function of VGAM2407 is therefore inhibition of LOC145676 (Accession XM_085202). Accordingly, utilities of VGAM2407 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145676. LOC90459 (Accession XM_031826) is another VGAM2407 host target gene. LOC90459 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90459, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90459 BINDING SITE, designated SEQ ID:31490, to the nucleotide sequence of VGAM2407 RNA, herein designated VGAM RNA, also designated SEQ ID:5118.

[81596] Another function of VGAM2407 is therefore inhibition of LOC90459 (Accession XM_031826). Accordingly, utilities

of VGAM2407 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90459. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2408 (VGAM2408) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81597] VGAM2408 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2408 was detected is described hereinabove with reference to Figs. 1-8.

[81598] VGAM2408 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2408 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81599] VGAM2408 gene encodes a VGAM2408 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2408 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2408 precursor RNA is designated SEQ ID:2394, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2394 is located at position 36819 relative to the genome of Goatpox Virus.

[81600] VGAM2408 precursor RNA folds onto itself, forming VGAM2408 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81601] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2408 folded precursor RNA into VGAM2408 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2408 RNA is designated SEQ ID:5119, and

is provided hereinbelow with reference to the sequence listing part.

[81602] VGAM2408 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2408 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2408 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81603] VGAM2408 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2408 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2408 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2408 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2408 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81604] The complementary binding of VGAM2408 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2408 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2408 host target RNA into VGAM2408 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81605] It is appreciated that VGAM2408 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2408 host target genes. The mRNA of each one of this plurality of VGAM2408 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2408 RNA, herein designated VGAM RNA, and which when bound by VGAM2408 RNA causes inhibition of translation of respective one or more VGAM2408 host target proteins.

[81606] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2408 gene, herein designated VGAM GENE, on one or more VGAM2408 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81607] It is yet further appreciated that a function of VGAM2408 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2408 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2408 correlate with, and may be deduced from, the identity of the host target genes which VGAM2408 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81608] Nucleotide sequences of the VGAM2408 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2408 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2408 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2408 are further described hereinbelow with reference to Table 1.

[81609] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2408 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2408 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81610] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2408 gene, herein designated VGAM is inhibition of expression of VGAM2408 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2408 correlate with, and may be deduced from, the identity of the target genes which VGAM2408 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81611] Myeloma Overexpressed Gene (in a subset of t(11;14) Positive Multiple Myelomas) (MYEOV, Accession NM_138768) is a VGAM2408 host target gene. MYEOV BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MYEOV, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYEOV BINDING SITE, designated SEQ ID:28998, to the nucleotide sequence of VGAM2408 RNA, herein designated VGAM RNA, also designated SEQ ID:5119.

[81612] A function of VGAM2408 is therefore inhibition of Myeloma Overexpressed Gene (in a subset of t(11;14) Positive Multiple Myelomas) (MYEOV, Accession NM_138768), a gene which is encoded by MYELOMA OVEREXPRESSED GENE. Accordingly, utilities of VGAM2408

include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYEOV. The function of MYEOV and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM471.JDD1 (Accession XM_032515) is another VGAM2408 host target gene. JDD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by JDD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JDD1 BINDING SITE, designated SEQ ID:31667, to the nucleotide sequence of VGAM2408 RNA, herein designated VGAM RNA, also designated SEQ ID:5119.

[81613] Another function of VGAM2408 is therefore inhibition of JDD1 (Accession XM_032515). Accordingly, utilities of VGAM2408 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JDD1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2409 (VGAM2409) viral gene, which modulates expression

of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81614] VGAM2409 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2409 was detected is described hereinabove with reference to Figs. 1-8.

[81615] VGAM2409 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2409 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81616] VGAM2409 gene encodes a VGAM2409 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2409 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2409 precursor RNA is designated SEQ ID:2395, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2395 is located at position 109177 relative to the genome of Goatpox Virus.

[81617] VGAM2409 precursor RNA folds onto itself, forming VGAM2409 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81618] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2409 folded precursor RNA into VGAM2409 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 55%) nucleotide sequence of VGAM2409 RNA is designated SEQ ID:5120, and is provided hereinbelow with reference to the sequence listing part.

[81619] VGAM2409 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2409 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2409 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81620] VGAM2409 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2409 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2409 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2409 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2409 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81621] The complementary binding of VGAM2409 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2409 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2409 host target RNA into VGAM2409 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81622] It is appreciated that VGAM2409 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2409 host target genes. The mRNA of each one of this plurality of VGAM2409 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2409 RNA, herein designated VGAM RNA, and which when bound by VGAM2409 RNA causes inhibition of translation of respective one or more VGAM2409 host target proteins.

[81623] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2409 gene, herein designated VGAM GENE, on one or more VGAM2409 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81624] It is yet further appreciated that a function of VGAM2409 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2409 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2409 correlate with, and may be deduced from, the identity of the host target genes which VGAM2409 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[81625] Nucleotide sequences of the VGAM2409 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2409 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2409 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2409 are further described hereinbelow with reference to Table 1.

[81626] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2409 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2409 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81627] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2409 gene, herein designated VGAM is inhibition of expression of VGAM2409 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2409 correlate with, and may be deduced from, the identity of the target genes which VGAM2409 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81628] Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession NM_033285) is a VGAM2409 host target gene. TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TP53INP1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TP53INP1 BINDING SITE1 and TP53INP1 BINDING SITE2, designated SEQ ID:27105 and SEQ ID:36116 respectively, to the nucleotide sequence of VGAM2409 RNA, herein designated VGAM RNA, also designated SEQ ID:5120.

[81629] A function of VGAM2409 is therefore inhibition of Tumor Protein P53 Inducible Nuclear Protein 1 (TP53INP1, Accession NM_033285). Accordingly, utilities of VGAM2409 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53INP1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2410 (VGAM2410) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81630] VGAM2410 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2410 was detected is described hereinabove with reference to Figs. 1-8.

[81631] VGAM2410 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2410 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81632] VGAM2410 gene encodes a VGAM2410 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2410 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2410 precursor RNA is designated SEQ ID:2396, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2396 is located at position 118894 relative to the genome of Goatpox Virus.

[81633] VGAM2410 precursor RNA folds onto itself, forming VGAM2410 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81634] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2410 folded precursor RNA into VGAM2410 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2410 RNA is designated SEQ ID:5121, and is provided hereinbelow with reference to the sequence listing part.

[81635] VGAM2410 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2410 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2410 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[81636] VGAM2410 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2410 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2410 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2410 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2410 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81637] The complementary binding of VGAM2410 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2410 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2410 host target RNA into VGAM2410 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81638] It is appreciated that VGAM2410 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2410 host target genes. The mRNA of each one of this plurality of VGAM2410 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2410 RNA, herein designated VGAM RNA, and which when bound by VGAM2410 RNA causes inhibition of translation of respective one or more VGAM2410 host target proteins.

[81639] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2410 gene, herein designated VGAM GENE, on one or more VGAM2410 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81640] It is yet further appreciated that a function of VGAM2410 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2410 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2410 correlate with, and may be deduced from, the identity of the host target genes which VGAM2410 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81641] Nucleotide sequences of the VGAM2410 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2410 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2410 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2410 are further described hereinbelow with reference to Table 1.

[81642] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2410 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2410 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81643] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2410 gene, herein designated VGAM is inhibition of expression of VGAM2410 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2410 correlate with, and may be deduced from, the identity of the target genes which VGAM2410 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81644] SPF30 (Accession NM_005871) is a VGAM2410 host target gene. SPF30 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by SPF30, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPF30 BINDING SITE, designated SEQ ID:12490, to the nucleotide sequence of VGAM2410 RNA, herein designated VGAM RNA, also designated SEQ ID:5121.

[81645] A function of VGAM2410 is therefore inhibition of SPF30 (Accession NM_005871). Accordingly, utilities of VGAM2410 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPF30. LOC153339 (Accession XM_098362) is another VGAM2410 host target gene. LOC153339 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153339, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153339 BINDING SITE, designated SEQ ID:41614, to the nucleotide sequence of VGAM2410 RNA, herein designated VGAM RNA, also designated SEQ ID:5121.

[81646] Another function of VGAM2410 is therefore inhibition of

LOC153339 (Accession XM_098362). Accordingly, utilities of VGAM2410 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153339. LOC154739 (Accession XM_098602) is another VGAM2410 host target gene. LOC154739 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154739, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154739 BINDING SITE, designated SEQ ID:41711, to the nucleotide sequence of VGAM2410 RNA, herein designated VGAM RNA, also designated SEQ ID:5121.

[81647] Another function of VGAM2410 is therefore inhibition of LOC154739 (Accession XM_098602). Accordingly, utilities of VGAM2410 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154739. LOC92573 (Accession XM_045884) is another VGAM2410 host target gene. LOC92573 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92573, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of LOC92573 BINDING SITE, designated SEQ ID:34596, to the nucleotide sequence of VGAM2410 RNA, herein designated VGAM RNA, also designated SEQ ID:5121.

[81648] Another function of VGAM2410 is therefore inhibition of LOC92573 (Accession XM_045884). Accordingly, utilities of VGAM2410 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92573. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2411 (VGAM2411) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81649] VGAM2411 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2411 was detected is described hereinabove with reference to Figs. 1-8.

[81650] VGAM2411 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2411 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[81651] VGAM2411 gene encodes a VGAM2411 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2411 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2411 precursor RNA is designated SEQ ID:2397, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2397 is located at position 74764 relative to the genome of Goatpox Virus.

[81652] VGAM2411 precursor RNA folds onto itself, forming VGAM2411 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81653] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2411 folded precursor RNA into VGAM2411 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2411 RNA is designated SEQ ID:5122, and is provided hereinbelow with reference to the sequence listing part.

[81654] VGAM2411 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2411 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2411 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81655] VGAM2411 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2411 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2411 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2411 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2411 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81656] The complementary binding of VGAM2411 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2411 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2411 host target RNA into VGAM2411 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81657] It is appreciated that VGAM2411 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2411 host target genes. The mRNA of each one of this plurality of VGAM2411 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2411 RNA, herein designated VGAM RNA, and which when bound by VGAM2411 RNA causes inhibition of translation of respective one or more VGAM2411 host target proteins.

[81658] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2411 gene, herein designated VGAM GENE, on one or more VGAM2411 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81659] It is yet further appreciated that a function of VGAM2411 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2411 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2411 correlate with, and may be deduced from, the identity of the host target genes which VGAM2411 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81660] Nucleotide sequences of the VGAM2411 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2411 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2411 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2411 are further described hereinbelow with reference to Table 1.

[81661] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2411 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2411 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81662] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2411 gene, herein designated VGAM is inhibition of expression of VGAM2411 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2411 correlate with, and may be deduced from, the identity of the target genes which VGAM2411 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81663] Radixin (RDX, Accession NM_002906) is a VGAM2411 host target gene. RDX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RDX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RDX BINDING SITE, designated SEQ ID:8806, to the nucleotide sequence of VGAM2411 RNA, herein designated VGAM RNA, also designated SEQ ID:5122.

[81664] A function of VGAM2411 is therefore inhibition of Radixin

(RDX, Accession NM_002906), a gene which plays a crucial role in the binding of the barbed end of actin filaments to the plasma membrane. Accordingly, utilities of VGAM2411 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RDX. The function of RDX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM290.XT3 (Accession NM_020208) is another VGAM2411 host target gene. XT3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XT3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XT3 BINDING SITE, designated SEQ ID:21440, to the nucleotide sequence of VGAM2411 RNA, herein designated VGAM RNA, also designated SEQ ID:5122.

[81665] Another function of VGAM2411 is therefore inhibition of XT3 (Accession NM_020208), a gene which is a Kidney-specific orphan transporter. Accordingly, utilities of VGAM2411 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XT3. The function of XT3 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM21.FLJ10607 (Accession XM_085119) is another VGAM2411 host target gene. FLJ10607 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10607, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10607 BINDING SITE, designated SEQ ID:37832, to the nucleotide sequence of VGAM2411 RNA, herein designated VGAM RNA, also designated SEQ ID:5122.

[81666] Another function of VGAM2411 is therefore inhibition of FLJ10607 (Accession XM_085119). Accordingly, utilities of VGAM2411 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10607. KIAA1622 (Accession NM_058237) is another VGAM2411 host target gene. KIAA1622 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1622, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1622 BINDING SITE, designated SEQ ID:27762, to the nucleotide sequence of VGAM2411 RNA, herein designated VGAM RNA, also designated SEQ ID:5122.

[81667] Another function of VGAM2411 is therefore inhibition of KIAA1622 (Accession NM_058237). Accordingly, utilities of VGAM2411 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1622. LOC196812 (Accession XM_116868) is another VGAM2411 host target gene. LOC196812 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196812, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196812 BINDING SITE, designated SEQ ID:43131, to the nucleotide sequence of VGAM2411 RNA, herein designated VGAM RNA, also designated SEQ ID:5122.

[81668] Another function of VGAM2411 is therefore inhibition of LOC196812 (Accession XM_116868). Accordingly, utilities of VGAM2411 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196812. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2412 (VGAM2412) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81669] VGAM2412 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2412 was detected is described hereinabove with reference to Figs. 1-8.

[81670] VGAM2412 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2412 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81671] VGAM2412 gene encodes a VGAM2412 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2412 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2412 precursor RNA is designated SEQ ID:2398, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2398 is located at position 52802 relative to the

genome of Goatpox Virus.

[81672] VGAM2412 precursor RNA folds onto itself, forming VGAM2412 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81673] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2412 folded precursor RNA into VGAM2412 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 67%) nucleotide sequence of VGAM2412 RNA is designated SEQ ID:5123, and is provided hereinbelow with reference to the sequence listing part.

[81674] VGAM2412 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2412 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2412 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81675] VGAM2412 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2412 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2412 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2412 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2412 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81676] The complementary binding of VGAM2412 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2412 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2412 host target RNA into VGAM2412 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81677] It is appreciated that VGAM2412 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2412 host target genes. The mRNA of each one of this plurality of VGAM2412 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2412 RNA, herein designated VGAM RNA, and which when bound by VGAM2412 RNA causes inhibition of translation of respective one or more VGAM2412 host target proteins.

[81678] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2412 gene, herein designated VGAM GENE, on one or more VGAM2412 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81679] It is yet further appreciated that a function of VGAM2412 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2412 corre-

late with, and may be deduced from, the identity of the host target genes which VGAM2412 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81680] Nucleotide sequences of the VGAM2412 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2412 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2412 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2412 are further described hereinbelow with reference to Table 1.

[81681] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2412 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2412 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81682] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2412 gene, herein designated VGAM is inhibition of expression of VGAM2412 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2412 correlate with, and may be deduced

from, the identity of the target genes which VGAM2412 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81683] ATPase, Class VI, Type 11B (ATP11B, Accession XM_087254) is a VGAM2412 host target gene. ATP11B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP11B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP11B BINDING SITE, designated SEQ ID:39145, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also designated SEQ ID:5123.

[81684] A function of VGAM2412 is therefore inhibition of ATPase, Class VI, Type 11B (ATP11B, Accession XM_087254), a gene which is phosphorylated in their intermediate state, drives uphill transport of ions across membranes. Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP11B. The function of ATP11B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM665.Monoamine Oxidase

B (MAOB, Accession XM_010261) is another VGAM2412 host target gene. MAOB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAOB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAOB BINDING SITE, designated SEQ ID:30148, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also designated SEQ ID:5123.

[81685] Another function of VGAM2412 is therefore inhibition of Monoamine Oxidase B (MAOB, Accession XM_010261). Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAOB. Usher Syndrome 2A (autosomal recessive, mild) (USH2A, Accession NM_007123) is another VGAM2412 host target gene. USH2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by USH2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USH2A BINDING SITE, designated SEQ

ID:13981, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also designated SEQ ID:5123.

[81686] Another function of VGAM2412 is therefore inhibition of Usher Syndrome 2A (autosomal recessive, mild) (USH2A, Accession NM_007123). Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USH2A. Chromosome 3 Open Reading Frame 4 (C3orf4, Accession NM_019895) is another VGAM2412 host target gene. C3orf4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C3orf4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C3orf4 BINDING SITE, designated SEQ ID:21280, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also designated SEQ ID:5123.

[81687] Another function of VGAM2412 is therefore inhibition of Chromosome 3 Open Reading Frame 4 (C3orf4, Accession NM_019895). Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with C3orf4. Glia Maturation Factor, Beta (GMFB, Accession NM_004124) is another VGAM2412 host target gene. GMFB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GMFB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GMFB BINDING SITE, designated SEQ ID:10328, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also designated SEQ ID:5123.

[81688] Another function of VGAM2412 is therefore inhibition of Glia Maturation Factor, Beta (GMFB, Accession NM_004124). Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GMFB. KIAA0410 (Accession NM_014778) is another VGAM2412 host target gene. KIAA0410 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0410, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0410 BINDING SITE, designated SEQ

ID:16616, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also designated SEQ ID:5123.

[81689] Another function of VGAM2412 is therefore inhibition of KIAA0410 (Accession NM_014778). Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0410. KIAA1493 (Accession XM_034415) is another VGAM2412 host target gene. KIAA1493 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1493, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1493 BINDING SITE, designated SEQ ID:32093, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also designated SEQ ID:5123.

[81690] Another function of VGAM2412 is therefore inhibition of KIAA1493 (Accession XM_034415). Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1493. Nuclear Transcription Factor, X-box Binding 1 (NFX1, Accession NM_002504) is another VGAM2412 host

target gene. NFX1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NFX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFX1 BINDING SITE, designated SEQ ID:8327, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also designated SEQ ID:5123.

[81691] Another function of VGAM2412 is therefore inhibition of Nuclear Transcription Factor, X-box Binding 1 (NFX1, Accession NM_002504). Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFX1. LOC143425 (Accession XM_113695) is another VGAM2412 host target gene. LOC143425 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143425, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143425 BINDING SITE, designated SEQ ID:42356, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5123.

[81692] Another function of VGAM2412 is therefore inhibition of LOC143425 (Accession XM_113695). Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143425. LOC221540 (Accession XM_168133) is another VGAM2412 host target gene. LOC221540 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221540, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221540 BINDING SITE, designated SEQ ID:45046, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also designated SEQ ID:5123.

[81693] Another function of VGAM2412 is therefore inhibition of LOC221540 (Accession XM_168133). Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221540. LOC257545 (Accession XM_175217) is another VGAM2412 host target gene. LOC257545 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257545, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257545 BINDING SITE, designated SEQ ID:46694, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also designated SEQ ID:5123.

[81694] Another function of VGAM2412 is therefore inhibition of LOC257545 (Accession XM_175217). Accordingly, utilities of VGAM2412 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257545. LOC257598 (Accession XM_175295) is another VGAM2412 host target gene. LOC257598 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257598, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257598 BINDING SITE, designated SEQ ID:46751, to the nucleotide sequence of VGAM2412 RNA, herein designated VGAM RNA, also designated SEQ ID:5123.

[81695] Another function of VGAM2412 is therefore inhibition of LOC257598 (Accession XM_175295). Accordingly, utilities of VGAM2412 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC257598. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2413 (VGAM2413) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81696] VGAM2413 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2413 was detected is described hereinabove with reference to Figs. 1-8.

[81697] VGAM2413 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2413 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81698] VGAM2413 gene encodes a VGAM2413 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2413 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2413 precursor RNA is desig-

nated SEQ ID:2399, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2399 is located at position 77043 relative to the genome of Goatpox Virus.

[81699] VGAM2413 precursor RNA folds onto itself, forming VGAM2413 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81700] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2413 folded precursor RNA into VGAM2413 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2413 RNA is designated SEQ ID:5124, and is provided hereinbelow with reference to the sequence

listing part.

[81701] VGAM2413 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2413 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2413 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81702] VGAM2413 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2413 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2413 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2413 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2413 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81703] The complementary binding of VGAM2413 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2413 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2413 host target RNA into VGAM2413 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81704] It is appreciated that VGAM2413 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2413 host target genes. The mRNA of each one of this plurality of VGAM2413 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2413 RNA, herein designated VGAM

RNA, and which when bound by VGAM2413 RNA causes inhibition of translation of respective one or more VGAM2413 host target proteins.

[81705] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2413 gene, herein designated VGAM GENE, on one or more VGAM2413 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81706] It is yet further appreciated that a function of VGAM2413 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2413 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2413 correlate with, and may be deduced from, the identity of the host target genes which VGAM2413 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81707] Nucleotide sequences of the VGAM2413 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2413 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2413 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2413 are further described hereinbelow with reference to Table 1.

[81708] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2413 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2413 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81709] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2413 gene, herein designated VGAM is

inhibition of expression of VGAM2413 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2413 correlate with, and may be deduced from, the identity of the target genes which VGAM2413 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81710] KIAA1155 (Accession XM_030864) is a VGAM2413 host target gene. KIAA1155 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1155, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1155 BINDING SITE, designated SEQ ID:31197, to the nucleotide sequence of VGAM2413 RNA, herein designated VGAM RNA, also designated SEQ ID:5124.

[81711] A function of VGAM2413 is therefore inhibition of KIAA1155 (Accession XM_030864). Accordingly, utilities of VGAM2413 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1155. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2414 (VGAM2414) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81712] VGAM2414 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2414 was detected is described hereinabove with reference to Figs. 1-8.

[81713] VGAM2414 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2414 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81714] VGAM2414 gene encodes a VGAM2414 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2414 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2414 precursor RNA is designated SEQ ID:2400, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2400 is located at position 57820 relative to the genome of Goatpox Virus.

[81715] VGAM2414 precursor RNA folds onto itself, forming VGAM2414 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81716] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2414 folded precursor RNA into VGAM2414 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2414 RNA is designated SEQ ID:5125, and is provided hereinbelow with reference to the sequence listing part.

[81717] VGAM2414 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2414 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2414 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81718] VGAM2414 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2414 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2414 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2414 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2414 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81719] The complementary binding of VGAM2414 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2414 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2414 host target RNA into VGAM2414 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81720] It is appreciated that VGAM2414 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2414 host target genes. The mRNA of each one of this plurality of VGAM2414 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2414 RNA, herein designated VGAM RNA, and which when bound by VGAM2414 RNA causes inhibition of translation of respective one or more VGAM2414 host target proteins.

[81721] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2414 gene, herein designated VGAM GENE, on one or more VGAM2414 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81722] It is yet further appreciated that a function of VGAM2414 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2414 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2414 correlate with, and may be deduced from, the identity of the

host target genes which VGAM2414 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81723] Nucleotide sequences of the VGAM2414 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2414 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2414 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2414 are further described hereinbelow with reference to Table 1.

[81724] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2414 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2414 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81725] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2414 gene, herein designated VGAM is inhibition of expression of VGAM2414 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2414 correlate with, and may be deduced from, the identity of the target genes which VGAM2414

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81726] Mannosidase, Alpha, Class 2C, Member 1 (MAN2C1, Accession XM_053585) is a VGAM2414 host target gene. MAN2C1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAN2C1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAN2C1 BINDING SITE, designated SEQ ID:36101, to the nucleotide sequence of VGAM2414 RNA, herein designated VGAM RNA, also designated SEQ ID:5125.

[81727] A function of VGAM2414 is therefore inhibition of Mannosidase, Alpha, Class 2C, Member 1 (MAN2C1, Accession XM_053585), a gene which is Strongly similar to a region of rat ER alpha-mannosidase. Accordingly, utilities of VGAM2414 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAN2C1. The function of MAN2C1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM958.Proprotein Convertase Subtil-

isin/kexin Type 2 (PCSK2, Accession NM_002594) is another VGAM2414 host target gene. PCSK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCSK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCSK2 BINDING SITE, designated SEQ ID:8455, to the nucleotide sequence of VGAM2414 RNA, herein designated VGAM RNA, also designated SEQ ID:5125.

[81728] Another function of VGAM2414 is therefore inhibition of Proprotein Convertase Subtilisin/kexin Type 2 (PCSK2, Accession NM_002594), a gene which is involved in the processing of hormone and other protein precursors at sites comprised of pairs of basic amino acid residues. Accordingly, utilities of VGAM2414 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCSK2. The function of PCSK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1120.Phosphorylase Kinase, Alpha 2 (liver) (PHKA2, Accession NM_000292) is another VGAM2414 host target gene. PHKA2 BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PHKA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PHKA2 BINDING SITE, designated SEQ ID:5835, to the nucleotide sequence of VGAM2414 RNA, herein designated VGAM RNA, also designated SEQ ID:5125.

[81729] Another function of VGAM2414 is therefore inhibition of Phosphorylase Kinase, Alpha 2 (liver) (PHKA2, Accession NM_000292). Accordingly, utilities of VGAM2414 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHKA2. KIAA1458 (Accession XM_044434) is another VGAM2414 host target gene. KIAA1458 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1458, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1458 BINDING SITE, designated SEQ ID:34208, to the nucleotide sequence of VGAM2414 RNA, herein designated VGAM RNA, also designated SEQ ID:5125.

[81730] Another function of VGAM2414 is therefore inhibition of KIAA1458 (Accession XM_044434). Accordingly, utilities of VGAM2414 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1458. Rabip4R (Accession NM_017987) is another VGAM2414 host target gene. Rabip4R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Rabip4R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Rabip4R BINDING SITE, designated SEQ ID:19715, to the nucleotide sequence of VGAM2414 RNA, herein designated VGAM RNA, also designated SEQ ID:5125.

[81731] Another function of VGAM2414 is therefore inhibition of Rabip4R (Accession NM_017987). Accordingly, utilities of VGAM2414 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Rabip4R. Sulfotransferase Family 4A, Member 1 (SULT4A1, Accession XM_043609) is another VGAM2414 host target gene. SULT4A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SULT4A1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SULT4A1 BINDING SITE, designated SEQ ID:33974, to the nucleotide sequence of VGAM2414 RNA, herein designated VGAM RNA, also designated SEQ ID:5125.

[81732] Another function of VGAM2414 is therefore inhibition of Sulfotransferase Family 4A, Member 1 (SULT4A1, Accession XM_043609). Accordingly, utilities of VGAM2414 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SULT4A1. LOC146958 (Accession XM_097142) is another VGAM2414 host target gene. LOC146958 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146958, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146958 BINDING SITE, designated SEQ ID:40773, to the nucleotide sequence of VGAM2414 RNA, herein designated VGAM RNA, also designated SEQ ID:5125.

[81733] Another function of VGAM2414 is therefore inhibition of LOC146958 (Accession XM_097142). Accordingly, utilities

of VGAM2414 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146958. LOC257443 (Accession XM_171072) is another VGAM2414 host target gene. LOC257443 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257443, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257443 BINDING SITE, designated SEQ ID:45876, to the nucleotide sequence of VGAM2414 RNA, herein designated VGAM RNA, also designated SEQ ID:5125.

[81734] Another function of VGAM2414 is therefore inhibition of LOC257443 (Accession XM_171072). Accordingly, utilities of VGAM2414 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257443. LOC90643 (Accession XM_033145) is another VGAM2414 host target gene. LOC90643 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90643, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC90643 BINDING SITE, designated SEQ ID:31854, to the nucleotide sequence of VGAM2414 RNA, herein designated VGAM RNA, also designated SEQ ID:5125.

[81735] Another function of VGAM2414 is therefore inhibition of LOC90643 (Accession XM_033145). Accordingly, utilities of VGAM2414 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90643. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2415 (VGAM2415) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81736] VGAM2415 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2415 was detected is described hereinabove with reference to Figs. 1-8.

[81737] VGAM2415 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2415 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81738] VGAM2415 gene encodes a VGAM2415 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2415 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2415 precursor RNA is designated SEQ ID:2401, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2401 is located at position 96068 relative to the genome of Goatpox Virus.

[81739] VGAM2415 precursor RNA folds onto itself, forming VGAM2415 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81740] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2415 folded precursor RNA into VGAM2415 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2415 RNA is designated SEQ ID:5126, and is provided hereinbelow with reference to the sequence listing part.

[81741] VGAM2415 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2415 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2415 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81742] VGAM2415 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2415 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2415 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2415 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2415 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81743] The complementary binding of VGAM2415 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2415 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2415 host target RNA into VGAM2415 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81744] It is appreciated that VGAM2415 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2415 host target genes. The mRNA of each one of this plurality of VGAM2415 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2415 RNA, herein designated VGAM RNA, and which when bound by VGAM2415 RNA causes inhibition of translation of respective one or more VGAM2415 host target proteins.

[81745] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2415 gene, herein designated VGAM GENE, on one or more VGAM2415 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81746] It is yet further appreciated that a function of VGAM2415 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2415 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2415 correlate with, and may be deduced from, the identity of the host target genes which VGAM2415 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81747] Nucleotide sequences of the VGAM2415 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2415 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2415 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2415 are further described hereinbelow with reference to Table 1.

[81748] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2415 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2415 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81749] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2415 gene, herein designated VGAM is inhibition of expression of VGAM2415 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2415 correlate with, and may be deduced from, the identity of the target genes which VGAM2415 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81750] LanC Lantibiotic Synthetase Component C-like 2 (bacterial) (LANCL2, Accession NM_018697) is a VGAM2415 host target gene. LANCL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LANCL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LANCL2 BINDING SITE, designated SEQ ID:20779, to the nucleotide sequence of VGAM2415 RNA, herein designated VGAM RNA, also designated SEQ ID:5126.

[81751] A function of VGAM2415 is therefore inhibition of LanC Lantibiotic Synthetase Component C-like 2 (bacterial) (LANCL2, Accession NM_018697). Accordingly, utilities of VGAM2415 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LANCL2. Makorin, Ring Finger Protein, 1 (MKRN1, Accession NM_013446) is another VGAM2415 host target gene. MKRN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MKRN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MKRN1 BINDING SITE, designated SEQ ID:15114, to the nucleotide sequence of VGAM2415 RNA, herein designated VGAM RNA, also designated SEQ ID:5126.

[81752] Another function of VGAM2415 is therefore inhibition of Makorin, Ring Finger Protein, 1 (MKRN1, Accession NM_013446). Accordingly, utilities of VGAM2415 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKRN1. RTP801 (Accession NM_019058) is another VGAM2415 host target gene. RTP801 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by RTP801, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RTP801 BINDING SITE, designated SEQ ID:21140, to the nucleotide sequence of VGAM2415 RNA, herein designated VGAM RNA, also designated SEQ ID:5126.

[81753] Another function of VGAM2415 is therefore inhibition of RTP801 (Accession NM_019058). Accordingly, utilities of VGAM2415 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RTP801. LOC158450 (Accession XM_088580) is another VGAM2415 host target gene. LOC158450 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158450, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158450 BINDING SITE, designated SEQ ID:39843, to the nucleotide sequence of VGAM2415 RNA, herein designated VGAM RNA, also designated SEQ ID:5126.

[81754] Another function of VGAM2415 is therefore inhibition of

LOC158450 (Accession XM_088580). Accordingly, utilities of VGAM2415 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158450. LOC158504 (Accession XM_088591) is another VGAM2415 host target gene. LOC158504 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158504, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158504 BINDING SITE, designated SEQ ID:39854, to the nucleotide sequence of VGAM2415 RNA, herein designated VGAM RNA, also designated SEQ ID:5126.

[81755] Another function of VGAM2415 is therefore inhibition of LOC158504 (Accession XM_088591). Accordingly, utilities of VGAM2415 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158504. LOC253613 (Accession XM_171225) is another VGAM2415 host target gene. LOC253613 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253613, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC253613 BINDING SITE, designated SEQ ID:46011, to the nucleotide sequence of VGAM2415 RNA, herein designated VGAM RNA, also designated SEQ ID:5126.

[81756] Another function of VGAM2415 is therefore inhibition of LOC253613 (Accession XM_171225). Accordingly, utilities of VGAM2415 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253613. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2416 (VGAM2416) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81757] VGAM2416 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2416 was detected is described hereinabove with reference to Figs. 1-8.

[81758] VGAM2416 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2416 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[81759] VGAM2416 gene encodes a VGAM2416 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2416 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2416 precursor RNA is designated SEQ ID:2402, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2402 is located at position 126030 relative to the genome of Goatpox Virus.

[81760] VGAM2416 precursor RNA folds onto itself, forming VGAM2416 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81761] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2416 folded precursor RNA into VGAM2416 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2416 RNA is designated SEQ ID:5127, and is provided hereinbelow with reference to the sequence listing part.

[81762] VGAM2416 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2416 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2416 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81763] VGAM2416 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2416 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2416 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2416 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2416 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81764] The complementary binding of VGAM2416 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2416 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2416 host target RNA into VGAM2416 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81765] It is appreciated that VGAM2416 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2416 host target genes. The mRNA of each one of this plurality of VGAM2416 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2416 RNA, herein designated VGAM RNA, and which when bound by VGAM2416 RNA causes inhibition of translation of respective one or more VGAM2416 host target proteins.

[81766] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2416 gene, herein designated VGAM GENE, on one or more VGAM2416 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81767] It is yet further appreciated that a function of VGAM2416 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2416 correlate with, and may be deduced from, the identity of the host target genes which VGAM2416 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81768] Nucleotide sequences of the VGAM2416 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2416 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2416 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2416 are further described hereinbelow with reference to Table 1.

[81769] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2416 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2416 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81770] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2416 gene, herein designated VGAM is inhibition of expression of VGAM2416 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2416 correlate with, and may be deduced from, the identity of the target genes which VGAM2416 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81771] Core-binding Factor, Beta Subunit (CBFB, Accession NM_001755) is a VGAM2416 host target gene. CBFB BINDING SITE1 and CBFB BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CBFB, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBFB BINDING SITE1 and CBFB BINDING SITE2, designated SEQ ID:7509 and SEQ ID:23150 respectively, to the nucleotide sequence of VGAM2416

RNA, herein designated VGAM RNA, also designated SEQ ID:5127.

[81772] A function of VGAM2416 is therefore inhibition of Core-binding Factor, Beta Subunit (CBFB, Accession NM_001755), a gene which is beta subunit of the transcription factor CBF which causes leukemia. Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFB. The function of CBFB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM98.Secreted Frizzled-related Protein 1 (SFRP1, Accession NM_003012) is another VGAM2416 host target gene. SFRP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFRP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRP1 BINDING SITE, designated SEQ ID:8925, to the nucleotide sequence of VGAM2416 RNA, herein designated VGAM RNA, also designated SEQ ID:5127.

[81773] Another function of VGAM2416 is therefore inhibition of

Secreted Frizzled-related Protein 1 (SFRP1, Accession NM_003012), a gene which is a receptor for wnt proteins that may have an anti-apoptotic function. Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRP1. The function of SFRP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM250.Synaptotagmin IV (SYT4, Accession XM_031162) is another VGAM2416 host target gene. SYT4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYT4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYT4 BINDING SITE, designated SEQ ID:31294, to the nucleotide sequence of VGAM2416 RNA, herein designated VGAM RNA, also designated SEQ ID:5127.

[81774] Another function of VGAM2416 is therefore inhibition of Synaptotagmin IV (SYT4, Accession XM_031162), a gene which may be involved in ca2+-dependent exocytosis of secretory vesicles or may serve as ca2+ sensors in the process of vesicular trafficking and exocytosis. Accord-

ingly, utilities of VGAM2416 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYT4. The function of SYT4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Transient Receptor Potential Cation Channel, Subfamily C, Member 5 (TRPC5, Accession NM_012471) is another VGAM2416 host target gene. TRPC5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRPC5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPC5 BINDING SITE, designated SEQ ID:14852, to the nucleotide sequence of VGAM2416 RNA, herein designated VGAM RNA, also designated SEQ ID:5127.

[81775] Another function of VGAM2416 is therefore inhibition of Transient Receptor Potential Cation Channel, Subfamily C, Member 5 (TRPC5, Accession NM_012471). Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRPC5. MIG2 (Accession XM_051693) is another

VGAM2416 host target gene. MIG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MIG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MIG2 BINDING SITE, designated SEQ ID:35864, to the nucleotide sequence of VGAM2416 RNA, herein designated VGAM RNA, also designated SEQ ID:5127.

[81776] Another function of VGAM2416 is therefore inhibition of MIG2 (Accession XM_051693). Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MIG2. Nudix (nucleoside diphosphate linked moiety X)-type Motif 4 (NUDT4, Accession NM_019094) is another VGAM2416 host target gene. NUDT4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NUDT4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NUDT4 BINDING SITE, designated SEQ ID:21170, to the nucleotide sequence of VGAM2416 RNA, herein designated VGAM RNA,

also designated SEQ ID:5127.

[81777] Another function of VGAM2416 is therefore inhibition of Nudix (nucleoside diphosphate linked moiety X)-type Motif 4 (NUDT4, Accession NM_019094). Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NUDT4. PRO2012 (Accession NM_018614) is another VGAM2416 host target gene. PRO2012 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2012, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2012 BINDING SITE, designated SEQ ID:20682, to the nucleotide sequence of VGAM2416 RNA, herein designated VGAM RNA, also designated SEQ ID:5127.

[81778] Another function of VGAM2416 is therefore inhibition of PRO2012 (Accession NM_018614). Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2012. Synovial Sarcoma Translocation Gene On Chromosome 18-like 1 (SS18L1, Accession XM_037202) is another VGAM2416 host target gene. SS18L1 BINDING SITE

is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SS18L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SS18L1 BINDING SITE, designated SEQ ID:32566, to the nucleotide sequence of VGAM2416 RNA, herein designated VGAM RNA, also designated SEQ ID:5127.

[81779] Another function of VGAM2416 is therefore inhibition of Synovial Sarcoma Translocation Gene On Chromosome 18-like 1 (SS18L1, Accession XM_037202). Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SS18L1. Signal Transducing Adaptor Molecule (SH3 domain and ITAM motif) 2 (STAM2, Accession NM_005843) is another VGAM2416 host target gene. STAM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STAM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAM2 BINDING SITE, designated SEQ ID:12461, to the nucleotide sequence of VGAM2416 RNA,

herein designated VGAM RNA, also designated SEQ ID:5127.

[81780] Another function of VGAM2416 is therefore inhibition of Signal Transducing Adaptor Molecule (SH3 domain and ITAM motif) 2 (STAM2, Accession NM_005843). Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAM2. LOC139221 (Accession XM_066558) is another VGAM2416 host target gene. LOC139221 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC139221, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC139221 BINDING SITE, designated SEQ ID:37334, to the nucleotide sequence of VGAM2416 RNA, herein designated VGAM RNA, also designated SEQ ID:5127.

[81781] Another function of VGAM2416 is therefore inhibition of LOC139221 (Accession XM_066558). Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139221. LOC161734 (Accession XM_102109) is another VGAM2416 host target gene. LOC161734 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC161734, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161734 BINDING SITE, designated SEQ ID:42111, to the nucleotide sequence of VGAM2416 RNA, herein designated VGAM RNA, also designated SEQ ID:5127.

[81782] Another function of VGAM2416 is therefore inhibition of LOC161734 (Accession XM_102109). Accordingly, utilities of VGAM2416 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161734. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2417 (VGAM2417) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81783] VGAM2417 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2417 was detected is described hereinabove with reference to Figs. 1-8.

[81784] VGAM2417 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2417 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81785] VGAM2417 gene encodes a VGAM2417 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2417 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2417 precursor RNA is designated SEQ ID:2403, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2403 is located at position 96899 relative to the genome of Goatpox Virus.

[81786] VGAM2417 precursor RNA folds onto itself, forming VGAM2417 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[81787] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2417 folded precursor RNA into VGAM2417 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2417 RNA is designated SEQ ID:5128, and is provided hereinbelow with reference to the sequence listing part.

[81788] VGAM2417 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2417 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2417 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81789] VGAM2417 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2417 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2417 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2417 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2417 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81790] The complementary binding of VGAM2417 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2417 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2417 host target RNA into VGAM2417 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81791] It is appreciated that VGAM2417 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2417 host target genes. The mRNA of each one of this plurality of VGAM2417 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2417 RNA, herein designated VGAM RNA, and which when bound by VGAM2417 RNA causes inhibition of translation of respective one or more VGAM2417 host target proteins.

[81792] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2417 gene, herein designated VGAM GENE, on one or more VGAM2417 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81793] It is yet further appreciated that a function of VGAM2417 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2417 correlate with, and may be deduced from, the identity of the host target genes which VGAM2417 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81794] Nucleotide sequences of the VGAM2417 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2417 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2417 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2417 are further described hereinbelow with reference to Table 1.

[81795] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2417 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2417 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81796] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2417 gene, herein designated VGAM is inhibition of expression of VGAM2417 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2417 correlate with, and may be deduced from, the identity of the target genes which VGAM2417 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81797] Cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1, Accession NM_053056) is a VGAM2417 host target gene. CCND1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CCND1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of CCND1 BINDING SITE, designated SEQ ID:27601, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81798] A function of VGAM2417 is therefore inhibition of Cyclin D1 (PRAD1: parathyroid adenomatosis 1) (CCND1, Accession NM_053056), a gene which is involved in the control of cell cycle and is required for Schwann cell proliferation to proceed normally during Wallerian degeneration. Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCND1. The function of CCND1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM220.CD164 Antigen, Sialomucin (CD164, Accession NM_006016) is another VGAM2417 host target gene. CD164 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD164, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD164 BIND-

ING SITE, designated SEQ ID:12629, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81799] Another function of VGAM2417 is therefore inhibition of CD164 Antigen, Sialomucin (CD164, Accession NM_006016), a gene which plays a role in hematopoiesis by facilitating the adhesion of CD34+ cells to bone marrow stroma and negatively regulates CD34+ hematopoietic progenitor cell growth. Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD164. The function of CD164 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM75.Crystallin, Zeta (quinone reductase) (CRYZ, Accession NM_001889) is another VGAM2417 host target gene. CRYZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRYZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRYZ BINDING SITE, designated SEQ ID:7618, to the nucleotide sequence of VGAM2417 RNA, herein

designated VGAM RNA, also designated SEQ ID:5128.

[81800] Another function of VGAM2417 is therefore inhibition of Crystallin, Zeta (quinone reductase) (CRYZ, Accession NM_001889), a gene which may act in the detoxification of xenobiotics. Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRYZ. The function of CRYZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM323.FLJ12960 (Accession NM_024638) is another VGAM2417 host target gene. FLJ12960 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12960, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12960 BINDING SITE, designated SEQ ID:23919, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81801] Another function of VGAM2417 is therefore inhibition of FLJ12960 (Accession NM_024638). Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12960. KIAA0478 (Accession NM_014870) is another VGAM2417 host target gene. KIAA0478 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0478, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0478 BINDING SITE, designated SEQ ID:16984, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81802] Another function of VGAM2417 is therefore inhibition of KIAA0478 (Accession NM_014870). Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0478. KIAA1116 (Accession NM_014892) is another VGAM2417 host target gene. KIAA1116 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1116, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1116 BINDING SITE, designated SEQ ID:17040, to the

nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81803] Another function of VGAM2417 is therefore inhibition of KIAA1116 (Accession NM_014892). Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1116. KIAA1559 (Accession XM_054472) is another VGAM2417 host target gene. KIAA1559 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1559, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1559 BINDING SITE, designated SEQ ID:36165, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81804] Another function of VGAM2417 is therefore inhibition of KIAA1559 (Accession XM_054472). Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1559. PB1 (Accession NM_018165) is another VGAM2417 host target gene. PB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by PB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PB1 BINDING SITE, designated SEQ ID:19981, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81805] Another function of VGAM2417 is therefore inhibition of PB1 (Accession NM_018165). Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PB1. PRO0641 (Accession NM_014135) is another VGAM2417 host target gene. PRO0641 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO0641, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0641 BINDING SITE, designated SEQ ID:15402, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81806] Another function of VGAM2417 is therefore inhibition of PRO0641 (Accession NM_014135). Accordingly, utilities of

VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0641. SH3 Domain Binding Glutamic Acid-rich Protein Like 2 (SH3BGRL2, Accession NM_031469) is another VGAM2417 host target gene. SH3BGRL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3BGRL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3BGRL2 BINDING SITE, designated SEQ ID:25523, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81807] Another function of VGAM2417 is therefore inhibition of SH3 Domain Binding Glutamic Acid-rich Protein Like 2 (SH3BGRL2, Accession NM_031469). Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3BGRL2. Signal Sequence Receptor, Gamma (translocon-associated protein gamma) (SSR3, Accession NM_007107) is another VGAM2417 host target gene. SSR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SSR3, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SSR3 BINDING SITE, designated SEQ ID:13972, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81808] Another function of VGAM2417 is therefore inhibition of Signal Sequence Receptor, Gamma (translocon-associated protein gamma) (SSR3, Accession NM_007107). Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSR3. LOC144871 (Accession XM_096698) is another VGAM2417 host target gene. LOC144871 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144871, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144871 BINDING SITE, designated SEQ ID:40471, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81809] Another function of VGAM2417 is therefore inhibition of LOC144871 (Accession XM_096698). Accordingly, utilities

of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144871. LOC151473 (Accession XM_087215) is another VGAM2417 host target gene. LOC151473 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151473, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151473 BINDING SITE, designated SEQ ID:39121, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81810] Another function of VGAM2417 is therefore inhibition of LOC151473 (Accession XM_087215). Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151473. LOC158428 (Accession XM_047249) is another VGAM2417 host target gene. LOC158428 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158428, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC158428 BINDING SITE, designated SEQ ID:34922, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81811] Another function of VGAM2417 is therefore inhibition of LOC158428 (Accession XM_047249). Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158428. LOC197287 (Accession XM_027541) is another VGAM2417 host target gene. LOC197287 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197287, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197287 BINDING SITE, designated SEQ ID:30523, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81812] Another function of VGAM2417 is therefore inhibition of LOC197287 (Accession XM_027541). Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197287. LOC255265 (Accession XM_170902) is another VGAM2417 host target gene. LOC255265 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255265 BINDING SITE, designated SEQ ID:45658, to the nucleotide sequence of VGAM2417 RNA, herein designated VGAM RNA, also designated SEQ ID:5128.

[81813] Another function of VGAM2417 is therefore inhibition of LOC255265 (Accession XM_170902). Accordingly, utilities of VGAM2417 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255265. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2418 (VGAM2418) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81814] VGAM2418 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2418 was detected is described hereinabove with reference to Figs. 1-8.

[81815] VGAM2418 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2418 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81816] VGAM2418 gene encodes a VGAM2418 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2418 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2418 precursor RNA is designated SEQ ID:2404, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2404 is located at position 117185 relative to the genome of Goatpox Virus.

[81817] VGAM2418 precursor RNA folds onto itself, forming VGAM2418 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[81818] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2418 folded precursor RNA into VGAM2418 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2418 RNA is designated SEQ ID:5129, and is provided hereinbelow with reference to the sequence listing part.

[81819] VGAM2418 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2418 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2418 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81820] VGAM2418 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2418 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2418 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2418 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2418 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81821] The complementary binding of VGAM2418 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2418 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2418 host target RNA into VGAM2418 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81822] It is appreciated that VGAM2418 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2418 host target genes. The mRNA of each one of this plurality of VGAM2418 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2418 RNA, herein designated VGAM RNA, and which when bound by VGAM2418 RNA causes inhibition of translation of respective one or more VGAM2418 host target proteins.

[81823] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2418 gene, herein designated VGAM GENE, on one or more VGAM2418 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81824] It is yet further appreciated that a function of VGAM2418 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2418 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2418 correlate with, and may be deduced from, the identity of the host target genes which VGAM2418 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81825] Nucleotide sequences of the VGAM2418 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2418 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2418 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2418 are further described hereinbelow with reference to Table 1.

[81826] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2418 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2418 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81827] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2418 gene, herein designated VGAM is inhibition of expression of VGAM2418 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2418 correlate with, and may be deduced from, the identity of the target genes which VGAM2418 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81828] Netrin 4 (NTN4, Accession XM_031896) is a VGAM2418 host target gene. NTN4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NTN4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of NTN4 BINDING SITE, designated SEQ ID:31508, to the nucleotide sequence of VGAM2418 RNA, herein designated VGAM RNA, also designated SEQ ID:5129.

[81829] A function of VGAM2418 is therefore inhibition of Netrin 4 (NTN4, Accession XM_031896). Accordingly, utilities of VGAM2418 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTN4. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2419 (VGAM2419) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81830] VGAM2419 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2419 was detected is described hereinabove with reference to Figs. 1-8.

[81831] VGAM2419 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2419 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81832] VGAM2419 gene encodes a VGAM2419 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2419 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2419 precursor RNA is designated SEQ ID:2405, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2405 is located at position 104440 relative to the genome of Goatpox Virus.

[81833] VGAM2419 precursor RNA folds onto itself, forming VGAM2419 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81834] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2419 folded precursor RNA into VGAM2419 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2419 RNA is designated SEQ ID:5130, and is provided hereinbelow with reference to the sequence listing part.

[81835] VGAM2419 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2419 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2419 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81836] VGAM2419 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2419 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2419 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2419 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2419 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81837] The complementary binding of VGAM2419 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2419 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2419 host target RNA into VGAM2419 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81838] It is appreciated that VGAM2419 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2419 host target genes. The mRNA of each one of this plurality of VGAM2419 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2419 RNA, herein designated VGAM RNA, and which when bound by VGAM2419 RNA causes inhibition of translation of respective one or more VGAM2419 host target proteins.

[81839] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2419 gene, herein designated VGAM GENE, on one or more VGAM2419 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81840] It is yet further appreciated that a function of VGAM2419 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2419 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2419 correlate with, and may be deduced from, the identity of the host target genes which VGAM2419 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81841] Nucleotide sequences of the VGAM2419 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2419 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2419 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2419 are further described hereinbelow with reference to Table 1.

[81842] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2419 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2419 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81843] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2419 gene, herein designated VGAM is inhibition of expression of VGAM2419 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2419 correlate with, and may be deduced from, the identity of the target genes which VGAM2419 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81844] Calbindin 1, 28kDa (CALB1, Accession NM_004929) is a VGAM2419 host target gene. CALB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CALB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CALB1 BINDING SITE, designated SEQ ID:11369, to the nucleotide sequence of VGAM2419 RNA, herein designated VGAM RNA, also designated SEQ ID:5130.

[81845] A function of VGAM2419 is therefore inhibition of Cal-

bindin 1, 28kDa (CALB1, Accession NM_004929), a gene which buffers cytosolic calcium. Accordingly, utilities of VGAM2419 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CALB1. The function of CALB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM266.F-box and Leucine-rich Repeat Protein 2 (FBXL2, Accession NM_012157) is another VGAM2419 host target gene. FBXL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBXL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXL2 BINDING SITE, designated SEQ ID:14453, to the nucleotide sequence of VGAM2419 RNA, herein designated VGAM RNA, also designated SEQ ID:5130.

[81846] Another function of VGAM2419 is therefore inhibition of F-box and Leucine-rich Repeat Protein 2 (FBXL2, Accession NM_012157). Accordingly, utilities of VGAM2419 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXL2. SMT3 Suppres-

sor of Mif Two 3 Homolog 1 (yeast) (SMT3H1, Accession XM_009805) is another VGAM2419 host target gene. SMT3H1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMT3H1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMT3H1 BINDING SITE, designated SEQ ID:30123, to the nucleotide sequence of VGAM2419 RNA, herein designated VGAM RNA, also designated SEQ ID:5130.

[81847] Another function of VGAM2419 is therefore inhibition of SMT3 Suppressor of Mif Two 3 Homolog 1 (yeast) (SMT3H1, Accession XM_009805), a gene which is involved in the function and/or structure of the eukaryotic kinetochore. Accordingly, utilities of VGAM2419 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMT3H1. The function of SMT3H1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM119.DKFZP434P0721 (Accession XM_033181) is another VGAM2419 host target gene. DKFZP434P0721

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434P0721, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434P0721 BINDING SITE, designated SEQ ID:31873, to the nucleotide sequence of VGAM2419 RNA, herein designated VGAM RNA, also designated SEQ ID:5130.

[81848] Another function of VGAM2419 is therefore inhibition of DKFZP434P0721 (Accession XM_033181). Accordingly, utilities of VGAM2419 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434P0721. KIAA1084 (Accession NM_014910) is another VGAM2419 host target gene. KIAA1084 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1084, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1084 BINDING SITE, designated SEQ ID:17134, to the nucleotide sequence of VGAM2419 RNA, herein designated VGAM RNA, also designated SEQ ID:5130.

[81849] Another function of VGAM2419 is therefore inhibition of KIAA1084 (Accession NM_014910). Accordingly, utilities of VGAM2419 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1084. MGC10911 (Accession NM_032302) is another VGAM2419 host target gene. MGC10911 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC10911, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10911 BINDING SITE, designated SEQ ID:26084, to the nucleotide sequence of VGAM2419 RNA, herein designated VGAM RNA, also designated SEQ ID:5130.

[81850] Another function of VGAM2419 is therefore inhibition of MGC10911 (Accession NM_032302). Accordingly, utilities of VGAM2419 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10911. Solute Carrier Family 38, Member 4 (SLC38A4, Accession NM_018018) is another VGAM2419 host target gene. SLC38A4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC38A4, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC38A4 BINDING SITE, designated SEQ ID:19758, to the nucleotide sequence of VGAM2419 RNA, herein designated VGAM RNA, also designated SEQ ID:5130.

[81851] Another function of VGAM2419 is therefore inhibition of Solute Carrier Family 38, Member 4 (SLC38A4, Accession NM_018018). Accordingly, utilities of VGAM2419 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC38A4. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2420 (VGAM2420) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81852] VGAM2420 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2420 was detected is described hereinabove with reference to Figs. 1-8.

[81853] VGAM2420 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus.

VGAM2420 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81854] VGAM2420 gene encodes a VGAM2420 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2420 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2420 precursor RNA is designated SEQ ID:2406, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2406 is located at position 138753 relative to the genome of Goatpox Virus.

[81855] VGAM2420 precursor RNA folds onto itself, forming VGAM2420 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81856] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2420 folded precursor RNA into VGAM2420 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2420 RNA is designated SEQ ID:5131, and is provided hereinbelow with reference to the sequence listing part.

[81857] VGAM2420 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2420 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2420 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81858] VGAM2420 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2420 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2420 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2420 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2420 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81859] The complementary binding of VGAM2420 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2420 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2420 host target RNA into VGAM2420 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81860] It is appreciated that VGAM2420 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2420 host target genes. The mRNA of each one of this plurality of VGAM2420 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2420 RNA, herein designated VGAM RNA, and which when bound by VGAM2420 RNA causes inhibition of translation of respective one or more VGAM2420 host target proteins.

[81861] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2420 gene, herein designated VGAM GENE, on one or more VGAM2420 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81862] It is yet further appreciated that a function of VGAM2420 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2420 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2420 correlate with, and may be deduced from, the identity of the host target genes which VGAM2420 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81863] Nucleotide sequences of the VGAM2420 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2420 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2420 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2420 are further described hereinbelow with reference to Table 1.

[81864] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2420 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2420 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81865] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2420 gene, herein designated VGAM is inhibition of expression of VGAM2420 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2420 correlate with, and may be deduced from, the identity of the target genes which VGAM2420 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81866] Ankyrin 2, Neuronal (ANK2, Accession NM_001148) is a VGAM2420 host target gene. ANK2 BINDING SITE1 and ANK2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ANK2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ANK2 BINDING SITE1 and ANK2 BINDING SITE2,

designated SEQ ID:6819 and SEQ ID:21963 respectively, to the nucleotide sequence of VGAM2420 RNA, herein designated VGAM RNA, also designated SEQ ID:5131.

[81867] A function of VGAM2420 is therefore inhibition of Ankyrin 2, Neuronal (ANK2, Accession NM_001148), a gene which attaches integral membrane proteins to cytoskeletal elements. also binds to cytoskeletal proteins. Accordingly, utilities of VGAM2420 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ANK2. The function of ANK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM769.TEM8 (Accession NM_032208) is another VGAM2420 host target gene. TEM8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TEM8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEM8 BINDING SITE, designated SEQ ID:25915, to the nucleotide sequence of VGAM2420 RNA, herein designated VGAM RNA, also designated SEQ ID:5131.

[81868] Another function of VGAM2420 is therefore inhibition of

TEM8 (Accession NM_032208), a gene which is a tumor-specific endothelial marker. Accordingly, utilities of VGAM2420 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEM8. The function of TEM8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1489.Zinc Finger Protein 138 (clone pHZ-32) (ZNF138, Accession XM_088081) is another VGAM2420 host target gene. ZNF138 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF138, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF138 BINDING SITE, designated SEQ ID:39507, to the nucleotide sequence of VGAM2420 RNA, herein designated VGAM RNA, also designated SEQ ID:5131.

[81869] Another function of VGAM2420 is therefore inhibition of Zinc Finger Protein 138 (clone pHZ-32) (ZNF138, Accession XM_088081). Accordingly, utilities of VGAM2420 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF138. PB1 (Accession

NM_018313) is another VGAM2420 host target gene. PB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PB1 BINDING SITE, designated SEQ ID:20306, to the nucleotide sequence of VGAM2420 RNA, herein designated VGAM RNA, also designated SEQ ID:5131.

[81870] Another function of VGAM2420 is therefore inhibition of PB1 (Accession NM_018313). Accordingly, utilities of VGAM2420 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PB1. PRO2086 (Accession NM_014111) is another VGAM2420 host target gene. PRO2086 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO2086, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2086 BINDING SITE, designated SEQ ID:15343, to the nucleotide sequence of VGAM2420 RNA, herein designated VGAM RNA, also designated SEQ ID:5131.

[81871] Another function of VGAM2420 is therefore inhibition of PRO2086 (Accession NM_014111). Accordingly, utilities of VGAM2420 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2086. LOC154930 (Accession XM_088080) is another VGAM2420 host target gene. LOC154930 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154930, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154930 BINDING SITE, designated SEQ ID:39504, to the nucleotide sequence of VGAM2420 RNA, herein designated VGAM RNA, also designated SEQ ID:5131.

[81872] Another function of VGAM2420 is therefore inhibition of LOC154930 (Accession XM_088080). Accordingly, utilities of VGAM2420 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154930. LOC199775 (Accession XM_114016) is another VGAM2420 host target gene. LOC199775 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC199775, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199775 BINDING SITE, designated SEQ ID:42614, to the nucleotide sequence of VGAM2420 RNA, herein designated VGAM RNA, also designated SEQ ID:5131.

[81873] Another function of VGAM2420 is therefore inhibition of LOC199775 (Accession XM_114016). Accordingly, utilities of VGAM2420 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199775. LOC51246 (Accession NM_016479) is another VGAM2420 host target gene. LOC51246 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51246, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51246 BINDING SITE, designated SEQ ID:18577, to the nucleotide sequence of VGAM2420 RNA, herein designated VGAM RNA, also designated SEQ ID:5131.

[81874] Another function of VGAM2420 is therefore inhibition of LOC51246 (Accession NM_016479). Accordingly, utilities of VGAM2420 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC51246. LOC51652 (Accession NM_016079) is another VGAM2420 host target gene. LOC51652 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51652, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51652 BINDING SITE, designated SEQ ID:18150, to the nucleotide sequence of VGAM2420 RNA, herein designated VGAM RNA, also designated SEQ ID:5131.

[81875] Another function of VGAM2420 is therefore inhibition of LOC51652 (Accession NM_016079). Accordingly, utilities of VGAM2420 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51652. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2421 (VGAM2421) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81876] VGAM2421 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2421 was detected is described hereinabove with reference to Figs. 1-8.

[81877] VGAM2421 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2421 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81878] VGAM2421 gene encodes a VGAM2421 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2421 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2421 precursor RNA is designated SEQ ID:2407, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2407 is located at position 87501 relative to the genome of Goatpox Virus.

[81879] VGAM2421 precursor RNA folds onto itself, forming VGAM2421 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81880] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2421 folded precursor RNA into VGAM2421 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2421 RNA is designated SEQ ID:5132, and is provided hereinbelow with reference to the sequence listing part.

[81881] VGAM2421 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2421 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2421 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81882] VGAM2421 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2421 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2421 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2421 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2421 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81883] The complementary binding of VGAM2421 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2421 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2421 host target RNA into VGAM2421 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81884] It is appreciated that VGAM2421 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2421 host target genes. The mRNA of each one of this plurality of VGAM2421 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2421 RNA, herein designated VGAM RNA, and which when bound by VGAM2421 RNA causes inhibition of translation of respective one or more VGAM2421 host target proteins.

[81885] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2421 gene, herein designated VGAM GENE, on one or more VGAM2421 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81886] It is yet further appreciated that a function of VGAM2421 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2421 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2421 correlate with, and may be deduced from, the identity of the host target genes which VGAM2421 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81887] Nucleotide sequences of the VGAM2421 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2421 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2421 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2421 are further described hereinbelow with reference to Table 1.

[81888] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2421 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2421 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81889] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2421 gene, herein designated VGAM is inhibition of expression of VGAM2421 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2421 correlate with, and may be deduced from, the identity of the target genes which VGAM2421 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81890] Phosphatidylinositol Glycan, Class H (PIGH, Accession NM_004569) is a VGAM2421 host target gene. PIGH BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIGH, correspond-

ing to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIGH BINDING SITE, designated SEQ ID:10911, to the nucleotide sequence of VGAM2421 RNA, herein designated VGAM RNA, also designated SEQ ID:5132.

[81891] A function of VGAM2421 is therefore inhibition of Phosphatidylinositol Glycan, Class H (PIGH, Accession NM_004569), a gene which catalyzes transfer of GlcNAc to PI. Accordingly, utilities of VGAM2421 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIGH. The function of PIGH has been established by previous studies. The PIGH gene encodes an enzyme involved in the biosynthesis of glycosylphosphatidylinositol anchor; see PIGA (OMIM Ref. No. 311770) and PIGF (OMIM Ref. No. 600153) for other components of the system. Kamitani et al. (1993) isolated cDNA for a human gene that repaired the defect in a complementation class H mutant cell line. They determined that PIGH encodes a predicted protein of 188 amino acids. Ware et al. (1994) demonstrated that the mouse Pigh gene is located on chromosome 12 in a region of homology of synteny with 14q11-q24. Watanabe et al. (1996) demonstrated

that the PIGA and PIGH proteins form a protein complex and are subunits of the GPI GlcNAc transferase of the endoplasmic reticulum (ER). They showed that PIGH is a cytoplasmic ER-associated protein. Using immunoprecipitation experiments, Watanabe et al. (1998) demonstrated that PIGQ (OMIM Ref. No. 605754) associates specifically with PIGA, PIGC (OMIM Ref. No. 601730), and PIGH and that all 4 proteins form a complex that has GPI-GlcNAc transferase (GPI-GnT) activity in vitro

[81892] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[81893] Watanabe, R.; Inoue, N.; Westfall, B.; Taron, C. H.; Orlean, P.; Takeda, J.; Kinoshita, T. : The first step of glycosylphosphatidylinositol biosynthesis is mediated by a complex of PIG-A, PIG-H, PIG-C and GPI1. EMBO J. 17: 877-885, 1998. ; and

[81894] Watanabe, R.; Kinoshita, T.; Masaki, R.; Yamamoto, A.; Takeda, J.; Inoue, N. : PIG-A and PIG-H, which participate in glycosylphosphatidylinositol anchor biosynthesis, form a protein comp.

[81895] Further studies establishing the function and utilities of PIGH are found in John Hopkins OMIM database record ID

600154, and in sited publications numbered 133 and 8105-8107 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.DCMP Deaminase (DCTD, Accession NM_001921) is another VGAM2421 host target gene. DCTD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCTD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCTD BINDING SITE, designated SEQ ID:7636, to the nucleotide sequence of VGAM2421 RNA, herein designated VGAM RNA, also designated SEQ ID:5132.

[81896] Another function of VGAM2421 is therefore inhibition of DCMP Deaminase (DCTD, Accession NM_001921). Accordingly, utilities of VGAM2421 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DCTD. FLJ14906 (Accession NM_032859) is another VGAM2421 host target gene. FLJ14906 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14906, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of FLJ14906 BINDING SITE, designated SEQ ID:26664, to the nucleotide sequence of VGAM2421 RNA, herein designated VGAM RNA, also designated SEQ ID:5132.

[81897] Another function of VGAM2421 is therefore inhibition of FLJ14906 (Accession NM_032859). Accordingly, utilities of VGAM2421 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14906. LOC138389 (Accession XM_072534) is another VGAM2421 host target gene. LOC138389 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC138389, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC138389 BINDING SITE, designated SEQ ID:37503, to the nucleotide sequence of VGAM2421 RNA, herein designated VGAM RNA, also designated SEQ ID:5132.

[81898] Another function of VGAM2421 is therefore inhibition of LOC138389 (Accession XM_072534). Accordingly, utilities of VGAM2421 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC138389. LOC145622 (Accession XM_085186) is an-

other VGAM2421 host target gene. LOC145622 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145622, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145622 BINDING SITE, designated SEQ ID:37916, to the nucleotide sequence of VGAM2421 RNA, herein designated VGAM RNA, also designated SEQ ID:5132.

[81899] Another function of VGAM2421 is therefore inhibition of LOC145622 (Accession XM_085186). Accordingly, utilities of VGAM2421 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145622. LOC54499 (Accession XM_047479) is another VGAM2421 host target gene. LOC54499 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC54499, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC54499 BINDING SITE, designated SEQ ID:34968, to the nucleotide sequence of VGAM2421 RNA, herein designated VGAM RNA, also designated SEQ ID:5132.

[81900] Another function of VGAM2421 is therefore inhibition of LOC54499 (Accession XM_047479). Accordingly, utilities of VGAM2421 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC54499. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2422 (VGAM2422) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81901] VGAM2422 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2422 was detected is described hereinabove with reference to Figs. 1-8.

[81902] VGAM2422 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2422 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81903] VGAM2422 gene encodes a VGAM2422 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2422 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2422 precursor RNA is designated SEQ ID:2408, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2408 is located at position 83441 relative to the genome of Goatpox Virus.

[81904] VGAM2422 precursor RNA folds onto itself, forming VGAM2422 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81905] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2422 folded precursor RNA into VGAM2422 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2422 RNA is designated SEQ ID:5133, and is provided hereinbelow with reference to the sequence listing part.

[81906] VGAM2422 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2422 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2422 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81907] VGAM2422 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2422 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2422 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2422 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2422 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81908] The complementary binding of VGAM2422 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2422 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2422 host target RNA into VGAM2422 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81909] It is appreciated that VGAM2422 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2422 host target genes. The mRNA of each one of this plurality of VGAM2422 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2422 RNA, herein designated VGAM RNA, and which when bound by VGAM2422 RNA causes inhibition of translation of respective one or more VGAM2422 host target proteins.

[81910] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2422 gene, herein designated VGAM GENE, on one or more VGAM2422 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81911] It is yet further appreciated that a function of VGAM2422 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2422 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2422 correlate with, and may be deduced from, the identity of the host target genes which VGAM2422 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81912] Nucleotide sequences of the VGAM2422 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2422 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2422 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2422 are further described hereinbelow with reference to Table 1.

[81913] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2422 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2422 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[81914] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2422 gene, herein designated VGAM is inhibition of expression of VGAM2422 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2422 correlate with, and may be deduced from, the identity of the target genes which VGAM2422 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81915] N-ethylmaleimide-sensitive Factor Attachment Protein, Beta (NAPB, Accession XM_046652) is a VGAM2422 host target gene. NAPB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NAPB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NAPB BINDING SITE, designated SEQ ID:34765, to the nucleotide sequence of VGAM2422 RNA, herein designated VGAM RNA, also designated SEQ ID:5133.

[81916] A function of VGAM2422 is therefore inhibition of N-ethylmaleimide-sensitive Factor Attachment Protein, Beta (NAPB, Accession XM_046652). Accordingly, utilities of

VGAM2422 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAPB. NCK-associated Protein 1 (NCKAP1, Accession NM_013436) is another VGAM2422 host target gene. NCKAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NCKAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCKAP1 BINDING SITE, designated SEQ ID:15094, to the nucleotide sequence of VGAM2422 RNA, herein designated VGAM RNA, also designated SEQ ID:5133.

[81917] Another function of VGAM2422 is therefore inhibition of NCK-associated Protein 1 (NCKAP1, Accession NM_013436). Accordingly, utilities of VGAM2422 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCKAP1. ATPase, Class V, Type 10D (ATP10D, Accession XM_054907) is another VGAM2422 host target gene. ATP10D BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP10D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP10D BINDING SITE, designated SEQ ID:36199, to the nucleotide sequence of VGAM2422 RNA, herein designated VGAM RNA, also designated SEQ ID:5133.

[81918] Another function of VGAM2422 is therefore inhibition of ATPase, Class V, Type 10D (ATP10D, Accession XM_054907). Accordingly, utilities of VGAM2422 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP10D. FLJ12085 (Accession NM_022771) is another VGAM2422 host target gene. FLJ12085 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12085, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12085 BINDING SITE, designated SEQ ID:23031, to the nucleotide sequence of VGAM2422 RNA, herein designated VGAM RNA, also designated SEQ ID:5133.

[81919] Another function of VGAM2422 is therefore inhibition of FLJ12085 (Accession NM_022771). Accordingly, utilities of VGAM2422 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ12085. SCLY (Accession NM_016510) is another VGAM2422 host target gene. SCLY BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCLY, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCLY BINDING SITE, designated SEQ ID:18587, to the nucleotide sequence of VGAM2422 RNA, herein designated VGAM RNA, also designated SEQ ID:5133.

[81920] Another function of VGAM2422 is therefore inhibition of SCLY (Accession NM_016510). Accordingly, utilities of VGAM2422 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCLY. LOC143879 (Accession XM_084666) is another VGAM2422 host target gene. LOC143879 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143879, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143879 BINDING SITE, designated SEQ ID:37657, to

the nucleotide sequence of VGAM2422 RNA, herein designated VGAM RNA, also designated SEQ ID:5133.

[81921] Another function of VGAM2422 is therefore inhibition of LOC143879 (Accession XM_084666). Accordingly, utilities of VGAM2422 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143879. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2423 (VGAM2423) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81922] VGAM2423 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2423 was detected is described hereinabove with reference to Figs. 1-8.

[81923] VGAM2423 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus.
VGAM2423 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81924] VGAM2423 gene encodes a VGAM2423 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2423 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2423 precursor RNA is designated SEQ ID:2409, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2409 is located at position 74429 relative to the genome of Goatpox Virus.

[81925] VGAM2423 precursor RNA folds onto itself, forming VGAM2423 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81926] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2423 folded precursor RNA into VGAM2423 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2423 RNA is designated SEQ ID:5134, and is provided hereinbelow with reference to the sequence listing part.

[81927] VGAM2423 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2423 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2423 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81928] VGAM2423 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2423 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2423 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2423 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2423 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81929] The complementary binding of VGAM2423 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2423 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2423 host target RNA into VGAM2423 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81930] It is appreciated that VGAM2423 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2423 host target genes. The mRNA of each one of this plurality of VGAM2423 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2423 RNA, herein designated VGAM RNA, and which when bound by VGAM2423 RNA causes inhibition of translation of respective one or more VGAM2423 host target proteins.

[81931] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2423 gene, herein designated VGAM GENE, on one or more VGAM2423 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81932] It is yet further appreciated that a function of VGAM2423 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2423 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2423 correlate with, and may be deduced from, the identity of the host target genes which VGAM2423 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81933] Nucleotide sequences of the VGAM2423 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2423 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2423 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2423 are further described hereinbelow with reference to Table 1.

[81934] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2423 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2423 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81935] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2423 gene, herein designated VGAM is inhibition of expression of VGAM2423 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2423 correlate with, and may be deduced from, the identity of the target genes which VGAM2423 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81936] Interleukin 17 (cytotoxic T-lymphocyte-associated serine esterase 8) (IL17, Accession NM_002190) is a VGAM2423 host target gene. IL17 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL17, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL17 BINDING SITE, designated SEQ ID:7947, to the nucleotide sequence of VGAM2423 RNA, herein designated VGAM RNA, also designated SEQ ID:5134.

[81937] A function of VGAM2423 is therefore inhibition of Inter-

leukin 17 (cytotoxic T-lymphocyte-associated serine esterase 8) (IL17, Accession NM_002190), a gene which induces stromal cells to produce proinflammatory and hematopoietic cytokines. Accordingly, utilities of VGAM2423 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL17. The function of IL17 has been established by previous studies. Rouvier et al. (1993) used subtractive library screening to isolate a novel rodent gene, termed CTLA8, that was expressed specifically in cytotoxic T cells. Although Rouvier et al. (1993) described CTLA8 as a mouse gene, Kennedy et al. (1996) showed that it is actually the rat IL17 homolog. Rouvier et al. (1993) noted that the CTLA8 polypeptide sequence is 56.8% identical to that of the immediate-early gene 13 of Herpesvirus saimiri (OMIM Ref. No. HVS-13). The CTLA8 3-prime untranslated region contains AU-rich repeats typically found in the mRNA of cytokines and growth factors. Yao et al. (1995) cloned a human IL17 cDNA. The cDNA encodes a 155-amino acid polypeptide that contains an N-terminal hydrophobic signal sequence. Northern blot analysis revealed that the gene is expressed as a 1.9-kb mRNA in stimulated, but not resting, T cells; the transcript could not be detected in

any human tissues. Expressed recombinant IL17 was secreted in both glycosylated and nonglycosylated forms. IL17 protein applied to fibroblasts induced the production of IL6 (OMIM Ref. No. 147620) and IL8 (OMIM Ref. No. 146930) and enhanced surface expression of intracellular adhesion molecule-1 (ICAM1; 147840).

[81938] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[81939] Kennedy, J.; Rossi, D. L.; Zurawski, S. M.; Vega, F., Jr. : Kastelein, R. A.; Wagner, J. L.; Hannum, C. H.; Zlotnick, A.: Mouse IL-17: a cytokine preferentially expressed by alpha beta TCR + CD4-CD8-T cells. J. Interferon Cytokine Res. 16: 611-617, 1996. ; and

[81940] Yao, Z.; Painter, S. L.; Fanslow, W. C.; Ulrich, D.; Macduff, B. M.; Spriggs, M. K.; Armitage, R. J. : Human IL-17: a novel cytokine derived from T cells. J. Immun. 155: 5483-5486, 1995.

[81941] Further studies establishing the function and utilities of IL17 are found in John Hopkins OMIM database record ID 603149, and in sited publications numbered 5428-5431 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.FK506 Binding Pro-

tein 5 (FKBP5, Accession NM_004117) is another VGAM2423 host target gene. FKBP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FKBP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FKBP5 BINDING SITE, designated SEQ ID:10326, to the nucleotide sequence of VGAM2423 RNA, herein designated VGAM RNA, also designated SEQ ID:5134.

[81942] Another function of VGAM2423 is therefore inhibition of FK506 Binding Protein 5 (FKBP5, Accession NM_004117). Accordingly, utilities of VGAM2423 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKBP5. KIAA1383 (Accession XM_045859) is another VGAM2423 host target gene. KIAA1383 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1383, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1383 BINDING SITE, designated SEQ ID:34584, to the nucleotide sequence of VGAM2423 RNA,

herein designated VGAM RNA, also designated SEQ ID:5134.

[81943] Another function of VGAM2423 is therefore inhibition of KIAA1383 (Accession XM_045859). Accordingly, utilities of VGAM2423 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1383. Phospholipase A2, Group III (PLA2G3, Accession NM_015715) is another VGAM2423 host target gene. PLA2G3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLA2G3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLA2G3 BINDING SITE, designated SEQ ID:17929, to the nucleotide sequence of VGAM2423 RNA, herein designated VGAM RNA, also designated SEQ ID:5134.

[81944] Another function of VGAM2423 is therefore inhibition of Phospholipase A2, Group III (PLA2G3, Accession NM_015715). Accordingly, utilities of VGAM2423 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLA2G3. LOC120103 (Accession XM_058449) is another VGAM2423 host target

gene. LOC120103 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120103, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120103 BINDING SITE, designated SEQ ID:36618, to the nucleotide sequence of VGAM2423 RNA, herein designated VGAM RNA, also designated SEQ ID:5134.

[81945] Another function of VGAM2423 is therefore inhibition of LOC120103 (Accession XM_058449). Accordingly, utilities of VGAM2423 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120103. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2424 (VGAM2424) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81946] VGAM2424 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2424 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[81947] VGAM2424 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2424 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81948] VGAM2424 gene encodes a VGAM2424 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2424 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2424 precursor RNA is designated SEQ ID:2410, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2410 is located at position 134679 relative to the genome of Goatpox Virus.

[81949] VGAM2424 precursor RNA folds onto itself, forming VGAM2424 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81950] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2424 folded precursor RNA into VGAM2424 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2424 RNA is designated SEQ ID:5135, and is provided hereinbelow with reference to the sequence listing part.

[81951] VGAM2424 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2424 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2424 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81952] VGAM2424 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2424 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2424 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2424 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2424 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81953] The complementary binding of VGAM2424 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2424 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2424 host target RNA into VGAM2424 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81954] It is appreciated that VGAM2424 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2424 host target genes. The mRNA of each one of this plurality of VGAM2424 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2424 RNA, herein designated VGAM RNA, and which when bound by VGAM2424 RNA causes inhibition of translation of respective one or more VGAM2424 host target proteins.

[81955] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2424 gene, herein designated VGAM GENE, on one or more VGAM2424 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81956] It is yet further appreciated that a function of VGAM2424 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2424 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2424 correlate with, and may be deduced from, the identity of the host target genes which VGAM2424 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81957] Nucleotide sequences of the VGAM2424 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2424 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2424 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2424 are further described hereinbelow with reference to Table 1.

[81958] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2424 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2424 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81959] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2424 gene, herein designated VGAM is inhibition of expression of VGAM2424 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2424 correlate with, and may be deduced from, the identity of the target genes which VGAM2424 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81960] Exostoses (multiple) 2 (EXT2, Accession NM_000401) is a VGAM2424 host target gene. EXT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EXT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EXT2 BINDING SITE, designated SEQ ID:5977, to the nucleotide sequence of VGAM2424 RNA, herein designated VGAM RNA, also designated SEQ ID:5135.

[81961] A function of VGAM2424 is therefore inhibition of Exostoses (multiple) 2 (EXT2, Accession NM_000401). Accordingly, utilities of VGAM2424 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EXT2. FLJ23047 (Accession NM_024548) is another VGAM2424 host target gene. FLJ23047 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23047, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23047 BINDING SITE, designated SEQ ID:23761, to the nucleotide sequence of VGAM2424 RNA, herein designated VGAM RNA, also designated SEQ ID:5135.

[81962] Another function of VGAM2424 is therefore inhibition of FLJ23047 (Accession NM_024548). Accordingly, utilities of VGAM2424 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ23047. Hect Domain and RLD 3 (HERC3, Accession NM_014606) is another VGAM2424 host target gene. HERC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HERC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HERC3 BINDING SITE, designated SEQ ID:15970, to the nucleotide sequence of VGAM2424 RNA, herein designated VGAM RNA, also designated SEQ ID:5135.

[81963] Another function of VGAM2424 is therefore inhibition of Hect Domain and RLD 3 (HERC3, Accession NM_014606). Accordingly, utilities of VGAM2424 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HERC3. LOC200933 (Accession XM_117294) is another VGAM2424 host target gene. LOC200933 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200933, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200933 BINDING SITE, desig-

nated SEQ ID:43361, to the nucleotide sequence of VGAM2424 RNA, herein designated VGAM RNA, also designated SEQ ID:5135.

[81964] Another function of VGAM2424 is therefore inhibition of LOC200933 (Accession XM_117294). Accordingly, utilities of VGAM2424 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200933. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2425 (VGAM2425) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[81965] VGAM2425 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2425 was detected is described hereinabove with reference to Figs. 1-8.

[81966] VGAM2425 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2425 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81967] VGAM2425 gene encodes a VGAM2425 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2425 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2425 precursor RNA is designated SEQ ID:2411, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2411 is located at position 148298 relative to the genome of Goatpox Virus.

[81968] VGAM2425 precursor RNA folds onto itself, forming VGAM2425 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81969] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2425 folded precursor RNA into VGAM2425 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2425 RNA is designated SEQ ID:5136, and is provided hereinbelow with reference to the sequence listing part.

[81970] VGAM2425 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2425 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2425 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81971] VGAM2425 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2425 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2425 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2425 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2425 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[81972] The complementary binding of VGAM2425 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2425 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2425 host target RNA into VGAM2425 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81973] It is appreciated that VGAM2425 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2425 host target genes. The mRNA of each one of this plurality of VGAM2425 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2425 RNA, herein designated VGAM RNA, and which when bound by VGAM2425 RNA causes inhibition of translation of respective one or more VGAM2425 host target proteins.

[81974] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2425 gene, herein designated VGAM GENE, on one or more VGAM2425 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[81975] It is yet further appreciated that a function of VGAM2425 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2425 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2425 correlate with, and may be deduced from, the identity of the host target genes which VGAM2425 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[81976] Nucleotide sequences of the VGAM2425 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2425 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2425 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2425 are further described hereinbelow with reference to Table 1.

[81977] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2425 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2425 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[81978] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2425 gene, herein designated VGAM is inhibition of expression of VGAM2425 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2425 correlate with, and may be deduced from, the identity of the target genes which VGAM2425 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[81979] Carbonic Anhydrase III, Muscle Specific (CA3, Accession NM_005181) is a VGAM2425 host target gene. CA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CA3 BINDING SITE, designated SEQ ID:11679, to the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, also designated SEQ ID:5136.

[81980] A function of VGAM2425 is therefore inhibition of Car-

bonic Anhydrase III, Muscle Specific (CA3, Accession NM_005181), a gene which has a muscle-specific function of reversible hydratation of carbon dioxide. Accordingly, utilities of VGAM2425 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CA3. The function of CA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1911.Fas (TNFRSF6)-associated Via Death Domain (FADD, Accession NM_003824) is another VGAM2425 host target gene. FADD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FADD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FADD BINDING SITE, designated SEQ ID:9917, to the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, also designated SEQ ID:5136.

[81981] Another function of VGAM2425 is therefore inhibition of Fas (TNFRSF6)-associated Via Death Domain (FADD, Accession NM_003824), a gene which may play an important role in the proximal signal transduction of FAS. Accord-

ingly, utilities of VGAM2425 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FADD. The function of FADD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM995.DKFZP547E2110 (Accession XM_165676) is another VGAM2425 host target gene. DKFZP547E2110 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP547E2110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP547E2110 BINDING SITE, designated SEQ ID:43732, to the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, also designated SEQ ID:5136.

[81982] Another function of VGAM2425 is therefore inhibition of DKFZP547E2110 (Accession XM_165676). Accordingly, utilities of VGAM2425 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP547E2110. KIAA0767 (Accession XM_027105) is another VGAM2425 host target gene. KIAA0767 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by KIAA0767, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0767 BINDING SITE, designated SEQ ID:30409, to the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, also designated SEQ ID:5136.

[81983] Another function of VGAM2425 is therefore inhibition of KIAA0767 (Accession XM_027105). Accordingly, utilities of VGAM2425 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0767. KIAA1464 (Accession XM_043069) is another VGAM2425 host target gene. KIAA1464 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1464, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1464 BINDING SITE, designated SEQ ID:33886, to the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, also designated SEQ ID:5136.

[81984] Another function of VGAM2425 is therefore inhibition of KIAA1464 (Accession XM_043069). Accordingly, utilities

of VGAM2425 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1464. LOC122830 (Accession XM_058661) is another VGAM2425 host target gene. LOC122830 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC122830, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122830 BINDING SITE, designated SEQ ID:36709, to the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, also designated SEQ ID:5136.

[81985] Another function of VGAM2425 is therefore inhibition of LOC122830 (Accession XM_058661). Accordingly, utilities of VGAM2425 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122830. LOC144481 (Accession XM_096611) is another VGAM2425 host target gene. LOC144481 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144481, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC144481 BINDING SITE, designated SEQ ID:40419, to the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, also designated SEQ ID:5136.

[81986] Another function of VGAM2425 is therefore inhibition of LOC144481 (Accession XM_096611). Accordingly, utilities of VGAM2425 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144481. LOC144501 (Accession XM_096612) is another VGAM2425 host target gene. LOC144501 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144501, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144501 BINDING SITE, designated SEQ ID:40421, to the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, also designated SEQ ID:5136.

[81987] Another function of VGAM2425 is therefore inhibition of LOC144501 (Accession XM_096612). Accordingly, utilities of VGAM2425 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144501. LOC168667 (Accession XM_166592) is another VGAM2425 host target gene. LOC168667 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC168667, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC168667 BINDING SITE, designated SEQ ID:44564, to the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, also designated SEQ ID:5136.

[81988] Another function of VGAM2425 is therefore inhibition of LOC168667 (Accession XM_166592). Accordingly, utilities of VGAM2425 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC168667. LOC254045 (Accession XM_172882) is another VGAM2425 host target gene. LOC254045 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254045, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254045 BINDING SITE, designated SEQ ID:46161, to the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, also designated SEQ ID:5136.

[81989] Another function of VGAM2425 is therefore inhibition of

LOC254045 (Accession XM_172882). Accordingly, utilities of VGAM2425 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254045. LOC51068 (Accession NM_015938) is another VGAM2425 host target gene. LOC51068 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51068, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51068 BINDING SITE, designated SEQ ID:18058, to the nucleotide sequence of VGAM2425 RNA, herein designated VGAM RNA, also designated SEQ ID:5136.

[81990] Another function of VGAM2425 is therefore inhibition of LOC51068 (Accession NM_015938). Accordingly, utilities of VGAM2425 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51068. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2426 (VGAM2426) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[81991] VGAM2426 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2426 was detected is described hereinabove with reference to Figs. 1-8.

[81992] VGAM2426 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2426 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[81993] VGAM2426 gene encodes a VGAM2426 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2426 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2426 precursor RNA is designated SEQ ID:2412, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2412 is located at position 51036 relative to the genome of Goatpox Virus.

[81994] VGAM2426 precursor RNA folds onto itself, forming VGAM2426 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[81995] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2426 folded precursor RNA into VGAM2426 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2426 RNA is designated SEQ ID:5137, and is provided hereinbelow with reference to the sequence listing part.

[81996] VGAM2426 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2426 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2426 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[81997] VGAM2426 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2426 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2426 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2426 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2426 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[81998] The complementary binding of VGAM2426 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2426 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2426 host target RNA into VGAM2426 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[81999] It is appreciated that VGAM2426 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2426 host target genes. The mRNA of each one of this plurality of VGAM2426 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2426 RNA, herein designated VGAM RNA, and which when bound by VGAM2426 RNA causes inhibition of translation of respective one or more VGAM2426 host target proteins.

[82000] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2426 gene, herein designated VGAM GENE, on one

or more VGAM2426 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82001] It is yet further appreciated that a function of VGAM2426 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2426 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2426 correlate with, and may be deduced from, the identity of the host target genes which VGAM2426 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82002] Nucleotide sequences of the VGAM2426 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2426 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2426 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2426 are further described hereinbelow with reference to Table 1.

[82003] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2426 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2426 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82004] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2426 gene, herein designated VGAM is inhibition of expression of VGAM2426 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2426 correlate with, and may be deduced from, the identity of the target genes which VGAM2426 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82005] Archain 1 (ARCN1, Accession NM_001655) is a VGAM2426

host target gene. ARCN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARCN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARCN1 BINDING SITE, designated SEQ ID:7366, to the nucleotide sequence of VGAM2426 RNA, herein designated VGAM RNA, also designated SEQ ID:5137.

[82006] A function of VGAM2426 is therefore inhibition of Archain 1 (ARCN1, Accession NM_001655), a gene which plays a fundamental role in eukaryotic cell biology. Accordingly, utilities of VGAM2426 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARCN1. The function of ARCN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1226.Retinoblastoma 1 (including osteosarcoma) (RB1, Accession XM_165641) is another VGAM2426 host target gene. RB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RB1 BINDING SITE, designated SEQ ID:43704, to the nucleotide sequence of VGAM2426 RNA, herein designated VGAM RNA, also designated SEQ ID:5137.

[82007] Another function of VGAM2426 is therefore inhibition of Retinoblastoma 1 (including osteosarcoma) (RB1, Accession XM_165641), a gene which probably acts as a regulator of other genes. Accordingly, utilities of VGAM2426 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RB1. The function of RB1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM795.MCJ (Accession NM_013238) is another VGAM2426 host target gene. MCJ BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MCJ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MCJ BINDING SITE, designated SEQ ID:14898, to the nucleotide sequence of VGAM2426 RNA, herein designated VGAM RNA, also designated SEQ ID:5137.

[82008] Another function of VGAM2426 is therefore inhibition of MCJ (Accession NM_013238). Accordingly, utilities of VGAM2426 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCJ. PLU-1 (Accession XM_113375) is another VGAM2426 host target gene. PLU-1 BINDING SITE1 and PLU-1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PLU-1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLU-1 BINDING SITE1 and PLU-1 BINDING SITE2, designated SEQ ID:42251 and SEQ ID:13402 respectively, to the nucleotide sequence of VGAM2426 RNA, herein designated VGAM RNA, also designated SEQ ID:5137.

[82009] Another function of VGAM2426 is therefore inhibition of PLU-1 (Accession XM_113375). Accordingly, utilities of VGAM2426 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLU-1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2427 (VGAM2427) viral gene, which modulates expression

of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82010] VGAM2427 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2427 was detected is described hereinabove with reference to Figs. 1-8.

[82011] VGAM2427 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2427 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82012] VGAM2427 gene encodes a VGAM2427 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2427 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2427 precursor RNA is designated SEQ ID:2413, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2413 is located at position 48019 relative to the genome of Goatpox Virus.

[82013] VGAM2427 precursor RNA folds onto itself, forming VGAM2427 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82014] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2427 folded precursor RNA into VGAM2427 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2427 RNA is designated SEQ ID:5138, and is provided hereinbelow with reference to the sequence listing part.

[82015] VGAM2427 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2427 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2427 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82016] VGAM2427 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2427 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2427 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2427 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2427 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82017] The complementary binding of VGAM2427 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2427 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2427 host target RNA into VGAM2427 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82018] It is appreciated that VGAM2427 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2427 host target genes. The mRNA of each one of this plurality of VGAM2427 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2427 RNA, herein designated VGAM RNA, and which when bound by VGAM2427 RNA causes inhibition of translation of respective one or more VGAM2427 host target proteins.

[82019] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2427 gene, herein designated VGAM GENE, on one or more VGAM2427 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82020] It is yet further appreciated that a function of VGAM2427 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2427 correlate with, and may be deduced from, the identity of the host target genes which VGAM2427 binds and inhibits, and the function of these host target genes, as elaborated

hereinbelow.

[82021] Nucleotide sequences of the VGAM2427 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2427 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2427 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2427 are further described hereinbelow with reference to Table 1.

[82022] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2427 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2427 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82023] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2427 gene, herein designated VGAM is inhibition of expression of VGAM2427 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2427 correlate with, and may be deduced from, the identity of the target genes which VGAM2427 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82024] ATP-binding Cassette, Sub-family D (ALD), Member 2 (ABCD2, Accession NM_005164) is a VGAM2427 host target gene. ABCD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCD2 BINDING SITE, designated SEQ ID:11658, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82025] A function of VGAM2427 is therefore inhibition of ATP-binding Cassette, Sub-family D (ALD), Member 2 (ABCD2, Accession NM_005164), a gene which probable transporter. Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCD2. The function of ABCD2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM229.NAD(P)H Dehydrogenase, Quinone 1 (NQO1, Accession NM_000903) is another VGAM2427 host target gene. NQO1 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by NQO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NQO1 BINDING SITE, designated SEQ ID:6606, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82026] Another function of VGAM2427 is therefore inhibition of NAD(P)H Dehydrogenase, Quinone 1 (NQO1, Accession NM_000903), a gene which is cytochrome b5 reductase which reduces redox dyes and quinones. Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NQO1. The function of NQO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM923.RAB18, Member RAS Oncogene Family (RAB18, Accession NM_021252) is another VGAM2427 host target gene. RAB18 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB18, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of RAB18 BINDING SITE, designated SEQ ID:22224, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82027] Another function of VGAM2427 is therefore inhibition of RAB18, Member RAS Oncogene Family (RAB18, Accession NM_021252), a gene which plays a role in apical endocytosis/recycling. Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB18. The function of RAB18 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM120.RAD23 Homolog B (S. cerevisiae) (RAD23B, Accession NM_002874) is another VGAM2427 host target gene. RAD23B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAD23B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD23B BINDING SITE, designated SEQ ID:8785, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ

ID:5138.

[82028] Another function of VGAM2427 is therefore inhibition of RAD23 Homolog B (S. cerevisiae) (RAD23B, Accession NM_002874), a gene which is involved in dna excision repair. Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD23B. The function of RAD23B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM178.REV3-like, Catalytic Subunit of DNA Polymerase Zeta (yeast) (REV3L, Accession NM_002912) is another VGAM2427 host target gene. REV3L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by REV3L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of REV3L BINDING SITE, designated SEQ ID:8816, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82029] Another function of VGAM2427 is therefore inhibition of REV3-like, Catalytic Subunit of DNA Polymerase Zeta

(yeast) (REV3L, Accession NM_002912), a gene which is a catalytic subunit of DNA polymerase zeta and acts in translation replication and mutagenesis. Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with REV3L. The function of REV3L has been established by previous studies. To get a better understanding of mutagenic mechanisms in humans, Gibbs et al. (1998) cloned and sequenced the human homolog of the Saccharomyces cerevisiae REV3 gene. The yeast gene encodes the catalytic subunit of DNA polymerase zeta, a nonessential enzyme that is thought to carry out translesion replication and is responsible for virtually all DNA damage-induced mutagenesis and the majority of spontaneous mutagenesis. The human gene encodes an expected protein of 3,130 residues, about twice the size of the yeast protein, which has 1,504 amino acids. The 2 proteins are 29% identical in an amino-terminal region of approximately 340 residues, 39% identical in a carboxy-terminal region of approximately 850 residues, and 29% identical in a 55-residue region in the middle of the 2 genes. The sequence of the expected protein strongly predicted that it is the catalytic subunit of a DNA polymerase of the poly-

merase-zeta type; the carboxy-terminal domain possesses, in the right order, the 6 motifs characteristic of eukaryotic DNA polymerases, most closely resembles yeast polymerase-zeta among all polymerases in the GenBank database, and is different from the human alpha (POLA; 312040), delta (POLD1; 174761), and epsilon (POLE; 174762) enzymes. Human cells expressing high levels of an REV3 antisense RNA fragment grow normally, but show little or no UV-induced mutagenesis and are slightly more sensitive to killing by UV. The human gene therefore appears to carry out a function similar to that of its yeast counterpart. Xiao et al. (1998) identified human cDNA clones from 3 different libraries whose deduced amino acid sequences bore remarkable homology to yeast REV3. By in situ hybridization, they mapped the human REV3 gene to 1p33-p32. The gene encodes an mRNA of more than 10 kb. Its expression varies in different tissues and appeared to be elevated in some but not all of the tumor cell lines examined. In a study of genes involved in tumor suppression from 6q21, Morelli et al. (1998) identified the same sequence as that reported by Gibbs et al. (1998). The REV3L gene contains 33 exons (3 noncoding at the 5-prime end) and spans approximately 200 kb of

genomic DNA. The chromosome 6 assignment is the more likely (AFS).

[82030] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[82031] Gibbs, P. E. M.; McGregor, W. G.; Maher, V. M.; Nisson, P.; Lawrence, C. W. : A human homolog of the Saccharomyces cerevisiae REV3 gene, which encodes the catalytic subunit of DNA polymerase zeta. Proc. Nat. Acad. Sci. 95: 6876-6880, 1998. ; and

[82032] Xiao, W.; Lechler, T.; Chow, B. L.; Fontanie, T.; Agustus, M.; Carter, K. C.; Wei, Y.-F. : Identification, chromosomal mapping and tissue-specific expression of hREV3 encoding a putativ.

[82033] Further studies establishing the function and utilities of REV3L are found in John Hopkins OMIM database record ID 602776, and in sited publications numbered 7650-7652 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Tumor Necrosis Factor Receptor Superfamily, Member 9 (TNFRSF9, Accession NM_001561) is another VGAM2427 host target gene. TNFRSF9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by TNFRSF9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFRSF9 BINDING SITE, designated SEQ ID:7291, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82034] Another function of VGAM2427 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 9 (TNFRSF9, Accession NM_001561), a gene which inhibits proliferation of activated T lymphocytes. Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF9. The function of TNFRSF9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1954.Activin A Receptor, Type II (ACVR2, Accession NM_001616) is another VGAM2427 host target gene. ACVR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ACVR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of ACVR2 BINDING SITE, designated SEQ ID:7322, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82035] Another function of VGAM2427 is therefore inhibition of Activin A Receptor, Type II (ACVR2, Accession NM_001616). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACVR2. Chromosome 9 Open Reading Frame 14 (C9orf14, Accession XM_098859) is another VGAM2427 host target gene. C9orf14 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C9orf14, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C9orf14 BINDING SITE, designated SEQ ID:41913, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82036] Another function of VGAM2427 is therefore inhibition of Chromosome 9 Open Reading Frame 14 (C9orf14, Accession XM_098859). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with C9orf14. DKFZP586M0622 (Accession NM_015583) is another VGAM2427 host target gene. DKFZP586M0622 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP586M0622, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586M0622 BINDING SITE, designated SEQ ID:17850, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82037] Another function of VGAM2427 is therefore inhibition of DKFZP586M0622 (Accession NM_015583). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586M0622. FLJ10697 (Accession NM_018181) is another VGAM2427 host target gene. FLJ10697 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10697, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

FLJ10697 BINDING SITE, designated SEQ ID:20017, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82038] Another function of VGAM2427 is therefore inhibition of FLJ10697 (Accession NM_018181). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10697. FLJ13057 (Accession XM_171006) is another VGAM2427 host target gene. FLJ13057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13057 BINDING SITE, designated SEQ ID:45778, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82039] Another function of VGAM2427 is therefore inhibition of FLJ13057 (Accession XM_171006). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13057. KIAA0121 (Accession XM_052386) is another VGAM2427 host target gene. KIAA0121 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0121 BINDING SITE, designated SEQ ID:35973, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82040] Another function of VGAM2427 is therefore inhibition of KIAA0121 (Accession XM_052386). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0121. KIAA0265 (Accession XM_045954) is another VGAM2427 host target gene. KIAA0265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0265 BINDING SITE, designated SEQ ID:34622, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82041] Another function of VGAM2427 is therefore inhibition of

KIAA0265 (Accession XM_045954). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0265. KIAA1948 (Accession XM_091984) is another VGAM2427 host target gene. KIAA1948 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1948, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1948 BINDING SITE, designated SEQ ID:40084, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82042] Another function of VGAM2427 is therefore inhibition of KIAA1948 (Accession XM_091984). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1948. KIAA1950 (Accession XM_166532) is another VGAM2427 host target gene. KIAA1950 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1950, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1950 BINDING SITE, designated SEQ ID:44491, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82043] Another function of VGAM2427 is therefore inhibition of KIAA1950 (Accession XM_166532). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1950. KIAA1979 (Accession XM_113984) is another VGAM2427 host target gene. KIAA1979 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1979, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1979 BINDING SITE, designated SEQ ID:42592, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82044] Another function of VGAM2427 is therefore inhibition of KIAA1979 (Accession XM_113984). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1979. NYD-SP15 (Accession NM_030911) is another

VGAM2427 host target gene. NYD-SP15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NYD-SP15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NYD-SP15 BINDING SITE, designated SEQ ID:25178, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82045] Another function of VGAM2427 is therefore inhibition of NYD-SP15 (Accession NM_030911). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NYD-SP15. Protein Tyrosine Phosphatase, Non-receptor Type Substrate 1 (PTPNS1, Accession NM_080792) is another VGAM2427 host target gene. PTPNS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPNS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPNS1 BINDING SITE, designated SEQ ID:28059, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM

RNA, also designated SEQ ID:5138.

[82046] Another function of VGAM2427 is therefore inhibition of Protein Tyrosine Phosphatase, Non-receptor Type Substrate 1 (PTPNS1, Accession NM_080792). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPNS1. SMAP-5 (Accession NM_030799) is another VGAM2427 host target gene. SMAP-5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMAP-5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMAP-5 BINDING SITE, designated SEQ ID:25100, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82047] Another function of VGAM2427 is therefore inhibition of SMAP-5 (Accession NM_030799). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMAP-5. LOC112609 (Accession XM_053013) is another VGAM2427 host target gene. LOC112609 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC112609, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112609 BINDING SITE, designated SEQ ID:36059, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82048] Another function of VGAM2427 is therefore inhibition of LOC112609 (Accession XM_053013). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112609. LOC219540 (Accession XM_168047) is another VGAM2427 host target gene. LOC219540 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219540, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219540 BINDING SITE, designated SEQ ID:44960, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82049] Another function of VGAM2427 is therefore inhibition of LOC219540 (Accession XM_168047). Accordingly, utilities

of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219540. LOC254485 (Accession XM_170782) is another VGAM2427 host target gene. LOC254485 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254485, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254485 BINDING SITE, designated SEQ ID:45550, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82050] Another function of VGAM2427 is therefore inhibition of LOC254485 (Accession XM_170782). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254485. LOC256940 (Accession XM_172879) is another VGAM2427 host target gene. LOC256940 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256940, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC256940 BINDING SITE, designated SEQ ID:46156, to the nucleotide sequence of VGAM2427 RNA, herein designated VGAM RNA, also designated SEQ ID:5138.

[82051] Another function of VGAM2427 is therefore inhibition of LOC256940 (Accession XM_172879). Accordingly, utilities of VGAM2427 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256940. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2428 (VGAM2428) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82052] VGAM2428 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2428 was detected is described hereinabove with reference to Figs. 1-8.

[82053] VGAM2428 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2428 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82054] VGAM2428 gene encodes a VGAM2428 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2428 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2428 precursor RNA is designated SEQ ID:2414, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2414 is located at position 91853 relative to the genome of Goatpox Virus.

[82055] VGAM2428 precursor RNA folds onto itself, forming VGAM2428 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82056] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2428 folded precursor RNA into VGAM2428 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2428 RNA is designated SEQ ID:5139, and is provided hereinbelow with reference to the sequence listing part.

[82057] VGAM2428 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2428 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2428 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82058] VGAM2428 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2428 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2428 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2428 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2428 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82059] The complementary binding of VGAM2428 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2428 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2428 host target RNA into VGAM2428 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82060] It is appreciated that VGAM2428 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2428 host target genes. The mRNA of each one of this plurality of VGAM2428 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2428 RNA, herein designated VGAM RNA, and which when bound by VGAM2428 RNA causes inhibition of translation of respective one or more VGAM2428 host target proteins.

[82061] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2428 gene, herein designated VGAM GENE, on one or more VGAM2428 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82062] It is yet further appreciated that a function of VGAM2428 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2428 correlate with, and may be deduced from, the identity of the host target genes which VGAM2428 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82063] Nucleotide sequences of the VGAM2428 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2428 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2428 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2428 are further described hereinbelow with reference to Table 1.

[82064] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2428 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2428 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82065] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2428 gene, herein designated VGAM is inhibition of expression of VGAM2428 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2428 correlate with, and may be deduced from, the identity of the target genes which VGAM2428 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82066] Adenosine Deaminase, RNA-specific (ADAR, Accession NM_001111) is a VGAM2428 host target gene. ADAR BINDING SITE1 through ADAR BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ADAR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADAR BINDING SITE1 through ADAR BINDING SITE3, designated SEQ ID:6774, SEQ ID:17967 and SEQ ID:17960 respectively, to the nucleotide sequence of VGAM2428 RNA, herein designated

VGAM RNA, also designated SEQ ID:5139.

[82067] A function of VGAM2428 is therefore inhibition of Adenosine Deaminase, RNA-specific (ADAR, Accession NM_001111), a gene which converts adenosine to inosine in double-stranded RNA. Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADAR. The function of ADAR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM323.Matrix Metalloproteinase 19 (MMP19, Accession NM_022792) is another VGAM2428 host target gene. MMP19 BINDING SITE1 through MMP19 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MMP19, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MMP19 BINDING SITE1 through MMP19 BINDING SITE4, designated SEQ ID:23082, SEQ ID:23077, SEQ ID:23079 and SEQ ID:8269 respectively, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82068] Another function of VGAM2428 is therefore inhibition of Matrix Metalloproteinase 19 (MMP19, Accession NM_022792). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMP19. FLJ12704 (Accession NM_024998) is another VGAM2428 host target gene. FLJ12704 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12704, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12704 BINDING SITE, designated SEQ ID:24565, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82069] Another function of VGAM2428 is therefore inhibition of FLJ12704 (Accession NM_024998). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12704. H326 (Accession NM_015726) is another VGAM2428 host target gene. H326 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by H326, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H326 BINDING SITE, designated SEQ ID:17938, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82070] Another function of VGAM2428 is therefore inhibition of H326 (Accession NM_015726). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H326. KIAA0594 (Accession XM_036117) is another VGAM2428 host target gene. KIAA0594 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0594, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0594 BINDING SITE, designated SEQ ID:32387, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82071] Another function of VGAM2428 is therefore inhibition of KIAA0594 (Accession XM_036117). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0594. KIAA1634 (Accession XM_032749) is another VGAM2428 host target gene. KIAA1634 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1634, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1634 BINDING SITE, designated SEQ ID:31750, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82072] Another function of VGAM2428 is therefore inhibition of KIAA1634 (Accession XM_032749). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1634. KIAA1831 (Accession XM_033366) is another VGAM2428 host target gene. KIAA1831 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1831, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1831 BINDING SITE, designated SEQ ID:31905, to the

nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82073] Another function of VGAM2428 is therefore inhibition of KIAA1831 (Accession XM_033366). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1831. Purinergic Receptor P2X-like 1, Orphan Receptor (P2RXL1, Accession NM_005446) is another VGAM2428 host target gene. P2RXL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P2RXL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P2RXL1 BINDING SITE, designated SEQ ID:11932, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82074] Another function of VGAM2428 is therefore inhibition of Purinergic Receptor P2X-like 1, Orphan Receptor (P2RXL1, Accession NM_005446). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RXL1. PRP8 Pre-mRNA Processing Factor 8 Homolog

(yeast) (PRPF8, Accession XM_028335) is another VGAM2428 host target gene. PRPF8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRPF8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRPF8 BINDING SITE, designated SEQ ID:30680, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82075] Another function of VGAM2428 is therefore inhibition of PRP8 Pre-mRNA Processing Factor 8 Homolog (yeast) (PRPF8, Accession XM_028335). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRPF8. LOC120534 (Accession XM_058476) is another VGAM2428 host target gene. LOC120534 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120534, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120534 BINDING SITE, designated SEQ ID:36626, to

the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82076] Another function of VGAM2428 is therefore inhibition of LOC120534 (Accession XM_058476). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120534. LOC131870 (Accession XM_059544) is another VGAM2428 host target gene. LOC131870 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC131870, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC131870 BINDING SITE, designated SEQ ID:37016, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82077] Another function of VGAM2428 is therefore inhibition of LOC131870 (Accession XM_059544). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC131870. LOC144866 (Accession XM_096699) is another VGAM2428 host target gene. LOC144866 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC144866, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144866 BINDING SITE, designated SEQ ID:40476, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82078] Another function of VGAM2428 is therefore inhibition of LOC144866 (Accession XM_096699). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144866. LOC146774 (Accession XM_085584) is another VGAM2428 host target gene. LOC146774 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146774, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146774 BINDING SITE, designated SEQ ID:38234, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82079] Another function of VGAM2428 is therefore inhibition of LOC146774 (Accession XM_085584). Accordingly, utilities

of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146774. LOC150848 (Accession XM_097959) is another VGAM2428 host target gene. LOC150848 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150848, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150848 BINDING SITE, designated SEQ ID:41254, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82080] Another function of VGAM2428 is therefore inhibition of LOC150848 (Accession XM_097959). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150848. LOC151610 (Accession XM_087245) is another VGAM2428 host target gene. LOC151610 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151610, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC151610 BINDING SITE, designated SEQ ID:39134, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82081] Another function of VGAM2428 is therefore inhibition of LOC151610 (Accession XM_087245). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151610. LOC152317 (Accession XM_098189) is another VGAM2428 host target gene. LOC152317 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152317, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152317 BINDING SITE, designated SEQ ID:41467, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82082] Another function of VGAM2428 is therefore inhibition of LOC152317 (Accession XM_098189). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152317. LOC203378 (Accession XM_117541) is another VGAM2428 host target gene. LOC203378 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203378, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203378 BINDING SITE, designated SEQ ID:43558, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82083] Another function of VGAM2428 is therefore inhibition of LOC203378 (Accession XM_117541). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203378. LOC219347 (Accession XM_167564) is another VGAM2428 host target gene. LOC219347 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219347, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219347 BINDING SITE, designated SEQ ID:44678, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82084] Another function of VGAM2428 is therefore inhibition of

LOC219347 (Accession XM_167564). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219347. LOC91561 (Accession XM_039218) is another VGAM2428 host target gene. LOC91561 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91561, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91561 BINDING SITE, designated SEQ ID:33021, to the nucleotide sequence of VGAM2428 RNA, herein designated VGAM RNA, also designated SEQ ID:5139.

[82085] Another function of VGAM2428 is therefore inhibition of LOC91561 (Accession XM_039218). Accordingly, utilities of VGAM2428 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91561. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2429 (VGAM2429) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[82086] VGAM2429 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2429 was detected is described hereinabove with reference to Figs. 1-8.

[82087] VGAM2429 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2429 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82088] VGAM2429 gene encodes a VGAM2429 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2429 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2429 precursor RNA is designated SEQ ID:2415, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2415 is located at position 58421 relative to the genome of Goatpox Virus.

[82089] VGAM2429 precursor RNA folds onto itself, forming VGAM2429 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82090] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2429 folded precursor RNA into VGAM2429 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2429 RNA is designated SEQ ID:5140, and is provided hereinbelow with reference to the sequence listing part.

[82091] VGAM2429 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2429 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2429 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82092] VGAM2429 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2429 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2429 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2429 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2429 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[82093] The complementary binding of VGAM2429 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2429 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2429 host target RNA into VGAM2429 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82094] It is appreciated that VGAM2429 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2429 host target genes. The mRNA of each one of this plurality of VGAM2429 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2429 RNA, herein designated VGAM RNA, and which when bound by VGAM2429 RNA causes inhibition of translation of respective one or more VGAM2429 host target proteins.

[82095] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2429 gene, herein designated VGAM GENE, on one

or more VGAM2429 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82096] It is yet further appreciated that a function of VGAM2429 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2429 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2429 correlate with, and may be deduced from, the identity of the host target genes which VGAM2429 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82097] Nucleotide sequences of the VGAM2429 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2429 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2429 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2429 are further described hereinbelow with reference to Table 1.

[82098] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2429 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2429 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82099] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2429 gene, herein designated VGAM is inhibition of expression of VGAM2429 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2429 correlate with, and may be deduced from, the identity of the target genes which VGAM2429 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82100] Apical Protein-like (Xenopus laevis) (APXL, Accession

NM_001649) is a VGAM2429 host target gene. APXL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APXL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APXL BINDING SITE, designated SEQ ID:7356, to the nucleotide sequence of VGAM2429 RNA, herein designated VGAM RNA, also designated SEQ ID:5140.

[82101] A function of VGAM2429 is therefore inhibition of Apical Protein-like (Xenopus laevis) (APXL, Accession NM_001649), a gene which is implicated in amiloride-sensitive sodium channel activity. Accordingly, utilities of VGAM2429 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APXL. The function of APXL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.Eukaryotic Translation Initiation Factor 2, Subunit 3 Gamma, 52kDa (EIF2S3, Accession NM_001415) is another VGAM2429 host target gene. EIF2S3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF2S3, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF2S3 BINDING SITE, designated SEQ ID:7110, to the nucleotide sequence of VGAM2429 RNA, herein designated VGAM RNA, also designated SEQ ID:5140.

[82102] Another function of VGAM2429 is therefore inhibition of Eukaryotic Translation Initiation Factor 2, Subunit 3 Gamma, 52kDa (EIF2S3, Accession NM_001415), a gene which functions in the early steps of protein synthesis. Accordingly, utilities of VGAM2429 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF2S3. The function of EIF2S3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1254.Lumican (LUM, Accession NM_002345) is another VGAM2429 host target gene. LUM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LUM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LUM BINDING SITE, designated SEQ ID:8145,

to the nucleotide sequence of VGAM2429 RNA, herein designated VGAM RNA, also designated SEQ ID:5140.

[82103] Another function of VGAM2429 is therefore inhibition of Lumican (LUM, Accession NM_002345). Accordingly, utilities of VGAM2429 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LUM. ERp44 (Accession XM_088476) is another VGAM2429 host target gene. ERp44 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERp44, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERp44 BINDING SITE, designated SEQ ID:39726, to the nucleotide sequence of VGAM2429 RNA, herein designated VGAM RNA, also designated SEQ ID:5140.

[82104] Another function of VGAM2429 is therefore inhibition of ERp44 (Accession XM_088476). Accordingly, utilities of VGAM2429 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERp44. PNPASE (Accession XM_048088) is another VGAM2429 host target gene. PNPASE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by PNPASE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PNPASE BINDING SITE, designated SEQ ID:35102, to the nucleotide sequence of VGAM2429 RNA, herein designated VGAM RNA, also designated SEQ ID:5140.

[82105] Another function of VGAM2429 is therefore inhibition of PNPASE (Accession XM_048088). Accordingly, utilities of VGAM2429 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PNPASE. LOC115648 (Accession NM_145326) is another VGAM2429 host target gene. LOC115648 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115648, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115648 BINDING SITE, designated SEQ ID:29829, to the nucleotide sequence of VGAM2429 RNA, herein designated VGAM RNA, also designated SEQ ID:5140.

[82106] Another function of VGAM2429 is therefore inhibition of LOC115648 (Accession NM_145326). Accordingly, utilities

of VGAM2429 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115648. LOC255308 (Accession XM_170536) is another VGAM2429 host target gene. LOC255308 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255308 BINDING SITE, designated SEQ ID:45353, to the nucleotide sequence of VGAM2429 RNA, herein designated VGAM RNA, also designated SEQ ID:5140.

[82107] Another function of VGAM2429 is therefore inhibition of LOC255308 (Accession XM_170536). Accordingly, utilities of VGAM2429 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255308. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2430 (VGAM2430) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82108] VGAM2430 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2430 was detected is described hereinabove with reference to Figs. 1-8.

[82109] VGAM2430 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2430 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82110] VGAM2430 gene encodes a VGAM2430 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2430 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2430 precursor RNA is designated SEQ ID:2416, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2416 is located at position 123911 relative to the genome of Goatpox Virus.

[82111] VGAM2430 precursor RNA folds onto itself, forming VGAM2430 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82112] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2430 folded precursor RNA into VGAM2430 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2430 RNA is designated SEQ ID:5141, and is provided hereinbelow with reference to the sequence listing part.

[82113] VGAM2430 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2430 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2430 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[82114] VGAM2430 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2430 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2430 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2430 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2430 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82115] The complementary binding of VGAM2430 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2430 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2430 host target RNA into VGAM2430 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82116] It is appreciated that VGAM2430 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2430 host target genes. The mRNA of each one of this plurality of VGAM2430 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2430 RNA, herein designated VGAM RNA, and which when bound by VGAM2430 RNA causes inhibition of translation of respective one or more VGAM2430 host target proteins.

[82117] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2430 gene, herein designated VGAM GENE, on one or more VGAM2430 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82118] It is yet further appreciated that a function of VGAM2430 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2430 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2430 correlate with, and may be deduced from, the identity of the host target genes which VGAM2430 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82119] Nucleotide sequences of the VGAM2430 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2430 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2430 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2430 are further described hereinbelow with reference to Table 1.

[82120] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2430 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2430 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82121] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2430 gene, herein designated VGAM is inhibition of expression of VGAM2430 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2430 correlate with, and may be deduced from, the identity of the target genes which VGAM2430 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82122] Ceroid-lipofuscinosis, Neuronal 5 (CLN5, Accession NM_006493) is a VGAM2430 host target gene. CLN5

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLN5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLN5 BINDING SITE, designated SEQ ID:13230, to the nucleotide sequence of VGAM2430 RNA, herein designated VGAM RNA, also designated SEQ ID:5141.

[82123] A function of VGAM2430 is therefore inhibition of Ceroid-lipofuscinosis, Neuronal 5 (CLN5, Accession NM_006493). Accordingly, utilities of VGAM2430 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLN5. DKFZP434I0714 (Accession XM_098247) is another VGAM2430 host target gene. DKFZP434I0714 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434I0714, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434I0714 BINDING SITE, designated SEQ ID:41529, to the nucleotide sequence of VGAM2430 RNA, herein designated VGAM RNA, also designated SEQ ID:5141.

[82124] Another function of VGAM2430 is therefore inhibition of DKFZP434I0714 (Accession XM_098247). Accordingly, utilities of VGAM2430 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434I0714. DKFZP564F013 (Accession XM_168479) is another VGAM2430 host target gene. DKFZP564F013 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564F013, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564F013 BINDING SITE, designated SEQ ID:45200, to the nucleotide sequence of VGAM2430 RNA, herein designated VGAM RNA, also designated SEQ ID:5141.

[82125] Another function of VGAM2430 is therefore inhibition of DKFZP564F013 (Accession XM_168479). Accordingly, utilities of VGAM2430 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564F013. KIAA1674 (Accession XM_044065) is another VGAM2430 host target gene. KIAA1674 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1674, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1674 BINDING SITE, designated SEQ ID:34111, to the nucleotide sequence of VGAM2430 RNA, herein designated VGAM RNA, also designated SEQ ID:5141.

[82126] Another function of VGAM2430 is therefore inhibition of KIAA1674 (Accession XM_044065). Accordingly, utilities of VGAM2430 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1674. LOC145773 (Accession XM_085237) is another VGAM2430 host target gene. LOC145773 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145773, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145773 BINDING SITE, designated SEQ ID:37984, to the nucleotide sequence of VGAM2430 RNA, herein designated VGAM RNA, also designated SEQ ID:5141.

[82127] Another function of VGAM2430 is therefore inhibition of LOC145773 (Accession XM_085237). Accordingly, utilities of VGAM2430 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC145773. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2431 (VGAM2431) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82128] VGAM2431 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2431 was detected is described hereinabove with reference to Figs. 1-8.

[82129] VGAM2431 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2431 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82130] VGAM2431 gene encodes a VGAM2431 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2431 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2431 precursor RNA is desig-

nated SEQ ID:2417, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2417 is located at position 113097 relative to the genome of Goatpox Virus.

[82131] VGAM2431 precursor RNA folds onto itself, forming VGAM2431 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82132] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2431 folded precursor RNA into VGAM2431 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2431 RNA is designated SEQ ID:5142, and is provided hereinbelow with reference to the sequence

listing part.

[82133] VGAM2431 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2431 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2431 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82134] VGAM2431 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2431 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2431 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2431 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2431 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82135] The complementary binding of VGAM2431 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2431 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2431 host target RNA into VGAM2431 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82136] It is appreciated that VGAM2431 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2431 host target genes. The mRNA of each one of this plurality of VGAM2431 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2431 RNA, herein designated VGAM

RNA, and which when bound by VGAM2431 RNA causes inhibition of translation of respective one or more VGAM2431 host target proteins.

[82137] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2431 gene, herein designated VGAM GENE, on one or more VGAM2431 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82138] It is yet further appreciated that a function of VGAM2431 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2431 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2431 correlate with, and may be deduced from, the identity of the host target genes which VGAM2431 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82139] Nucleotide sequences of the VGAM2431 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2431 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2431 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2431 are further described hereinbelow with reference to Table 1.

[82140] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2431 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2431 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82141] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2431 gene, herein designated VGAM is

inhibition of expression of VGAM2431 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2431 correlate with, and may be deduced from, the identity of the target genes which VGAM2431 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82142] Cyclin F (CCNF, Accession NM_001761) is a VGAM2431 host target gene. CCNF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CCNF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCNF BINDING SITE, designated SEQ ID:7524, to the nucleotide sequence of VGAM2431 RNA, herein designated VGAM RNA, also designated SEQ ID:5142.

[82143] A function of VGAM2431 is therefore inhibition of Cyclin F (CCNF, Accession NM_001761), a gene which likely to be involved in the control of the cell cycle during s phase and g2. Accordingly, utilities of VGAM2431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCNF. The function of CCNF and its association with various diseases and clinical conditions,

has been established by previous studies, as described hereinabove with reference to VGAM367.Mitogen-activated Protein Kinase Kinase Kinase 1 (MAP3K1, Accession XM_042066) is another VGAM2431 host target gene. MAP3K1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K1 BINDING SITE, designated SEQ ID:33681, to the nucleotide sequence of VGAM2431 RNA, herein designated VGAM RNA, also designated SEQ ID:5142.

[82144] Another function of VGAM2431 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 1 (MAP3K1, Accession XM_042066), a gene which can phosphorylate and activate mapkk 1 and mapkk 2 (mek1/mek2) which leads to phosphorylation of map kinases. it is also a highly efficient activator of the jnk cascade. Accordingly, utilities of VGAM2431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K1. The function of MAP3K1 and its association with various diseases and clinical con-

ditions, has been established by previous studies, as described hereinabove with reference to VGAM469.C6.1A (Accession NM_024332) is another VGAM2431 host target gene. C6.1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C6.1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C6.1A BINDING SITE, designated SEQ ID:23639, to the nucleotide sequence of VGAM2431 RNA, herein designated VGAM RNA, also designated SEQ ID:5142.

[82145] Another function of VGAM2431 is therefore inhibition of C6.1A (Accession NM_024332). Accordingly, utilities of VGAM2431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C6.1A. KIAA1715 (Accession XM_042834) is another VGAM2431 host target gene. KIAA1715 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1715, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1715 BINDING SITE,

designated SEQ ID:33791, to the nucleotide sequence of VGAM2431 RNA, herein designated VGAM RNA, also designated SEQ ID:5142.

[82146] Another function of VGAM2431 is therefore inhibition of KIAA1715 (Accession XM_042834). Accordingly, utilities of VGAM2431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1715. LOC146839 (Accession XM_097107) is another VGAM2431 host target gene. LOC146839 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146839, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146839 BINDING SITE, designated SEQ ID:40752, to the nucleotide sequence of VGAM2431 RNA, herein designated VGAM RNA, also designated SEQ ID:5142.

[82147] Another function of VGAM2431 is therefore inhibition of LOC146839 (Accession XM_097107). Accordingly, utilities of VGAM2431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146839. LOC200609 (Accession XM_117256) is another VGAM2431 host target gene. LOC200609 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200609, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200609 BINDING SITE, designated SEQ ID:43324, to the nucleotide sequence of VGAM2431 RNA, herein designated VGAM RNA, also designated SEQ ID:5142.

[82148] Another function of VGAM2431 is therefore inhibition of LOC200609 (Accession XM_117256). Accordingly, utilities of VGAM2431 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200609. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2432 (VGAM2432) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82149] VGAM2432 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2432 was detected is described hereinabove with reference to Figs. 1-8.

[82150] VGAM2432 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2432 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82151] VGAM2432 gene encodes a VGAM2432 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2432 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2432 precursor RNA is designated SEQ ID:2418, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2418 is located at position 76475 relative to the genome of Goatpox Virus.

[82152] VGAM2432 precursor RNA folds onto itself, forming VGAM2432 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[82153] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2432 folded precursor RNA into VGAM2432 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 83%) nucleotide sequence of VGAM2432 RNA is designated SEQ ID:5143, and is provided hereinbelow with reference to the sequence listing part.

[82154] VGAM2432 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2432 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2432 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82155] VGAM2432 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2432 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2432 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2432 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2432 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82156] The complementary binding of VGAM2432 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2432 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2432 host target RNA into VGAM2432 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82157] It is appreciated that VGAM2432 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2432 host target genes. The mRNA of each one of this plurality of VGAM2432 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2432 RNA, herein designated VGAM RNA, and which when bound by VGAM2432 RNA causes inhibition of translation of respective one or more VGAM2432 host target proteins.

[82158] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2432 gene, herein designated VGAM GENE, on one or more VGAM2432 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82159] It is yet further appreciated that a function of VGAM2432 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2432 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2432 correlate with, and may be deduced from, the identity of the host target genes which VGAM2432 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82160] Nucleotide sequences of the VGAM2432 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2432 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2432 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2432 are further described hereinbelow with reference to Table 1.

[82161] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2432 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2432 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82162] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2432 gene, herein designated VGAM is inhibition of expression of VGAM2432 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2432 correlate with, and may be deduced from, the identity of the target genes which VGAM2432 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82163] Crystallin, Zeta (quinone reductase) (CRYZ, Accession NM_001889) is a VGAM2432 host target gene. CRYZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRYZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of CRYZ BINDING SITE, designated SEQ ID:7616, to the nucleotide sequence of VGAM2432 RNA, herein designated VGAM RNA, also designated SEQ ID:5143.

[82164] A function of VGAM2432 is therefore inhibition of Crystallin, Zeta (quinone reductase) (CRYZ, Accession NM_001889), a gene which may act in the detoxification of xenobiotics. Accordingly, utilities of VGAM2432 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRYZ. The function of CRYZ and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM323.EphA3 (EPHA3, Accession NM_005233) is another VGAM2432 host target gene. EPHA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPHA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPHA3 BINDING SITE, designated SEQ ID:11738, to the nucleotide sequence of VGAM2432 RNA, herein designated VGAM RNA, also designated SEQ ID:5143.

[82165] Another function of VGAM2432 is therefore inhibition of EphA3 (EPHA3, Accession NM_005233), a gene which binds to ephrin-a2, -a3, -a4 and -a5. could play a role in lymphoid function. Accordingly, utilities of VGAM2432 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPHA3. The function of EPHA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM164.FLJ20686 (Accession NM_017925) is another VGAM2432 host target gene. FLJ20686 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20686, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20686 BINDING SITE, designated SEQ ID:19595, to the nucleotide sequence of VGAM2432 RNA, herein designated VGAM RNA, also designated SEQ ID:5143.

[82166] Another function of VGAM2432 is therefore inhibition of FLJ20686 (Accession NM_017925). Accordingly, utilities of VGAM2432 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ20686. KIAA0089 (Accession XM_046056) is another VGAM2432 host target gene. KIAA0089 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0089, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0089 BINDING SITE, designated SEQ ID:34669, to the nucleotide sequence of VGAM2432 RNA, herein designated VGAM RNA, also designated SEQ ID:5143.

[82167] Another function of VGAM2432 is therefore inhibition of KIAA0089 (Accession XM_046056). Accordingly, utilities of VGAM2432 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0089. KIAA0429 (Accession NM_014751) is another VGAM2432 host target gene. KIAA0429 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0429, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0429 BINDING SITE, designated SEQ ID:16465, to the nucleotide sequence of VGAM2432 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5143.

[82168] Another function of VGAM2432 is therefore inhibition of KIAA0429 (Accession NM_014751). Accordingly, utilities of VGAM2432 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0429. SEC15L (Accession XM_051147) is another VGAM2432 host target gene. SEC15L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC15L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC15L BINDING SITE, designated SEQ ID:35764, to the nucleotide sequence of VGAM2432 RNA, herein designated VGAM RNA, also designated SEQ ID:5143.

[82169] Another function of VGAM2432 is therefore inhibition of SEC15L (Accession XM_051147). Accordingly, utilities of VGAM2432 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC15L. LOC147341 (Accession XM_097223) is another VGAM2432 host target gene. LOC147341 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147341, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147341 BINDING SITE, designated SEQ ID:40825, to the nucleotide sequence of VGAM2432 RNA, herein designated VGAM RNA, also designated SEQ ID:5143.

[82170] Another function of VGAM2432 is therefore inhibition of LOC147341 (Accession XM_097223). Accordingly, utilities of VGAM2432 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147341. LOC256277 (Accession XM_170644) is another VGAM2432 host target gene. LOC256277 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256277, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256277 BINDING SITE, designated SEQ ID:45425, to the nucleotide sequence of VGAM2432 RNA, herein designated VGAM RNA, also designated SEQ ID:5143.

[82171] Another function of VGAM2432 is therefore inhibition of LOC256277 (Accession XM_170644). Accordingly, utilities of VGAM2432 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC256277. LOC86651 (Accession XM_044052) is another VGAM2432 host target gene. LOC86651 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC86651, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC86651 BINDING SITE, designated SEQ ID:34097, to the nucleotide sequence of VGAM2432 RNA, herein designated VGAM RNA, also designated SEQ ID:5143.

[82172] Another function of VGAM2432 is therefore inhibition of LOC86651 (Accession XM_044052). Accordingly, utilities of VGAM2432 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC86651. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2433 (VGAM2433) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82173] VGAM2433 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2433 was detected is described hereinabove with reference to Figs. 1-8.

[82174] VGAM2433 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2433 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82175] VGAM2433 gene encodes a VGAM2433 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2433 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2433 precursor RNA is designated SEQ ID:2419, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2419 is located at position 30434 relative to the genome of Goatpox Virus.

[82176] VGAM2433 precursor RNA folds onto itself, forming VGAM2433 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82177] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2433 folded precursor RNA into VGAM2433 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 86%) nucleotide sequence of VGAM2433 RNA is designated SEQ ID:5144, and is provided hereinbelow with reference to the sequence listing part.

[82178] VGAM2433 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2433 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2433 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82179] VGAM2433 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2433 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2433 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2433 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2433 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82180] The complementary binding of VGAM2433 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2433 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2433 host target RNA into VGAM2433 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82181] It is appreciated that VGAM2433 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2433 host target genes. The mRNA of each one of this plurality of VGAM2433 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2433 RNA, herein designated VGAM RNA, and which when bound by VGAM2433 RNA causes inhibition of translation of respective one or more VGAM2433 host target proteins.

[82182] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2433 gene, herein designated VGAM GENE, on one or more VGAM2433 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82183] It is yet further appreciated that a function of VGAM2433 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2433 correlate with, and may be deduced from, the identity of the host target genes which VGAM2433 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82184] Nucleotide sequences of the VGAM2433 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2433 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2433 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2433 are further described hereinbelow with reference to Table 1.

[82185] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2433 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2433 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82186] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2433 gene, herein designated VGAM is inhibition of expression of VGAM2433 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2433 correlate with, and may be deduced from, the identity of the target genes which VGAM2433 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82187] B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898) is a VGAM2433 host target gene. BCL11B BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by BCL11B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL11B BINDING SITE, designated SEQ ID:23164, to the nucleotide sequence of VGAM2433 RNA, herein designated VGAM RNA, also designated SEQ ID:5144.

[82188] A function of VGAM2433 is therefore inhibition of B-cell CLL/lymphoma 11B (zinc finger protein) (BCL11B, Accession NM_022898). Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL11B. Cystic Fibrosis Transmembrane Conductance Regulator, ATP-binding Cassette (sub-family C, member 7) (CFTR, Accession NM_000492) is another VGAM2433 host target gene. CFTR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CFTR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CFTR BINDING SITE, designated SEQ ID:6104, to the nucleotide sequence of VGAM2433 RNA, herein

designated VGAM RNA, also designated SEQ ID:5144.

[82189] Another function of VGAM2433 is therefore inhibition of Cystic Fibrosis Transmembrane Conductance Regulator, ATP-binding Cassette (sub-family C, member 7) (CFTR, Accession NM_000492). Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CFTR. COX15 Homolog, Cytochrome C Oxidase Assembly Protein (yeast) (COX15, Accession NM_078470) is another VGAM2433 host target gene. COX15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COX15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COX15 BINDING SITE, designated SEQ ID:27790, to the nucleotide sequence of VGAM2433 RNA, herein designated VGAM RNA, also designated SEQ ID:5144.

[82190] Another function of VGAM2433 is therefore inhibition of COX15 Homolog, Cytochrome C Oxidase Assembly Protein (yeast) (COX15, Accession NM_078470). Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with COX15. Replication Protein A3, 14kDa (RPA3, Accession NM_002947) is another VGAM2433 host target gene. RPA3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RPA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPA3 BINDING SITE, designated SEQ ID:8858, to the nucleotide sequence of VGAM2433 RNA, herein designated VGAM RNA, also designated SEQ ID:5144.

[82191] Another function of VGAM2433 is therefore inhibition of Replication Protein A3, 14kDa (RPA3, Accession NM_002947). Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPA3. Sodium Channel, Voltage-gated, Type III, Alpha Polypeptide (SCN3A, Accession NM_006922) is another VGAM2433 host target gene. SCN3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCN3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCN3A BINDING SITE, designated SEQ

ID:13798, to the nucleotide sequence of VGAM2433 RNA, herein designated VGAM RNA, also designated SEQ ID:5144.

[82192] Another function of VGAM2433 is therefore inhibition of Sodium Channel, Voltage-gated, Type III, Alpha Polypeptide (SCN3A, Accession NM_006922), a gene which may be important for maintaining neural membrane excitability. Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCN3A. The function of SCN3A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM124.FLJ23151 (Accession NM_024772) is another VGAM2433 host target gene. FLJ23151 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23151, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23151 BINDING SITE, designated SEQ ID:24135, to the nucleotide sequence of VGAM2433 RNA, herein designated VGAM RNA, also designated SEQ ID:5144.

[82193] Another function of VGAM2433 is therefore inhibition of FLJ23151 (Accession NM_024772). Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23151. KIAA1468 (Accession XM_166289) is another VGAM2433 host target gene. KIAA1468 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1468, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1468 BINDING SITE, designated SEQ ID:44102, to the nucleotide sequence of VGAM2433 RNA, herein designated VGAM RNA, also designated SEQ ID:5144.

[82194] Another function of VGAM2433 is therefore inhibition of KIAA1468 (Accession XM_166289). Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1468. LRP15 (Accession NM_052953) is another VGAM2433 host target gene. LRP15 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LRP15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LRP15 BINDING SITE, designated SEQ ID:27510, to the nucleotide sequence of VGAM2433 RNA, herein designated VGAM RNA, also designated SEQ ID:5144.

[82195] Another function of VGAM2433 is therefore inhibition of LRP15 (Accession NM_052953). Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LRP15. LOC121536 (Accession XM_058567) is another VGAM2433 host target gene. LOC121536 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC121536, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC121536 BINDING SITE, designated SEQ ID:36666, to the nucleotide sequence of VGAM2433 RNA, herein designated VGAM RNA, also designated SEQ ID:5144.

[82196] Another function of VGAM2433 is therefore inhibition of LOC121536 (Accession XM_058567). Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC121536. LOC254251 (Accession XM_171088) is another VGAM2433 host target gene. LOC254251 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254251, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254251 BINDING SITE, designated SEQ ID:45895, to the nucleotide sequence of VGAM2433 RNA, herein designated VGAM RNA, also designated SEQ ID:5144.

[82197] Another function of VGAM2433 is therefore inhibition of LOC254251 (Accession XM_171088). Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254251. LOC51301 (Accession NM_016591) is another VGAM2433 host target gene. LOC51301 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC51301, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51301 BINDING SITE, designated SEQ ID:18674, to the nucleotide sequence of VGAM2433 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5144.

[82198] Another function of VGAM2433 is therefore inhibition of LOC51301 (Accession NM_016591). Accordingly, utilities of VGAM2433 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51301. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2434 (VGAM2434) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82199] VGAM2434 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2434 was detected is described hereinabove with reference to Figs. 1-8.

[82200] VGAM2434 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2434 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82201] VGAM2434 gene encodes a VGAM2434 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2434 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2434 precursor RNA is designated SEQ ID:2420, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2420 is located at position 130867 relative to the genome of Goatpox Virus.

[82202] VGAM2434 precursor RNA folds onto itself, forming VGAM2434 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82203] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2434 folded precursor RNA into VGAM2434 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2434 RNA is designated SEQ ID:5145, and is provided hereinbelow with reference to the sequence listing part.

[82204] VGAM2434 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2434 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2434 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82205] VGAM2434 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2434 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2434 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2434 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2434 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82206] The complementary binding of VGAM2434 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2434 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2434 host target RNA into VGAM2434 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82207] It is appreciated that VGAM2434 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2434 host target genes. The mRNA of

each one of this plurality of VGAM2434 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2434 RNA, herein designated VGAM RNA, and which when bound by VGAM2434 RNA causes inhibition of translation of respective one or more VGAM2434 host target proteins.

[82208] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2434 gene, herein designated VGAM GENE, on one or more VGAM2434 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[82209] It is yet further appreciated that a function of VGAM2434 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2434 correlate with, and may be deduced from, the identity of the host target genes which VGAM2434 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82210] Nucleotide sequences of the VGAM2434 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2434 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2434 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2434 are further described hereinbelow with reference to Table 1.

[82211] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2434 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2434 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82212] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2434 gene, herein designated VGAM is inhibition of expression of VGAM2434 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2434 correlate with, and may be deduced from, the identity of the target genes which VGAM2434 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82213] Alpha-1-B Glycoprotein (A1BG, Accession NM_130786) is a VGAM2434 host target gene. A1BG BINDING SITE1 and A1BG BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by A1BG, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of A1BG BINDING SITE1 and A1BG BINDING SITE2, designated SEQ ID:28279 and SEQ ID:28280 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82214] A function of VGAM2434 is therefore inhibition of Alpha-1-B Glycoprotein (A1BG, Accession NM_130786), a gene

which a plasma protein of unknown function. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with A1BG. The function of A1BG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM172.Apoptotic Protease Activating Factor (APAF1, Accession NM_001160) is another VGAM2434 host target gene. APAF1 BINDING SITE1 through APAF1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by APAF1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APAF1 BINDING SITE1 through APAF1 BINDING SITE4, designated SEQ ID:6830, SEQ ID:6831, SEQ ID:14869 and SEQ ID:14870 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82215] Another function of VGAM2434 is therefore inhibition of Apoptotic Protease Activating Factor (APAF1, Accession NM_001160), a gene which functions in the mitochondrial apoptotic pathway that leads to caspase 9 dependent acti-

vation of caspase 3. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APAF1. The function of APAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM552.Aquaporin 6, Kidney Specific (AQP6, Accession NM_001652) is another VGAM2434 host target gene. AQP6 BINDING SITE1 and AQP6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AQP6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AQP6 BINDING SITE1 and AQP6 BINDING SITE2, designated SEQ ID:7361 and SEQ ID:27619 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82216] Another function of VGAM2434 is therefore inhibition of Aquaporin 6, Kidney Specific (AQP6, Accession NM_001652), a gene which participates in distinct physiologic function such as glomerular filtration, tubular endocytosis, and acid-base metabolism. Accordingly, utilities

of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AQP6. The function of AQP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM340.ATPase, Na+/K+ Transporting, Beta 2 Polypeptide (ATP1B2, Accession NM_001678) is another VGAM2434 host target gene. ATP1B2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP1B2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP1B2 BINDING SITE, designated SEQ ID:7393, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82217] Another function of VGAM2434 is therefore inhibition of ATPase, Na+/K+ Transporting, Beta 2 Polypeptide (ATP1B2, Accession NM_001678), a gene which catalyzes the hydrolysis of ATP coupled with the exchange of Na +/K+ ions across the plasma membrane. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with ATP1B2. The function of ATP1B2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.ATPase, Class I, Type 8B, Member 2 (ATP8B2, Accession XM_036933) is another VGAM2434 host target gene. ATP8B2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP8B2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP8B2 BINDING SITE, designated SEQ ID:32517, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82218] Another function of VGAM2434 is therefore inhibition of ATPase, Class I, Type 8B, Member 2 (ATP8B2, Accession XM_036933). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8B2. BRIP1 (Accession NM_032043) is another VGAM2434 host target gene. BRIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BRIP1, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRIP1 BINDING SITE, designated SEQ ID:25757, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82219] Another function of VGAM2434 is therefore inhibition of BRIP1 (Accession NM_032043). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRIP1. Chromosome 20 Open Reading Frame 1 (C20orf1, Accession NM_012112) is another VGAM2434 host target gene. C20orf1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf1 BINDING SITE, designated SEQ ID:14428, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82220] Another function of VGAM2434 is therefore inhibition of Chromosome 20 Open Reading Frame 1 (C20orf1, Accession NM_012112), a gene which is a nuclear proliferation-

associated protein. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf1. The function of C20orf1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Cold Autoinflammatory Syndrome 1 (CIAS1, Accession NM_004895) is another VGAM2434 host target gene. CIAS1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CIAS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CIAS1 BINDING SITE, designated SEQ ID:11322, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82221] Another function of VGAM2434 is therefore inhibition of Cold Autoinflammatory Syndrome 1 (CIAS1, Accession NM_004895), a gene which may mediate protein-protein interactions; contains a leucine rich repeat. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIAS1. The function of CIAS1 and its association with

various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM316.COX15 Homolog, Cytochrome C Oxidase Assembly Protein (yeast) (COX15, Accession NM_078470) is another VGAM2434 host target gene. COX15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COX15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COX15 BINDING SITE, designated SEQ ID:27789, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82222] Another function of VGAM2434 is therefore inhibition of COX15 Homolog, Cytochrome C Oxidase Assembly Protein (yeast) (COX15, Accession NM_078470). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COX15. Cartilage Associated Protein (CRTAP, Accession NM_006371) is another VGAM2434 host target gene. CRTAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRTAP,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRTAP BINDING SITE, designated SEQ ID:13063, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82223] Another function of VGAM2434 is therefore inhibition of Cartilage Associated Protein (CRTAP, Accession NM_006371), a gene which is a novel developmentally regulated chick embryo protein. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRTAP. The function of CRTAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.Chemokine (C-X-C motif) Ligand 16 (CXCL16, Accession NM_022059) is another VGAM2434 host target gene. CXCL16 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CXCL16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of CXCL16 BINDING SITE, designated SEQ ID:22598, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82224] Another function of VGAM2434 is therefore inhibition of Chemokine (C-X-C motif) Ligand 16 (CXCL16, Accession NM_022059), a gene which induces calcium mobilization. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXCL16. The function of CXCL16 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1845.Cytochrome P450, Subfamily I (aromatic compound-inducible), Polypeptide 2 (CYP1A2, Accession NM_000761) is another VGAM2434 host target gene. CYP1A2 BINDING SITE1 through CYP1A2 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CYP1A2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP1A2 BINDING SITE1 through CYP1A2 BINDING SITE4, desig-

nated SEQ ID:6413, SEQ ID:6411, SEQ ID:34255 and SEQ ID:34257 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82225] Another function of VGAM2434 is therefore inhibition of Cytochrome P450, Subfamily I (aromatic compound-inducible), Polypeptide 2 (CYP1A2, Accession NM_000761), a gene which intervenes in an NADPH-dependent electron transport pathway. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP1A2. The function of CYP1A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.DNA Fragmentation Factor, 40kDa, Beta Polypeptide (caspase-activated DNase) (DFFB, Accession XM_113366) is another VGAM2434 host target gene. DFFB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DFFB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DFFB BINDING SITE, designated SEQ ID:42246, to the nu-

cleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82226] Another function of VGAM2434 is therefore inhibition of DNA Fragmentation Factor, 40kDa, Beta Polypeptide (caspase-activated DNase) (DFFB, Accession XM_113366), a gene which induces DNA fragmentation and chromatin condensation during apoptosis. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DFFB. The function of DFFB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Disrupted In Schizophrenia 1 (DISC1, Accession NM_018662) is another VGAM2434 host target gene. DISC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DISC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DISC1 BINDING SITE, designated SEQ ID:20740, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82227] Another function of VGAM2434 is therefore inhibition of Disrupted In Schizophrenia 1 (DISC1, Accession NM_018662), a gene which has globular N-terminal domain(s) and a helical C-terminal domain. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DISC1. The function of DISC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Down Syndrome Critical Region Gene 3 (DSCR3, Accession NM_006052) is another VGAM2434 host target gene. DSCR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DSCR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DSCR3 BINDING SITE, designated SEQ ID:12688, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82228] Another function of VGAM2434 is therefore inhibition of Down Syndrome Critical Region Gene 3 (DSCR3, Accession NM_006052). Accordingly, utilities of VGAM2434 include

diagnosis, prevention and treatment of diseases and clinical conditions associated with DSCR3. EPB72 (Accession NM_004099) is another VGAM2434 host target gene. EPB72 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPB72, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPB72 BINDING SITE, designated SEQ ID:10307, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82229] Another function of VGAM2434 is therefore inhibition of EPB72 (Accession NM_004099), a gene which may regulate cation conductance. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPB72. The function of EPB72 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1560.Ellis Van Creveld Syndrome (EVC, Accession NM_014556) is another VGAM2434 host target gene. EVC BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by EVC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:15895, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82230] Another function of VGAM2434 is therefore inhibition of Ellis Van Creveld Syndrome (EVC, Accession NM_014556). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC. Fasciculation and Elongation Protein Zeta 1 (zygin I) (FEZ1, Accession NM_022549) is another VGAM2434 host target gene. FEZ1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FEZ1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FEZ1 BINDING SITE, designated SEQ ID:22879, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82231] Another function of VGAM2434 is therefore inhibition of

Fasciculation and Elongation Protein Zeta 1 (zygin I) (FEZ1, Accession NM_022549), a gene which Zygin 1; may have a role in axonal outgrowth; has similarity to C. elegans UNC-76. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FEZ1. The function of FEZ1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM37.Frizzled Homolog 4 (Drosophila) (FZD4, Accession NM_012193) is another VGAM2434 host target gene. FZD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FZD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FZD4 BINDING SITE, designated SEQ ID:14484, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82232] Another function of VGAM2434 is therefore inhibition of Frizzled Homolog 4 (Drosophila) (FZD4, Accession NM_012193), a gene which may function in cell polarity, cell fate specification and cancer; similar to frizzled re-

ceptor family, has seven transmembrane domains. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FZD4. The function of FZD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM309.GM2 Ganglioside Activator Protein (GM2A, Accession XM_041978) is another VGAM2434 host target gene. GM2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GM2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GM2A BINDING SITE, designated SEQ ID:33662, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82233] Another function of VGAM2434 is therefore inhibition of GM2 Ganglioside Activator Protein (GM2A, Accession XM_041978). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GM2A. G Protein-coupled Receptor 56 (GPR56, Accession NM_005682) is another

VGAM2434 host target gene. GPR56 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GPR56, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR56 BINDING SITE, designated SEQ ID:12239, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82234] Another function of VGAM2434 is therefore inhibition of G Protein-coupled Receptor 56 (GPR56, Accession NM_005682), a gene which transduces extracellular signals through heterotrimeric G proteins. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR56. The function of GPR56 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM782.G Protein-coupled Receptor 81 (GPR81, Accession NM_032554) is another VGAM2434 host target gene. GPR81 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPR81, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR81 BINDING SITE, designated SEQ ID:26281, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82235] Another function of VGAM2434 is therefore inhibition of G Protein-coupled Receptor 81 (GPR81, Accession NM_032554). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR81. GRAF (Accession NM_015071) is another VGAM2434 host target gene. GRAF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRAF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRAF BINDING SITE, designated SEQ ID:17445, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82236] Another function of VGAM2434 is therefore inhibition of GRAF (Accession NM_015071), a gene which ia a GTPase activating protein for p21-rac. Accordingly, utilities of

VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRAF. The function of GRAF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM430.HCS (Accession NM_018947) is another VGAM2434 host target gene. HCS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCS BINDING SITE, designated SEQ ID:21016, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82237] Another function of VGAM2434 is therefore inhibition of HCS (Accession NM_018947). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCS. High-mobility Group 20A (HMG20A, Accession NM_018200) is another VGAM2434 host target gene. HMG20A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

HMG20A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMG20A BINDING SITE, designated SEQ ID:20074, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82238] Another function of VGAM2434 is therefore inhibition of High-mobility Group 20A (HMG20A, Accession NM_018200). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMG20A. Isocitrate Dehydrogenase 3 (NAD+) Alpha (IDH3A, Accession NM_005530) is another VGAM2434 host target gene. IDH3A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IDH3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IDH3A BINDING SITE, designated SEQ ID:12051, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82239] Another function of VGAM2434 is therefore inhibition of Isocitrate Dehydrogenase 3 (NAD+) Alpha (IDH3A, Accession NM_005530), a gene which decarboxylates isocitrate into alpha-ketoglutarate in the TCA cycle. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IDH3A. The function of IDH3A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM349.Integrin, Alpha M (complement component receptor 3, alpha; also known as CD11b (p170), Macrophage Antigen Alpha Polypeptide) (ITGAM, Accession XM_050142) is another VGAM2434 host target gene. ITGAM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGAM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGAM BINDING SITE, designated SEQ ID:35565, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82240] Another function of VGAM2434 is therefore inhibition of

Integrin, Alpha M (complement component receptor 3, alpha; also known as CD11b (p170), Macrophage Antigen Alpha Polypeptide) (ITGAM, Accession XM_050142), a gene which is invovled in various adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGAM. The function of ITGAM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1386.Leucine Zipper, Putative Tumor Suppressor 1 (LZTS1, Accession NM_021020) is another VGAM2434 host target gene. LZTS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LZTS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LZTS1 BINDING SITE, designated SEQ ID:22007, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82241] Another function of VGAM2434 is therefore inhibition of Leucine Zipper, Putative Tumor Suppressor 1 (LZTS1, Accession NM_021020), a gene which Zygin 1; may have a role in axonal outgrowth; has similarity to C. elegans UNC-76. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LZTS1. The function of LZTS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM890.Male Germ Cell-associated Kinase (MAK, Accession NM_005906) is another VGAM2434 host target gene. MAK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAK BINDING SITE, designated SEQ ID:12531, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82242] Another function of VGAM2434 is therefore inhibition of Male Germ Cell-associated Kinase (MAK, Accession NM_005906), a gene which plays an important role in

spermatogenesis. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAK. The function of MAK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1322.MADS Box Transcription Enhancer Factor 2, Polypeptide A (myocyte enhancer factor 2A) (MEF2A, Accession NM_005587) is another VGAM2434 host target gene. MEF2A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MEF2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEF2A BINDING SITE, designated SEQ ID:12118, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82243] Another function of VGAM2434 is therefore inhibition of MADS Box Transcription Enhancer Factor 2, Polypeptide A (myocyte enhancer factor 2A) (MEF2A, Accession NM_005587), a gene which binds a consensus sequence that regulates transcription. Accordingly, utilities of

VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEF2A. The function of MEF2A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM46.Mediterranean Fever (MEFV, Accession NM_000243) is another VGAM2434 host target gene. MEFV BINDING SITE1 and MEFV BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MEFV, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MEFV BINDING SITE1 and MEFV BINDING SITE2, designated SEQ ID:5772 and SEQ ID:5771 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82244] Another function of VGAM2434 is therefore inhibition of Mediterranean Fever (MEFV, Accession NM_000243). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MEFV. MHC Class I Polypeptide-related Sequence B (MICB, Accession NM_005931) is another

VGAM2434 host target gene. MICB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MICB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MICB BINDING SITE, designated SEQ ID:12564, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82245] Another function of VGAM2434 is therefore inhibition of MHC Class I Polypeptide-related Sequence B (MICB, Accession NM_005931), a gene which involved in the presentation of foreign antigens to the immune system. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MICB. The function of MICB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Melan-A (MLANA, Accession NM_005511) is another VGAM2434 host target gene. MLANA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MLANA, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MLANA BINDING SITE, designated SEQ ID:12028, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82246] Another function of VGAM2434 is therefore inhibition of Melan-A (MLANA, Accession NM_005511). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLANA. Myeloproliferative Leukemia Virus Oncogene (MPL, Accession NM_005373) is another VGAM2434 host target gene. MPL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MPL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MPL BINDING SITE, designated SEQ ID:11848, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82247] Another function of VGAM2434 is therefore inhibition of Myeloproliferative Leukemia Virus Oncogene (MPL, Acces-

sion NM_005373). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MPL. V-myc Myelocytomatosis Viral Oncogene Homolog 2 (avian) (MYCL2, Accession NM_005377) is another VGAM2434 host target gene. MYCL2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYCL2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYCL2 BINDING SITE, designated SEQ ID:11855, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82248] Another function of VGAM2434 is therefore inhibition of V-myc Myelocytomatosis Viral Oncogene Homolog 2 (avian) (MYCL2, Accession NM_005377). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYCL2. Nuclear Receptor Coactivator 6 (NCOA6, Accession NM_014071) is another VGAM2434 host target gene. NCOA6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

NCOA6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NCOA6 BINDING SITE, designated SEQ ID:15293, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82249] Another function of VGAM2434 is therefore inhibition of Nuclear Receptor Coactivator 6 (NCOA6, Accession NM_014071), a gene which activates gene transcription through ligand-dependent association with coactivators. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NCOA6. The function of NCOA6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM25.Non-POU Domain Containing, Octamer-binding (NONO, Accession XM_088688) is another VGAM2434 host target gene. NONO BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NONO, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of NONO BINDING SITE, designated SEQ ID:39899, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82250] Another function of VGAM2434 is therefore inhibition of Non-POU Domain Containing, Octamer-binding (NONO, Accession XM_088688), a gene which is a nuclear protein which contains RNA recognition motifs. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NONO. The function of NONO and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM95.Protocadherin Beta 9 (PCDHB9, Accession NM_019119) is another VGAM2434 host target gene. PCDHB9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDHB9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDHB9 BINDING SITE, designated SEQ ID:21206, to the nucleotide sequence of VGAM2434 RNA,

herein designated VGAM RNA, also designated SEQ ID:5145.

[82251] Another function of VGAM2434 is therefore inhibition of Protocadherin Beta 9 (PCDHB9, Accession NM_019119), a gene which is a potential calcium-dependent cell-adhesion protein. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDHB9. The function of PCDHB9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Phosducin-like (PDCL, Accession NM_005388) is another VGAM2434 host target gene. PDCL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDCL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDCL BINDING SITE, designated SEQ ID:11866, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82252] Another function of VGAM2434 is therefore inhibition of Phosducin-like (PDCL, Accession NM_005388), a gene

which may regulate G-protein signaling and similar to phosducins. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDCL. The function of PDCL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1708.Phosphodiesterase 6B, CGMP-specific, Rod, Beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NM_000283) is another VGAM2434 host target gene. PDE6B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PDE6B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDE6B BINDING SITE, designated SEQ ID:5830, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82253] Another function of VGAM2434 is therefore inhibition of Phosphodiesterase 6B, CGMP-specific, Rod, Beta (congenital stationary night blindness 3, autosomal dominant) (PDE6B, Accession NM_000283). Accordingly, utili-

ties of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PDE6B. Period Homolog 2 (Drosophila) (PER2, Accession NM_022817) is another VGAM2434 host target gene. PER2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PER2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PER2 BINDING SITE, designated SEQ ID:23090, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82254] Another function of VGAM2434 is therefore inhibition of Period Homolog 2 (Drosophila) (PER2, Accession NM_022817), a gene which Period homolog 2; putative circadian clock protein; has a PAS dimerization domain. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PER2. The function of PER2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Phosphoinositide-3-kinase, Catalytic, Delta

Polypeptide (PIK3CD, Accession NM_005026) is another VGAM2434 host target gene. PIK3CD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIK3CD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIK3CD BINDING SITE, designated SEQ ID:11465, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82255] Another function of VGAM2434 is therefore inhibition of Phosphoinositide-3-kinase, Catalytic, Delta Polypeptide (PIK3CD, Accession NM_005026), a gene which regulating cell growth. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIK3CD. The function of PIK3CD has been established by previous studies. Vanhaesebroeck et al. (1997) classified p110-delta as a class I PI3K because it displayed broad in vitro lipid substrate specificity. Like p110-alpha and p110-beta, p110-delta binds p85 adaptor proteins and GTP-bound Ras. These 3 class I PI3Ks were indistinguishable at the level of p85 adaptor protein selection or recruitment to activated re-

ceptor complexes. However, unlike p110-alpha, p110-delta does not phosphorylate p85, but instead has an autophosphorylation activity Animal model experiments lend further support to the function of PIK3CD. Okkenhaug et al. (2002) generated mice expressing a catalytically inactive form of Pik3cd (asp910 to ala). They observed impaired signaling and attenuated immune responses by antigen receptors of B and T cells from these mice. The presence of Pik3ca and Pik3cb did not compensate for Pik3cd in immune function. The mutant mice also developed inflammatory bowel disease. Since the IBD7 susceptibility locus (OMIM Ref. No. 605225) maps to chromosome 1p36, the authors suggested that PIK3CD may be a candidate susceptibility gene

[82256] It is appreciated that the abovementioned animal model for PIK3CD is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[82257] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[82258] Okkenhaug, K.; Bilancio, A.; Farjot, G.; Priddle, H.; Sancho, S.; Peskett, E.; Pearce, W.; Meek, S. E.; Salpekar, A.; Water-

field, M. D.; Smith, A. J. H.; Vanhaesebroeck, B. : Impaired B and T cell antigen receptor signaling in p110-delta PI 3-kinase mutant mice. Science 297: 1031-1034, 2002. ; and

[82259] Vanhaesebroeck, B.; Welham, M. J.; Kotani, K.; Stein, R.; Warne, P. H.; Zvelebil, M. J.; Higashi, K.; Volinia, S.; Downward, J.; Waterfield, M. D. : p110-delta, a novel phosphoinositide 3-.

[82260] Further studies establishing the function and utilities of PIK3CD are found in John Hopkins OMIM database record ID 602839, and in sited publications numbered 1127-1130 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD, Accession NM_000302) is another VGAM2434 host target gene. PLOD BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PLOD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLOD BINDING SITE, designated SEQ ID:5845, to the nucleotide sequence of VGAM2434 RNA,

herein designated VGAM RNA, also designated SEQ ID:5145.

[82261] Another function of VGAM2434 is therefore inhibition of Procollagen-lysine, 2-oxoglutarate 5-dioxygenase (lysine hydroxylase, Ehlers-Danlos syndrome type VI) (PLOD, Accession NM_000302). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLOD. Prostaglandin E Synthase (PTGES, Accession NM_004878) is another VGAM2434 host target gene. PTGES BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTGES, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTGES BINDING SITE, designated SEQ ID:11313, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82262] Another function of VGAM2434 is therefore inhibition of Prostaglandin E Synthase (PTGES, Accession NM_004878). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGES. RNA Binding Motif Protein 8A

(RBM8A, Accession NM_005105) is another VGAM2434 host target gene. RBM8A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBM8A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBM8A BINDING SITE, designated SEQ ID:11582, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82263] Another function of VGAM2434 is therefore inhibition of RNA Binding Motif Protein 8A (RBM8A, Accession NM_005105), a gene which involves in the pathway of gene expression postsplicing nuclear preexport mRNPs, and newly exported cytoplasmic mRNPs. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBM8A. The function of RBM8A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1864.Rhesus Blood Group, D Antigen (RHD, Accession NM_016225) is another VGAM2434 host target gene. RHD BINDING SITE1 through RHD BIND-

ING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RHD, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RHD BINDING SITE1 through RHD BINDING SITE4, designated SEQ ID:18338, SEQ ID:18339, SEQ ID:18218 and SEQ ID:18219 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82264] Another function of VGAM2434 is therefore inhibition of Rhesus Blood Group, D Antigen (RHD, Accession NM_016225), a gene which Major antigen of the RH system. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RHD. The function of RHD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Spondyloepiphyseal Dysplasia, Late (SEDL, Accession NM_014563) is another VGAM2434 host target gene. SEDL BINDING SITE1 through SEDL BINDING SITE3 are HOST TARGET binding sites found in untranslated re-

gions of mRNA encoded by SEDL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEDL BINDING SITE1 through SEDL BINDING SITE3, designated SEQ ID:15911, SEQ ID:15912 and SEQ ID:15913 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82265] Another function of VGAM2434 is therefore inhibition of Spondyloepiphyseal Dysplasia, Late (SEDL, Accession NM_014563), a gene which may play role in vesicular transport from endoplasmic reticulum to golgi. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEDL. The function of SEDL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.SHC (Src homology 2 domain containing) Transforming Protein 1 (SHC1, Accession NM_003029) is another VGAM2434 host target gene. SHC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SHC1, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SHC1 BINDING SITE, designated SEQ ID:8969, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82266] Another function of VGAM2434 is therefore inhibition of SHC (Src homology 2 domain containing) Transforming Protein 1 (SHC1, Accession NM_003029), a gene which couples activated growth factor receptors to a signaling pathway. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHC1. The function of SHC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM53.TAL1 (SCL) Interrupting Locus (SIL, Accession NM_003035) is another VGAM2434 host target gene. SIL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIL BINDING SITE, designated SEQ ID:8984, to the nucleotide sequence of

VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82267] Another function of VGAM2434 is therefore inhibition of TAL1 (SCL) Interrupting Locus (SIL, Accession NM_003035), a gene which may be required for axial development and left-right specification. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIL. The function of SIL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1316.Solute Carrier Family 14 (urea transporter), Member 2 (SLC14A2, Accession NM_007163) is another VGAM2434 host target gene. SLC14A2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC14A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC14A2 BINDING SITE, designated SEQ ID:14012, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82268] Another function of VGAM2434 is therefore inhibition of

Solute Carrier Family 14 (urea transporter), Member 2 (SLC14A2, Accession NM_007163), a gene which is a renal urea transporter 2. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC14A2. The function of SLC14A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Solute Carrier Family 15 (oligopeptide transporter), Member 1 (SLC15A1, Accession NM_005073) is another VGAM2434 host target gene. SLC15A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC15A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC15A1 BINDING SITE, designated SEQ ID:11522, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82269] Another function of VGAM2434 is therefore inhibition of Solute Carrier Family 15 (oligopeptide transporter), Member 1 (SLC15A1, Accession NM_005073), a gene which is a H(+)-coupled peptide transporter. Accordingly, utilities of

VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC15A1. The function of SLC15A1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.SMAC (Accession NM_138930) is another VGAM2434 host target gene. SMAC BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SMAC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMAC BINDING SITE, designated SEQ ID:29049, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82270] Another function of VGAM2434 is therefore inhibition of SMAC (Accession NM_138930), a gene which promotes apoptosis via caspase activation. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMAC. The function of SMAC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference

to VGAM74.Sorting Nexin 15 (SNX15, Accession XM_057307) is another VGAM2434 host target gene. SNX15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SNX15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNX15 BINDING SITE, designated SEQ ID:36506, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82271] Another function of VGAM2434 is therefore inhibition of Sorting Nexin 15 (SNX15, Accession XM_057307). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNX15. Synovial Sarcoma Translocation, Chromosome 18 (SS18, Accession NM_005637) is another VGAM2434 host target gene. SS18 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SS18, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SS18 BINDING SITE,

designated SEQ ID:12165, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82272] Another function of VGAM2434 is therefore inhibition of Synovial Sarcoma Translocation, Chromosome 18 (SS18, Accession NM_005637), a gene which is a putative transcriptional activator. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SS18. The function of SS18 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Sulfotransferase Family, Cytosolic, 2B, Member 1 (SULT2B1, Accession NM_004605) is another VGAM2434 host target gene. SULT2B1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SULT2B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SULT2B1 BINDING SITE, designated SEQ ID:10949, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82273] Another function of VGAM2434 is therefore inhibition of Sulfotransferase Family, Cytosolic, 2B, Member 1 (SULT2B1, Accession NM_004605). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SULT2B1. TAP Binding Protein (tapasin) (TAPBP, Accession NM_003190) is another VGAM2434 host target gene. TAPBP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAPBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAPBP BINDING SITE, designated SEQ ID:9183, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82274] Another function of VGAM2434 is therefore inhibition of TAP Binding Protein (tapasin) (TAPBP, Accession NM_003190), a gene which is involved in MHC class I-restricted antigen processing. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAPBP. The function of TAPBP and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to VGAM122.Tyrosine Aminotransferase (TAT, Accession NM_000353) is another VGAM2434 host target gene. TAT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAT BINDING SITE, designated SEQ ID:5914, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82275] Another function of VGAM2434 is therefore inhibition of Tyrosine Aminotransferase (TAT, Accession NM_000353), a gene which is tyrosine aminotransferase and strongly similar to rat Rn.9947, which plays a role in gluconeogenesis. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAT. The function of TAT has been established by previous studies. Richner (1938) and Hanhart (1947) described an oculocutaneous syndrome characterized by herpetiform corneal ulcers and painful punctate keratoses of digits, palms, and soles. Richner (1938) described skin lesions in brother and sister. Only the

brother had corneal lesions. Hanhart (1947) reported that the parents of his patient were second cousins. Hanhart (1947) also described associated severe mental and somatic retardation. The pedigree he reported was reproduced by Waardenburg et al. (1961). Waardenburg et al. (1961) described children of a first-cousin marriage, one with the full syndrome and one with only corneal changes. Ventura et al. (1965) described the syndrome in 2 sons of first-cousin parents. Buist (1967) referred to studies of a child with tyrosinemia and tyrosine transaminase deficiency, but normal p-hydroxyphenylpyruvic acid oxidase. Phenylalanine level was normal. Hydroxyphenylpyruvic acid was elevated in the urine. Fellman et al. (1969) reported chemical studies on the same patient. Only the mitochondrial form of tyrosine aminotransferase (TAT) was present in the liver. The soluble form of TAT (EC 2.6.1.5) was lacking. The patient had markedly elevated tyrosine blood levels and an increase in urinary p-hydroxyphenylpyruvate and p-hydroxyphenyllactate. A regulator gene for tyrosine transaminase is X-linked (OMIM Ref. No. 314350). Goldsmith et al. (1973) demonstrated tyrosinemia and phenylaceticacidemia in this disorder. Their patient was the 14-year-old son of consan-

guineous Italian parents. The urine contained excessive P-hydroxyphenylactic acid. Urinary P-hydroxyphenylpyruvic acid was normal. Clinical and biochemical improvement accompanied low phenylalanine-low tyrosine diet. They suggested that soluble TAT may be deficient. Mitochondrial tyrosine transaminase is normal. Beinfang et al. (1976) described the ophthalmologic findings in the patient reported by Goldsmith et al. (1973). This condition is also known as tyrosinemia with palmar and plantar keratosis and keratitis. Garibaldi et al. (1977) observed this disorder, which they called oculocutaneous tyrosinosis, in a 42-month-old girl and her maternal aunt. The parents of the maternal aunt were first cousins. They emphasized the importance of early diagnosis in order to prevent mental retardation by means of a diet restricted in phenylalanine and tyrosine. Hunziker (1980) reported brother and sister with unusually late onset (about age 15). Their patients' skin lesions were improved with a diet restricted in phenylalanine and tyrosine. In a consanguineous sibship, Rehak et al. (1981) reported 4 cases of Richner-Hanhart syndrome. Cutaneous manifestations were typical but the eyes were not involved, suggesting heterogeneity in this disorder. Bohnert and Anton-Lamprecht (1982) re-

ported unique ultrastructural changes: thickening of the granular layer and increased synthesis of tonofibrils and keratohyalin; in the ridged palmar or plantar skin, large numbers of microtubules and unusually tight packing of tonofibrillar masses, which contained tubular channels or inclusions of microtubules. The authors assumed that increased cohesion and tight packing of tonofilaments prevent normal spreading of keratohyalin and result in its globular appearance. Further, they suggested that excessive amounts of intracellular tyrosine enhance crosslinks between aggregated tonofilaments. In an Ashkenazi Jewish family, Chitayat et al. (1992) observed 2 adult sibs, offspring of a first-cousin marriage, with persistent hypertyrosinemia. A curious feature was that the affected female sib, aged 41 years, had hypertyrosinemia and characteristic oculocutaneous signs; the brother, aged 39 years, had hypertyrosinemia but no oculocutaneous disease. Both sibs had 2 children; none had signs of metabolic fetopathy.

[82276] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[82277] Goldsmith, L. A.; Kang, E. S.; Bienfang, D. C.; Jimbow, K.;

Gerald, P. S.; Baden, H. P. : Tyrosinemia with plantar and palmar keratosis and keratitis. J. Pediat. 83: 798-805, 1973. ; and

[82278] Hunziker, N. : Richner-Hanhart syndrome and tyrosinemia type II. Dermatologica 160: 180-189, 1980.

[82279] Further studies establishing the function and utilities of TAT are found in John Hopkins OMIM database record ID 276600, and in sited publications numbered 8715-8728, 908 and 9088-9097 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Thromboxane A2 Receptor (TBXA2R, Accession NM_001060) is another VGAM2434 host target gene. TBXA2R BINDING SITE1 and TBXA2R BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TBXA2R, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBXA2R BINDING SITE1 and TBXA2R BINDING SITE2, designated SEQ ID:6729 and SEQ ID:6730 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82280] Another function of VGAM2434 is therefore inhibition of

Thromboxane A2 Receptor (TBXA2R, Accession NM_001060), a gene which activates Ca2+-activated chloride channels; stimulates platelet aggregation and smooth muscle constriction. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBXA2R. The function of TBXA2R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Tumor Necrosis Factor Receptor Superfamily, Member 10b (TNFRSF10B, Accession NM_003842) is another VGAM2434 host target gene. TNFRSF10B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFRSF10B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFRSF10B BINDING SITE, designated SEQ ID:9940, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82281] Another function of VGAM2434 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 10b

(TNFRSF10B, Accession NM_003842), a gene which forms complex that induces apoptosis. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF10B. The function of TNFRSF10B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM400.Tumor Necrosis Factor Receptor Superfamily, Member 9 (TNFRSF9, Accession NM_001561) is another VGAM2434 host target gene. TNFRSF9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNFRSF9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNFRSF9 BINDING SITE, designated SEQ ID:7289, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82282] Another function of VGAM2434 is therefore inhibition of Tumor Necrosis Factor Receptor Superfamily, Member 9 (TNFRSF9, Accession NM_001561), a gene which inhibits proliferation of activated T lymphocytes. Accordingly, util-

ities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNFRSF9. The function of TNFRSF9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1954.Tripartite Motif-containing 9 (TRIM9, Accession NM_015163) is another VGAM2434 host target gene. TRIM9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TRIM9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM9 BINDING SITE, designated SEQ ID:17519, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82283] Another function of VGAM2434 is therefore inhibition of Tripartite Motif-containing 9 (TRIM9, Accession NM_015163), a gene which may function as a positive regulator for mannosylphosphate transferase and is required to mediate mannosylphosphate transfer in both the core and outer chain portions of n-linked. oligosaccharides. Accordingly, utilities of VGAM2434 include diagno-

sis, prevention and treatment of diseases and clinical conditions associated with TRIM9. The function of TRIM9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Transient Receptor Potential Cation Channel, Subfamily V, Member 1 (TRPV1, Accession NM_018727) is another VGAM2434 host target gene. TRPV1 BINDING SITE1 through TRPV1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TRPV1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRPV1 BINDING SITE1 through TRPV1 BINDING SITE4, designated SEQ ID:20814, SEQ ID:27994, SEQ ID:28002 and SEQ ID:28010 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82284] Another function of VGAM2434 is therefore inhibition of Transient Receptor Potential Cation Channel, Subfamily V, Member 1 (TRPV1, Accession NM_018727), a gene which functions as a receptor for capsaicin. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with TRPV1. The function of TRPV1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM146.X-ray Repair Complementing Defective Repair In Chinese Hamster Cells 2 (XRCC2, Accession NM_005431) is another VGAM2434 host target gene. XRCC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by XRCC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XRCC2 BINDING SITE, designated SEQ ID:11901, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82285] Another function of VGAM2434 is therefore inhibition of X-ray Repair Complementing Defective Repair In Chinese Hamster Cells 2 (XRCC2, Accession NM_005431), a gene which involves in the homologous recombination repair (hrr) pathway of double-stranded dna. Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with XRCC2. The function of XRCC2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM241.Zinc Finger Protein 22 (KOX 15) (ZNF22, Accession XM_166153) is another VGAM2434 host target gene. ZNF22 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF22, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF22 BINDING SITE, designated SEQ ID:43971, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82286] Another function of VGAM2434 is therefore inhibition of Zinc Finger Protein 22 (KOX 15) (ZNF22, Accession XM_166153). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF22. Zinc Finger Protein 264 (ZNF264, Accession NM_003417) is another VGAM2434 host target gene. ZNF264 BINDING SITE1 and ZNF264 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by

ZNF264, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF264 BINDING SITE1 and ZNF264 BINDING SITE2, designated SEQ ID:9455 and SEQ ID:9460 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82287] Another function of VGAM2434 is therefore inhibition of Zinc Finger Protein 264 (ZNF264, Accession NM_003417). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF264. Ankyrin Repeat and SOCS Box-containing 16 (ASB16, Accession XM_046024) is another VGAM2434 host target gene. ASB16 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ASB16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ASB16 BINDING SITE, designated SEQ ID:34655, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82288] Another function of VGAM2434 is therefore inhibition of Ankyrin Repeat and SOCS Box-containing 16 (ASB16, Accession XM_046024). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB16. BA108L7.2 (Accession NM_030971) is another VGAM2434 host target gene. BA108L7.2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BA108L7.2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BA108L7.2 BINDING SITE, designated SEQ ID:25237, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82289] Another function of VGAM2434 is therefore inhibition of BA108L7.2 (Accession NM_030971). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BA108L7.2. BCL2-associated Athanogene 5 (BAG5, Accession NM_004873) is another VGAM2434 host target gene. BAG5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BAG5,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAG5 BINDING SITE, designated SEQ ID:11309, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82290] Another function of VGAM2434 is therefore inhibition of BCL2-associated Athanogene 5 (BAG5, Accession NM_004873). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAG5. Butyrophilin, Subfamily 3, Member A1 (BTN3A1, Accession NM_007048) is another VGAM2434 host target gene. BTN3A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTN3A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTN3A1 BINDING SITE, designated SEQ ID:13921, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82291] Another function of VGAM2434 is therefore inhibition of Butyrophilin, Subfamily 3, Member A1 (BTN3A1, Accession

NM_007048). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTN3A1. C1q and Tumor Necrosis Factor Related Protein 6 (C1QTNF6, Accession NM_031910) is another VGAM2434 host target gene. C1QTNF6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1QTNF6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1QTNF6 BINDING SITE, designated SEQ ID:25656, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82292] Another function of VGAM2434 is therefore inhibition of C1q and Tumor Necrosis Factor Related Protein 6 (C1QTNF6, Accession NM_031910). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QTNF6. C3F (Accession NM_005768) is another VGAM2434 host target gene. C3F BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C3F, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C3F BINDING SITE, designated SEQ ID:12331, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82293] Another function of VGAM2434 is therefore inhibition of C3F (Accession NM_005768). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C3F. C6orf5 (Accession NM_015524) is another VGAM2434 host target gene. C6orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C6orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C6orf5 BINDING SITE, designated SEQ ID:17780, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82294] Another function of VGAM2434 is therefore inhibition of C6orf5 (Accession NM_015524). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with C6orf5. Chromosome 9 Open Reading Frame 9 (C9orf9, Accession NM_018956) is another VGAM2434 host target gene. C9orf9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C9orf9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C9orf9 BINDING SITE, designated SEQ ID:21029, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82295] Another function of VGAM2434 is therefore inhibition of Chromosome 9 Open Reading Frame 9 (C9orf9, Accession NM_018956). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C9orf9. CDC14 Cell Division Cycle 14 Homolog B (S. cerevisiae) (CDC14B, Accession NM_033332) is another VGAM2434 host target gene. CDC14B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDC14B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of CDC14B BINDING SITE, designated SEQ ID:27174, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82296] Another function of VGAM2434 is therefore inhibition of CDC14 Cell Division Cycle 14 Homolog B (S. cerevisiae) (CDC14B, Accession NM_033332). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDC14B. Cat Eye Syndrome Chromosome Region, Candidate 1 (CECR1, Accession NM_017424) is another VGAM2434 host target gene. CECR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CECR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CECR1 BINDING SITE, designated SEQ ID:18884, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82297] Another function of VGAM2434 is therefore inhibition of Cat Eye Syndrome Chromosome Region, Candidate 1

(CECR1, Accession NM_017424). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR1. Chromatin Accessibility Complex 1 (CHRAC1, Accession NM_017444) is another VGAM2434 host target gene. CHRAC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHRAC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHRAC1 BINDING SITE, designated SEQ ID:18908, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82298] Another function of VGAM2434 is therefore inhibition of Chromatin Accessibility Complex 1 (CHRAC1, Accession NM_017444). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRAC1. CIP29 (Accession NM_032364) is another VGAM2434 host target gene. CIP29 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CIP29, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CIP29 BINDING SITE, designated SEQ ID:26148, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82299] Another function of VGAM2434 is therefore inhibition of CIP29 (Accession NM_032364). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIP29. Cleavage and Polyadenylation Specific Factor 2, 100kDa (CPSF2, Accession XM_029311) is another VGAM2434 host target gene. CPSF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CPSF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPSF2 BINDING SITE, designated SEQ ID:30862, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82300] Another function of VGAM2434 is therefore inhibition of Cleavage and Polyadenylation Specific Factor 2, 100kDa (CPSF2, Accession XM_029311). Accordingly, utilities of

VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPSF2. Cylicin, Basic Protein of Sperm Head Cytoskeleton 2 (CYLC2, Accession NM_001340) is another VGAM2434 host target gene. CYLC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYLC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYLC2 BINDING SITE, designated SEQ ID:7020, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82301] Another function of VGAM2434 is therefore inhibition of Cylicin, Basic Protein of Sperm Head Cytoskeleton 2 (CYLC2, Accession NM_001340). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYLC2. DKFZP434D146 (Accession NM_015595) is another VGAM2434 host target gene. DKFZP434D146 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434D146, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434D146 BINDING SITE, designated SEQ ID:17871, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82302] Another function of VGAM2434 is therefore inhibition of DKFZP434D146 (Accession NM_015595). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434D146. DKFZp434E2220 (Accession NM_017612) is another VGAM2434 host target gene. DKFZp434E2220 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp434E2220, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434E2220 BINDING SITE, designated SEQ ID:19111, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82303] Another function of VGAM2434 is therefore inhibition of DKFZp434E2220 (Accession NM_017612). Accordingly,

utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434E2220. DKFZP434F0318 (Accession NM_030817) is another VGAM2434 host target gene. DKFZP434F0318 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434F0318, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434F0318 BINDING SITE, designated SEQ ID:25143, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82304] Another function of VGAM2434 is therefore inhibition of DKFZP434F0318 (Accession NM_030817). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434F0318. DKFZP434J037 (Accession NM_030952) is another VGAM2434 host target gene. DKFZP434J037 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434J037, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING

SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434J037 BINDING SITE, designated SEQ ID:25220, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82305] Another function of VGAM2434 is therefore inhibition of DKFZP434J037 (Accession NM_030952). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434J037. DKFZp547H025 (Accession NM_020161) is another VGAM2434 host target gene. DKFZp547H025 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp547H025, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547H025 BINDING SITE, designated SEQ ID:21375, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82306] Another function of VGAM2434 is therefore inhibition of DKFZp547H025 (Accession NM_020161). Accordingly, utilities of VGAM2434 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZp547H025. DKFZP564O0523 (Accession NM_032120) is another VGAM2434 host target gene. DKFZP564O0523 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564O0523, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564O0523 BINDING SITE, designated SEQ ID:25805, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82307] Another function of VGAM2434 is therefore inhibition of DKFZP564O0523 (Accession NM_032120). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564O0523. DKFZp762L0311 (Accession NM_018719) is another VGAM2434 host target gene. DKFZp762L0311 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp762L0311, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the

nucleotide sequences of DKFZp762L0311 BINDING SITE, designated SEQ ID:20799, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82308] Another function of VGAM2434 is therefore inhibition of DKFZp762L0311 (Accession NM_018719). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762L0311. Ecotropic Viral Integration Site 5 (EVI5, Accession NM_005665) is another VGAM2434 host target gene. EVI5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EVI5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EVI5 BINDING SITE, designated SEQ ID:12215, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82309] Another function of VGAM2434 is therefore inhibition of Ecotropic Viral Integration Site 5 (EVI5, Accession NM_005665). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with EVI5. Fer-1-like 4 (C. elegans) (FER1L4, Accession NM_025206) is another VGAM2434 host target gene. FER1L4 BINDING SITE1 and FER1L4 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FER1L4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FER1L4 BINDING SITE1 and FER1L4 BINDING SITE2, designated SEQ ID:24875 and SEQ ID:24876 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82310] Another function of VGAM2434 is therefore inhibition of Fer-1-like 4 (C. elegans) (FER1L4, Accession NM_025206). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FER1L4. FLJ10232 (Accession NM_018033) is another VGAM2434 host target gene. FLJ10232 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10232, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10232 BINDING SITE, designated SEQ ID:19774, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82311] Another function of VGAM2434 is therefore inhibition of FLJ10232 (Accession NM_018033). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10232. FLJ10298 (Accession NM_018050) is another VGAM2434 host target gene. FLJ10298 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10298, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10298 BINDING SITE, designated SEQ ID:19809, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82312] Another function of VGAM2434 is therefore inhibition of FLJ10298 (Accession NM_018050). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ10298. FLJ10535 (Accession NM_018129) is another VGAM2434 host target gene. FLJ10535 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10535, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10535 BINDING SITE, designated SEQ ID:19917, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82313] Another function of VGAM2434 is therefore inhibition of FLJ10535 (Accession NM_018129). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10535. FLJ10713 (Accession NM_018189) is another VGAM2434 host target gene. FLJ10713 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10713, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10713 BINDING SITE, designated SEQ ID:20043, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM

RNA, also designated SEQ ID:5145.

[82314] Another function of VGAM2434 is therefore inhibition of FLJ10713 (Accession NM_018189). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10713. FLJ10901 (Accession NM_018265) is another VGAM2434 host target gene. FLJ10901 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10901, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10901 BINDING SITE, designated SEQ ID:20229, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82315] Another function of VGAM2434 is therefore inhibition of FLJ10901 (Accession NM_018265). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10901. FLJ11004 (Accession NM_018296) is another VGAM2434 host target gene. FLJ11004 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ11004, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11004 BINDING SITE, designated SEQ ID:20289, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82316] Another function of VGAM2434 is therefore inhibition of FLJ11004 (Accession NM_018296). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11004. FLJ11710 (Accession NM_024846) is another VGAM2434 host target gene. FLJ11710 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11710, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11710 BINDING SITE, designated SEQ ID:24275, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82317] Another function of VGAM2434 is therefore inhibition of FLJ11710 (Accession NM_024846). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ11710. FLJ12572 (Accession NM_022905) is another VGAM2434 host target gene. FLJ12572 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12572, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12572 BINDING SITE, designated SEQ ID:23197, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82318] Another function of VGAM2434 is therefore inhibition of FLJ12572 (Accession NM_022905). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12572. FLJ12586 (Accession NM_024620) is another VGAM2434 host target gene. FLJ12586 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12586, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12586 BINDING SITE, designated SEQ ID:23883, to the nucleotide

sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82319] Another function of VGAM2434 is therefore inhibition of FLJ12586 (Accession NM_024620). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12586. FLJ12687 (Accession NM_024917) is another VGAM2434 host target gene. FLJ12687 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12687, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12687 BINDING SITE, designated SEQ ID:24447, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82320] Another function of VGAM2434 is therefore inhibition of FLJ12687 (Accession NM_024917). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12687. FLJ12903 (Accession NM_022753) is another VGAM2434 host target gene. FLJ12903 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ12903, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12903 BINDING SITE, designated SEQ ID:22983, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82321] Another function of VGAM2434 is therefore inhibition of FLJ12903 (Accession NM_022753). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12903. FLJ12973 (Accession NM_024908) is another VGAM2434 host target gene. FLJ12973 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12973, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12973 BINDING SITE, designated SEQ ID:24408, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82322] Another function of VGAM2434 is therefore inhibition of FLJ12973 (Accession NM_024908). Accordingly, utilities of

VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12973. FLJ13193 (Accession NM_032177) is another VGAM2434 host target gene. FLJ13193 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13193, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13193 BINDING SITE, designated SEQ ID:25891, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82323] Another function of VGAM2434 is therefore inhibition of FLJ13193 (Accession NM_032177). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13193. FLJ14950 (Accession NM_032865) is another VGAM2434 host target gene. FLJ14950 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14950, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14950

BINDING SITE, designated SEQ ID:26675, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82324] Another function of VGAM2434 is therefore inhibition of FLJ14950 (Accession NM_032865). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14950. FLJ20034 (Accession NM_017630) is another VGAM2434 host target gene. FLJ20034 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20034, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20034 BINDING SITE, designated SEQ ID:19132, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82325] Another function of VGAM2434 is therefore inhibition of FLJ20034 (Accession NM_017630). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20034. FLJ20136 (Accession NM_017684) is another VGAM2434 host target gene. FLJ20136 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20136, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20136 BINDING SITE, designated SEQ ID:19232, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82326] Another function of VGAM2434 is therefore inhibition of FLJ20136 (Accession NM_017684). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20136. FLJ20342 (Accession NM_017774) is another VGAM2434 host target gene. FLJ20342 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20342, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20342 BINDING SITE, designated SEQ ID:19398, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82327] Another function of VGAM2434 is therefore inhibition of

FLJ20342 (Accession NM_017774). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20342. FLJ20344 (Accession NM_017776) is another VGAM2434 host target gene. FLJ20344 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20344, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20344 BINDING SITE, designated SEQ ID:19405, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82328] Another function of VGAM2434 is therefore inhibition of FLJ20344 (Accession NM_017776). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20344. FLJ20507 (Accession NM_017849) is another VGAM2434 host target gene. FLJ20507 BINDING SITE1 and FLJ20507 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ20507, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20507 BINDING SITE1 and FLJ20507 BINDING SITE2, designated SEQ ID:19510 and SEQ ID:30218 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82329] Another function of VGAM2434 is therefore inhibition of FLJ20507 (Accession NM_017849). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20507. FLJ22002 (Accession NM_024838) is another VGAM2434 host target gene. FLJ22002 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22002, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22002 BINDING SITE, designated SEQ ID:24249, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82330] Another function of VGAM2434 is therefore inhibition of FLJ22002 (Accession NM_024838). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ22002. FLJ22531 (Accession NM_024650) is another VGAM2434 host target gene. FLJ22531 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22531, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22531 BINDING SITE, designated SEQ ID:23946, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82331] Another function of VGAM2434 is therefore inhibition of FLJ22531 (Accession NM_024650). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22531. FLJ22794 (Accession XM_166220) is another VGAM2434 host target gene. FLJ22794 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22794 BINDING SITE, designated SEQ ID:44037, to the nucleotide

sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82332] Another function of VGAM2434 is therefore inhibition of FLJ22794 (Accession XM_166220). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22794. FLJ23024 (Accession NM_024936) is another VGAM2434 host target gene. FLJ23024 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23024, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23024 BINDING SITE, designated SEQ ID:24472, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82333] Another function of VGAM2434 is therefore inhibition of FLJ23024 (Accession NM_024936). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23024. FLJ23356 (Accession NM_032237) is another VGAM2434 host target gene. FLJ23356 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ23356, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23356 BINDING SITE, designated SEQ ID:25958, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82334] Another function of VGAM2434 is therefore inhibition of FLJ23356 (Accession NM_032237). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23356. FLJ23392 (Accession NM_024784) is another VGAM2434 host target gene. FLJ23392 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23392, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23392 BINDING SITE, designated SEQ ID:24160, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82335] Another function of VGAM2434 is therefore inhibition of FLJ23392 (Accession NM_024784). Accordingly, utilities of

VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23392. FLJ23563 (Accession XM_041701) is another VGAM2434 host target gene. FLJ23563 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23563, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23563 BINDING SITE, designated SEQ ID:33562, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82336] Another function of VGAM2434 is therefore inhibition of FLJ23563 (Accession XM_041701). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23563. FLJ25416 (Accession NM_145018) is another VGAM2434 host target gene. FLJ25416 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ25416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ25416

BINDING SITE, designated SEQ ID:29627, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82337] Another function of VGAM2434 is therefore inhibition of FLJ25416 (Accession NM_145018). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ25416. FLJ30532 (Accession NM_144724) is another VGAM2434 host target gene. FLJ30532 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ30532, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ30532 BINDING SITE, designated SEQ ID:29549, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82338] Another function of VGAM2434 is therefore inhibition of FLJ30532 (Accession NM_144724). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ30532. FLJ32865 (Accession NM_144613) is another VGAM2434 host target gene. FLJ32865 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ32865, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32865 BINDING SITE, designated SEQ ID:29426, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82339] Another function of VGAM2434 is therefore inhibition of FLJ32865 (Accession NM_144613). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32865. GAL3ST-4 (Accession NM_024637) is another VGAM2434 host target gene. GAL3ST-4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GAL3ST-4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAL3ST-4 BINDING SITE, designated SEQ ID:23910, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82340] Another function of VGAM2434 is therefore inhibition of

GAL3ST-4 (Accession NM_024637). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GAL3ST-4. GMPPB (Accession XM_171044) is another VGAM2434 host target gene. GMPPB BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GMPPB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GMPPB BINDING SITE, designated SEQ ID:45819, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82341] Another function of VGAM2434 is therefore inhibition of GMPPB (Accession XM_171044). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GMPPB. Guanine Nucleotide Binding Protein (G protein), Gamma 4 (GNG4, Accession NM_004485) is another VGAM2434 host target gene. GNG4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNG4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of GNG4 BINDING SITE, designated SEQ ID:10813, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82342] Another function of VGAM2434 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Gamma 4 (GNG4, Accession NM_004485). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNG4. Glycoprotein V (platelet) (GP5, Accession NM_004488) is another VGAM2434 host target gene. GP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GP5 BINDING SITE, designated SEQ ID:10819, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82343] Another function of VGAM2434 is therefore inhibition of Glycoprotein V (platelet) (GP5, Accession NM_004488). Accordingly, utilities of VGAM2434 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with GP5. GREB1 (Accession NM_014668) is another VGAM2434 host target gene. GREB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GREB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GREB1 BINDING SITE, designated SEQ ID:16124, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82344] Another function of VGAM2434 is therefore inhibition of GREB1 (Accession NM_014668). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GREB1. General Transcription Factor IIE, Polypeptide 1, Alpha 56kDa (GTF2E1, Accession NM_005513) is another VGAM2434 host target gene. GTF2E1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GTF2E1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTF2E1

BINDING SITE, designated SEQ ID:12036, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82345] Another function of VGAM2434 is therefore inhibition of General Transcription Factor IIE, Polypeptide 1, Alpha 56kDa (GTF2E1, Accession NM_005513). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2E1. GTPBG3 (Accession NM_032620) is another VGAM2434 host target gene. GTPBG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GTPBG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTPBG3 BINDING SITE, designated SEQ ID:26335, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82346] Another function of VGAM2434 is therefore inhibition of GTPBG3 (Accession NM_032620). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTPBG3. H-plk (Accession NM_015852) is another

VGAM2434 host target gene. H-plk BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by H-plk, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of H-plk BINDING SITE, designated SEQ ID:17986, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82347] Another function of VGAM2434 is therefore inhibition of H-plk (Accession NM_015852). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with H-plk. Histamine Receptor H4 (HRH4, Accession NM_021624) is another VGAM2434 host target gene. HRH4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HRH4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRH4 BINDING SITE, designated SEQ ID:22258, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82348] Another function of VGAM2434 is therefore inhibition of Histamine Receptor H4 (HRH4, Accession NM_021624). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRH4. ICK (Accession NM_014920) is another VGAM2434 host target gene. ICK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ICK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ICK BINDING SITE, designated SEQ ID:17196, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82349] Another function of VGAM2434 is therefore inhibition of ICK (Accession NM_014920). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ICK. Junctional Adhesion Molecule 1 (JAM1, Accession NM_144502) is another VGAM2434 host target gene. JAM1 BINDING SITE1 through JAM1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by JAM1, corresponding to HOST TAR-

GET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JAM1 BINDING SITE1 through JAM1 BINDING SITE4, designated SEQ ID:29331, SEQ ID:29342, SEQ ID:29352 and SEQ ID:18864 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82350] Another function of VGAM2434 is therefore inhibition of Junctional Adhesion Molecule 1 (JAM1, Accession NM_144502). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JAM1. KIAA0391 (Accession NM_014672) is another VGAM2434 host target gene. KIAA0391 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0391, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0391 BINDING SITE, designated SEQ ID:16136, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82351] Another function of VGAM2434 is therefore inhibition of KIAA0391 (Accession NM_014672). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0391. KIAA0426 (Accession NM_014724) is another VGAM2434 host target gene. KIAA0426 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0426, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0426 BINDING SITE, designated SEQ ID:16312, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82352] Another function of VGAM2434 is therefore inhibition of KIAA0426 (Accession NM_014724). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0426. KIAA0459 (Accession XM_027862) is another VGAM2434 host target gene. KIAA0459 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0459, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0459 BINDING SITE, designated SEQ ID:30578, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82353] Another function of VGAM2434 is therefore inhibition of KIAA0459 (Accession XM_027862). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0459. KIAA0475 (Accession NM_014864) is another VGAM2434 host target gene. KIAA0475 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0475, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:16951, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82354] Another function of VGAM2434 is therefore inhibition of KIAA0475 (Accession NM_014864). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0475. KIAA0495 (Accession XM_031397) is another VGAM2434 host target gene. KIAA0495 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0495, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0495 BINDING SITE, designated SEQ ID:31364, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82355] Another function of VGAM2434 is therefore inhibition of KIAA0495 (Accession XM_031397). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0495. KIAA0513 (Accession NM_014732) is another VGAM2434 host target gene. KIAA0513 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0513, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0513 BINDING SITE, designated SEQ ID:16361, to the nucleotide sequence of VGAM2434 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5145.

[82356] Another function of VGAM2434 is therefore inhibition of KIAA0513 (Accession NM_014732). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0513. KIAA0544 (Accession XM_048119) is another VGAM2434 host target gene. KIAA0544 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0544, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0544 BINDING SITE, designated SEQ ID:35117, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82357] Another function of VGAM2434 is therefore inhibition of KIAA0544 (Accession XM_048119). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0544. KIAA0557 (Accession XM_085507) is another VGAM2434 host target gene. KIAA0557 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0557, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0557 BINDING SITE, designated SEQ ID:38212, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82358] Another function of VGAM2434 is therefore inhibition of KIAA0557 (Accession XM_085507). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0557. KIAA0563 (Accession NM_014834) is another VGAM2434 host target gene. KIAA0563 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0563, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0563 BINDING SITE, designated SEQ ID:16841, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82359] Another function of VGAM2434 is therefore inhibition of KIAA0563 (Accession NM_014834). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0563. KIAA0594 (Accession XM_036117) is another VGAM2434 host target gene. KIAA0594 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0594, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0594 BINDING SITE, designated SEQ ID:32390, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82360] Another function of VGAM2434 is therefore inhibition of KIAA0594 (Accession XM_036117). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0594. KIAA0599 (Accession XM_085127) is another VGAM2434 host target gene. KIAA0599 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0599, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0599 BINDING SITE, designated SEQ ID:37859, to the

nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82361] Another function of VGAM2434 is therefore inhibition of KIAA0599 (Accession XM_085127). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0599. KIAA0650 (Accession XM_113962) is another VGAM2434 host target gene. KIAA0650 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0650, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0650 BINDING SITE, designated SEQ ID:42571, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82362] Another function of VGAM2434 is therefore inhibition of KIAA0650 (Accession XM_113962). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0650. KIAA0663 (Accession NM_014827) is another VGAM2434 host target gene. KIAA0663 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by KIAA0663, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0663 BINDING SITE, designated SEQ ID:16814, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82363] Another function of VGAM2434 is therefore inhibition of KIAA0663 (Accession NM_014827). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0663. KIAA0676 (Accession NM_015043) is another VGAM2434 host target gene. KIAA0676 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0676, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0676 BINDING SITE, designated SEQ ID:17395, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82364] Another function of VGAM2434 is therefore inhibition of KIAA0676 (Accession NM_015043). Accordingly, utilities

of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0676. KIAA0720 (Accession XM_030970) is another VGAM2434 host target gene. KIAA0720 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0720, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0720 BINDING SITE, designated SEQ ID:31232, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82365] Another function of VGAM2434 is therefore inhibition of KIAA0720 (Accession XM_030970). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0720. KIAA0841 (Accession XM_049237) is another VGAM2434 host target gene. KIAA0841 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0841 BINDING SITE, designated SEQ ID:35363, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82366] Another function of VGAM2434 is therefore inhibition of KIAA0841 (Accession XM_049237). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0841. KIAA0889 (Accession NM_015377) is another VGAM2434 host target gene. KIAA0889 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0889, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0889 BINDING SITE, designated SEQ ID:17680, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82367] Another function of VGAM2434 is therefore inhibition of KIAA0889 (Accession NM_015377). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0889. KIAA0924 (Accession NM_014897) is another VGAM2434 host target gene. KIAA0924 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0924, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0924 BINDING SITE, designated SEQ ID:17067, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82368] Another function of VGAM2434 is therefore inhibition of KIAA0924 (Accession NM_014897). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0924. KIAA1028 (Accession XM_166324) is another VGAM2434 host target gene. KIAA1028 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1028, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1028 BINDING SITE, designated SEQ ID:44164, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82369] Another function of VGAM2434 is therefore inhibition of

KIAA1028 (Accession XM_166324). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1028. KIAA1041 (Accession NM_014947) is another VGAM2434 host target gene. KIAA1041 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1041, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1041 BINDING SITE, designated SEQ ID:17266, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82370] Another function of VGAM2434 is therefore inhibition of KIAA1041 (Accession NM_014947). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1041. KIAA1054 (Accession XM_043493) is another VGAM2434 host target gene. KIAA1054 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA1054 BINDING SITE, designated SEQ ID:33957, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82371] Another function of VGAM2434 is therefore inhibition of KIAA1054 (Accession XM_043493). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1054. KIAA1165 (Accession XM_041162) is another VGAM2434 host target gene. KIAA1165 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1165, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1165 BINDING SITE, designated SEQ ID:33478, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82372] Another function of VGAM2434 is therefore inhibition of KIAA1165 (Accession XM_041162). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1165. KIAA1170 (Accession XM_045907) is another

VGAM2434 host target gene. KIAA1170 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1170, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1170 BINDING SITE, designated SEQ ID:34613, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82373] Another function of VGAM2434 is therefore inhibition of KIAA1170 (Accession XM_045907). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1170. KIAA1185 (Accession XM_031399) is another VGAM2434 host target gene. KIAA1185 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1185, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1185 BINDING SITE, designated SEQ ID:31369, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82374] Another function of VGAM2434 is therefore inhibition of KIAA1185 (Accession XM_031399). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1185. KIAA1198 (Accession XM_032674) is another VGAM2434 host target gene. KIAA1198 BINDING SITE1 and KIAA1198 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1198, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1198 BINDING SITE1 and KIAA1198 BINDING SITE2, designated SEQ ID:31716 and SEQ ID:31718 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82375] Another function of VGAM2434 is therefore inhibition of KIAA1198 (Accession XM_032674). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1198. KIAA1320 (Accession XM_045095) is another VGAM2434 host target gene. KIAA1320 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by KIAA1320, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1320 BINDING SITE, designated SEQ ID:34356, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82376] Another function of VGAM2434 is therefore inhibition of KIAA1320 (Accession XM_045095). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1320. KIAA1373 (Accession XM_048195) is another VGAM2434 host target gene. KIAA1373 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1373, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1373 BINDING SITE, designated SEQ ID:35128, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82377] Another function of VGAM2434 is therefore inhibition of KIAA1373 (Accession XM_048195). Accordingly, utilities

of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1373. KIAA1467 (Accession XM_049605) is another VGAM2434 host target gene. KIAA1467 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1467, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1467 BINDING SITE, designated SEQ ID:35454, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82378] Another function of VGAM2434 is therefore inhibition of KIAA1467 (Accession XM_049605). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1467. KIAA1497 (Accession XM_041431) is another VGAM2434 host target gene. KIAA1497 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1497, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1497 BINDING SITE, designated SEQ ID:33527, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82379] Another function of VGAM2434 is therefore inhibition of KIAA1497 (Accession XM_041431). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1497. KIAA1571 (Accession XM_027744) is another VGAM2434 host target gene. KIAA1571 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1571, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1571 BINDING SITE, designated SEQ ID:30566, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82380] Another function of VGAM2434 is therefore inhibition of KIAA1571 (Accession XM_027744). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1571. KIAA1615 (Accession XM_044021) is another VGAM2434 host target gene. KIAA1615 BINDING SITE1

and KIAA1615 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1615, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1615 BINDING SITE1 and KIAA1615 BINDING SITE2, designated SEQ ID:34082 and SEQ ID:34088 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82381] Another function of VGAM2434 is therefore inhibition of KIAA1615 (Accession XM_044021). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1615. KIAA1737 (Accession XM_041115) is another VGAM2434 host target gene. KIAA1737 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1737, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1737 BINDING SITE, designated SEQ ID:33448, to the nucleotide sequence of VGAM2434 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5145.

[82382] Another function of VGAM2434 is therefore inhibition of KIAA1737 (Accession XM_041115). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1737. KIAA1784 (Accession XM_036660) is another VGAM2434 host target gene. KIAA1784 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1784, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1784 BINDING SITE, designated SEQ ID:32486, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82383] Another function of VGAM2434 is therefore inhibition of KIAA1784 (Accession XM_036660). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1784. KIAA1829 (Accession XM_030378) is another VGAM2434 host target gene. KIAA1829 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1829, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1829 BINDING SITE, designated SEQ ID:31031, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82384] Another function of VGAM2434 is therefore inhibition of KIAA1829 (Accession XM_030378). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1829. KIAA1854 (Accession XM_049884) is another VGAM2434 host target gene. KIAA1854 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1854, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1854 BINDING SITE, designated SEQ ID:35537, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82385] Another function of VGAM2434 is therefore inhibition of KIAA1854 (Accession XM_049884). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1854. KIAA1922 (Accession XM_057040) is another VGAM2434 host target gene. KIAA1922 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1922, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1922 BINDING SITE, designated SEQ ID:36460, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82386] Another function of VGAM2434 is therefore inhibition of KIAA1922 (Accession XM_057040). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1922. KIAA1971 (Accession XM_058720) is another VGAM2434 host target gene. KIAA1971 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1971, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1971 BINDING SITE, designated SEQ ID:36731, to the

nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82387] Another function of VGAM2434 is therefore inhibition of KIAA1971 (Accession XM_058720). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1971. KIAA1987 (Accession XM_113870) is another VGAM2434 host target gene. KIAA1987 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1987, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1987 BINDING SITE, designated SEQ ID:42500, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82388] Another function of VGAM2434 is therefore inhibition of KIAA1987 (Accession XM_113870). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1987. Kallikrein 7 (chymotryptic, stratum corneum) (KLK7, Accession NM_139277) is another VGAM2434 host target gene. KLK7 BINDING SITE1 and KLK7 BINDING SITE2

are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KLK7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLK7 BINDING SITE1 and KLK7 BINDING SITE2, designated SEQ ID:29274 and SEQ ID:11477 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82389] Another function of VGAM2434 is therefore inhibition of Kallikrein 7 (chymotryptic, stratum corneum) (KLK7, Accession NM_139277). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLK7. LIECG3 (Accession XM_113371) is another VGAM2434 host target gene. LIECG3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LIECG3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIECG3 BINDING SITE, designated SEQ ID:42248, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ

ID:5145.

[82390] Another function of VGAM2434 is therefore inhibition of LIECG3 (Accession XM_113371). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIECG3. Lymphocyte Antigen 75 (LY75, Accession NM_002349) is another VGAM2434 host target gene. LY75 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LY75, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LY75 BINDING SITE, designated SEQ ID:8151, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82391] Another function of VGAM2434 is therefore inhibition of Lymphocyte Antigen 75 (LY75, Accession NM_002349). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LY75. MCLC (Accession NM_015127) is another VGAM2434 host target gene. MCLC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MCLC, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MCLC BINDING SITE, designated SEQ ID:17493, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82392] Another function of VGAM2434 is therefore inhibition of MCLC (Accession NM_015127). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCLC. MGC1842 (Accession XM_037797) is another VGAM2434 host target gene. MGC1842 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC1842, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC1842 BINDING SITE, designated SEQ ID:32689, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82393] Another function of VGAM2434 is therefore inhibition of MGC1842 (Accession XM_037797). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC1842. MGC4638 (Accession NM_031479) is another VGAM2434 host target gene. MGC4638 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4638, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4638 BINDING SITE, designated SEQ ID:25559, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82394] Another function of VGAM2434 is therefore inhibition of MGC4638 (Accession NM_031479). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4638. MGC5149 (Accession XM_051200) is another VGAM2434 host target gene. MGC5149 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC5149, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC5149 BINDING SITE, designated SEQ ID:35783, to the nucleotide

sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82395] Another function of VGAM2434 is therefore inhibition of MGC5149 (Accession XM_051200). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC5149. Melanoma-derived Leucine Zipper, Extra-nuclear Factor (MLZE, Accession NM_031415) is another VGAM2434 host target gene. MLZE BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MLZE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MLZE BINDING SITE, designated SEQ ID:25394, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82396] Another function of VGAM2434 is therefore inhibition of Melanoma-derived Leucine Zipper, Extra-nuclear Factor (MLZE, Accession NM_031415). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLZE. Matrix Metalloproteinase-like 1 (MMPL1, Accession

NM_004142) is another VGAM2434 host target gene. MMPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MMPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MMPL1 BINDING SITE, designated SEQ ID:10349, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82397] Another function of VGAM2434 is therefore inhibition of Matrix Metalloproteinase-like 1 (MMPL1, Accession NM_004142). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MMPL1. Molybdenum Cofactor Synthesis 3 (MOCS3, Accession NM_014484) is another VGAM2434 host target gene. MOCS3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MOCS3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MOCS3 BINDING SITE, designated SEQ ID:15831, to the nucleotide se-

quence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82398] Another function of VGAM2434 is therefore inhibition of Molybdenum Cofactor Synthesis 3 (MOCS3, Accession NM_014484). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOCS3. Mitochondrial Ribosomal Protein L44 (MRPL44, Accession NM_022915) is another VGAM2434 host target gene. MRPL44 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPL44, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPL44 BINDING SITE, designated SEQ ID:23227, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82399] Another function of VGAM2434 is therefore inhibition of Mitochondrial Ribosomal Protein L44 (MRPL44, Accession NM_022915). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPL44. Mitochondrial Ribosomal Protein S27 (MRPS27, Accession NM_015084) is

another VGAM2434 host target gene. MRPS27 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MRPS27, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MRPS27 BINDING SITE, designated SEQ ID:17476, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82400] Another function of VGAM2434 is therefore inhibition of Mitochondrial Ribosomal Protein S27 (MRPS27, Accession NM_015084). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MRPS27. NDP52 (Accession NM_005831) is another VGAM2434 host target gene. NDP52 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NDP52, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDP52 BINDING SITE, designated SEQ ID:12443, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ

ID:5145.

[82401] Another function of VGAM2434 is therefore inhibition of NDP52 (Accession NM_005831). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDP52. NADH Dehydrogenase (ubiquinone) 1, Subcomplex Unknown, 2, 14.5kDa (NDUFC2, Accession NM_004549) is another VGAM2434 host target gene. NDUFC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NDUFC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NDUFC2 BINDING SITE, designated SEQ ID:10895, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82402] Another function of VGAM2434 is therefore inhibition of NADH Dehydrogenase (ubiquinone) 1, Subcomplex Unknown, 2, 14.5kDa (NDUFC2, Accession NM_004549). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NDUFC2. Ninjurin 2 (NINJ2, Accession NM_016533) is another VGAM2434 host target gene.

NINJ2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NINJ2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NINJ2 BINDING SITE, designated SEQ ID:18605, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82403] Another function of VGAM2434 is therefore inhibition of Ninjurin 2 (NINJ2, Accession NM_016533). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NINJ2. Nup43 (Accession NM_024647) is another VGAM2434 host target gene. Nup43 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by Nup43, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of Nup43 BINDING SITE, designated SEQ ID:23936, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82404] Another function of VGAM2434 is therefore inhibition of

Nup43 (Accession NM_024647). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with Nup43. Oxysterol Binding Protein-like 2 (OSBPL2, Accession NM_014835) is another VGAM2434 host target gene. OSBPL2 BINDING SITE1 and OSBPL2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by OSBPL2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OSBPL2 BINDING SITE1 and OSBPL2 BINDING SITE2, designated SEQ ID:16852 and SEQ ID:29320 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82405] Another function of VGAM2434 is therefore inhibition of Oxysterol Binding Protein-like 2 (OSBPL2, Accession NM_014835). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OSBPL2. PRO0365 (Accession NM_014126) is another VGAM2434 host target gene. PRO0365 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded

by PRO0365, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0365 BINDING SITE, designated SEQ ID:15386, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82406] Another function of VGAM2434 is therefore inhibition of PRO0365 (Accession NM_014126). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0365. PRO1992 (Accession NM_014107) is another VGAM2434 host target gene. PRO1992 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1992, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1992 BINDING SITE, designated SEQ ID:15333, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82407] Another function of VGAM2434 is therefore inhibition of PRO1992 (Accession NM_014107). Accordingly, utilities of

VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1992. PRO2955 (Accession NM_018545) is another VGAM2434 host target gene. PRO2955 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO2955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2955 BINDING SITE, designated SEQ ID:20621, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82408] Another function of VGAM2434 is therefore inhibition of PRO2955 (Accession NM_018545). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2955. Proline-serine-threonine Phosphatase Interacting Protein 2 (PSTPIP2, Accession NM_024430) is another VGAM2434 host target gene. PSTPIP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSTPIP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PSTPIP2 BINDING SITE, designated SEQ ID:23680, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82409] Another function of VGAM2434 is therefore inhibition of Proline-serine-threonine Phosphatase Interacting Protein 2 (PSTPIP2, Accession NM_024430). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSTPIP2. RAB33B, Member RAS Oncogene Family (RAB33B, Accession NM_031296) is another VGAM2434 host target gene. RAB33B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB33B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB33B BINDING SITE, designated SEQ ID:25331, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82410] Another function of VGAM2434 is therefore inhibition of RAB33B, Member RAS Oncogene Family (RAB33B, Accession NM_031296). Accordingly, utilities of VGAM2434 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB33B. RAI (Accession NM_006663) is another VGAM2434 host target gene. RAI BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAI, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAI BINDING SITE, designated SEQ ID:13472, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82411] Another function of VGAM2434 is therefore inhibition of RAI (Accession NM_006663). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI. RES4-25 (Accession XM_035572) is another VGAM2434 host target gene. RES4-25 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RES4-25, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RES4-25 BINDING SITE, designated SEQ ID:32287, to the nucleotide sequence of

VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82412] Another function of VGAM2434 is therefore inhibition of RES4-25 (Accession XM_035572). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RES4-25. SEC24 Related Gene Family, Member A (S. cerevisiae) (SEC24A, Accession XM_094581) is another VGAM2434 host target gene. SEC24A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC24A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC24A BINDING SITE, designated SEQ ID:40235, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82413] Another function of VGAM2434 is therefore inhibition of SEC24 Related Gene Family, Member A (S. cerevisiae) (SEC24A, Accession XM_094581). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC24A. Small EDRK-rich Factor 1B (centromeric) (SERF1B,

Accession NM_022978) is another VGAM2434 host target gene. SERF1B BINDING SITE1 and SERF1B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SERF1B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERF1B BINDING SITE1 and SERF1B BINDING SITE2, designated SEQ ID:23258 and SEQ ID:23259 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82414] Another function of VGAM2434 is therefore inhibition of Small EDRK-rich Factor 1B (centromeric) (SERF1B, Accession NM_022978). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERF1B.

STAF65(gamma) (Accession NM_014860) is another VGAM2434 host target gene. STAF65(gamma) BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STAF65(gamma), corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of STAF65(gamma) BINDING SITE, designated SEQ ID:16923, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82415] Another function of VGAM2434 is therefore inhibition of STAF65(gamma) (Accession NM_014860). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAF65(gamma). Tripartite Motif-containing 6 (TRIM6, Accession NM_058166) is another VGAM2434 host target gene. TRIM6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TRIM6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM6 BINDING SITE, designated SEQ ID:27712, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82416] Another function of VGAM2434 is therefore inhibition of Tripartite Motif-containing 6 (TRIM6, Accession NM_058166). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with TRIM6. TU12B1-TY (Accession NM_016575) is another VGAM2434 host target gene. TU12B1-TY BINDING SITE1 through TU12B1-TY BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TU12B1-TY, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TU12B1-TY BINDING SITE1 through TU12B1-TY BINDING SITE3, designated SEQ ID:18646, SEQ ID:18647 and SEQ ID:18651 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82417] Another function of VGAM2434 is therefore inhibition of TU12B1-TY (Accession NM_016575). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TU12B1-TY. VDU1 (Accession NM_015017) is another VGAM2434 host target gene. VDU1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VDU1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of VDU1 BINDING SITE, designated SEQ ID:17382, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82418] Another function of VGAM2434 is therefore inhibition of VDU1 (Accession NM_015017). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VDU1. Vacuolar Protein Sorting 33A (yeast) (VPS33A, Accession NM_022916) is another VGAM2434 host target gene. VPS33A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VPS33A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS33A BINDING SITE, designated SEQ ID:23232, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82419] Another function of VGAM2434 is therefore inhibition of Vacuolar Protein Sorting 33A (yeast) (VPS33A, Accession NM_022916). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with VPS33A. Williams Beuren Syndrome Chromosome Region 20A (WBSCR20A, Accession NM_032158) is another VGAM2434 host target gene. WBSCR20A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by WBSCR20A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WBSCR20A BINDING SITE, designated SEQ ID:25859, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82420] Another function of VGAM2434 is therefore inhibition of Williams Beuren Syndrome Chromosome Region 20A (WBSCR20A, Accession NM_032158). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR20A. Williams-Beuren Syndrome Chromosome Region 23 (WBSCR23, Accession NM_025042) is another VGAM2434 host target gene. WBSCR23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WBSCR23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WBSCR23 BINDING SITE, designated SEQ ID:24641, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82421] Another function of VGAM2434 is therefore inhibition of Williams-Beuren Syndrome Chromosome Region 23 (WBSCR23, Accession NM_025042). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WBSCR23. Zinc Finger Protein 185 (LIM domain) (ZNF185, Accession NM_007150) is another VGAM2434 host target gene. ZNF185 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF185, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF185 BINDING SITE, designated SEQ ID:14004, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82422] Another function of VGAM2434 is therefore inhibition of Zinc Finger Protein 185 (LIM domain) (ZNF185, Accession

NM_007150). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF185. Zinc Finger Protein 338 (ZNF338, Accession NM_022088) is another VGAM2434 host target gene. ZNF338 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF338, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF338 BINDING SITE, designated SEQ ID:22633, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82423] Another function of VGAM2434 is therefore inhibition of Zinc Finger Protein 338 (ZNF338, Accession NM_022088). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF338. ZTL1 (Accession NM_024055) is another VGAM2434 host target gene. ZTL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZTL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of ZTL1 BINDING SITE, designated SEQ ID:23491, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82424] Another function of VGAM2434 is therefore inhibition of ZTL1 (Accession NM_024055). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZTL1. LOC112817 (Accession NM_138413) is another VGAM2434 host target gene. LOC112817 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC112817, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC112817 BINDING SITE, designated SEQ ID:28782, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82425] Another function of VGAM2434 is therefore inhibition of LOC112817 (Accession NM_138413). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC112817. LOC113675 (Accession NM_138432) is an-

other VGAM2434 host target gene. LOC113675 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC113675, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC113675 BINDING SITE, designated SEQ ID:28797, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82426] Another function of VGAM2434 is therefore inhibition of LOC113675 (Accession NM_138432). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC113675. LOC115219 (Accession XM_055499) is another VGAM2434 host target gene. LOC115219 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC115219, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115219 BINDING SITE, designated SEQ ID:36282, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82427] Another function of VGAM2434 is therefore inhibition of LOC115219 (Accession XM_055499). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115219. LOC120114 (Accession XM_061871) is another VGAM2434 host target gene. LOC120114 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC120114, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC120114 BINDING SITE, designated SEQ ID:37213, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82428] Another function of VGAM2434 is therefore inhibition of LOC120114 (Accession XM_061871). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC120114. LOC126364 (Accession XM_065047) is another VGAM2434 host target gene. LOC126364 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126364, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126364 BINDING SITE, designated SEQ ID:37273, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82429] Another function of VGAM2434 is therefore inhibition of LOC126364 (Accession XM_065047). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126364. LOC126661 (Accession XM_059061) is another VGAM2434 host target gene. LOC126661 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126661, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126661 BINDING SITE, designated SEQ ID:36856, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82430] Another function of VGAM2434 is therefore inhibition of LOC126661 (Accession XM_059061). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC126661. LOC126669 (Accession XM_060121) is another VGAM2434 host target gene. LOC126669 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126669, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126669 BINDING SITE, designated SEQ ID:37157, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82431] Another function of VGAM2434 is therefore inhibition of LOC126669 (Accession XM_060121). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126669. LOC132625 (Accession XM_067946) is another VGAM2434 host target gene. LOC132625 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC132625, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC132625 BINDING SITE, designated SEQ ID:37374, to the nucleotide sequence of VGAM2434 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5145.

[82432] Another function of VGAM2434 is therefore inhibition of LOC132625 (Accession XM_067946). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132625. LOC133686 (Accession XM_059667) is another VGAM2434 host target gene. LOC133686 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC133686, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC133686 BINDING SITE, designated SEQ ID:37054, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82433] Another function of VGAM2434 is therefore inhibition of LOC133686 (Accession XM_059667). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC133686. LOC135293 (Accession XM_072402) is another VGAM2434 host target gene. LOC135293 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC135293, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC135293 BINDING SITE, designated SEQ ID:37492, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82434] Another function of VGAM2434 is therefore inhibition of LOC135293 (Accession XM_072402). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135293. LOC135763 (Accession NM_138572) is another VGAM2434 host target gene. LOC135763 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC135763, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC135763 BINDING SITE, designated SEQ ID:28884, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82435] Another function of VGAM2434 is therefore inhibition of LOC135763 (Accession NM_138572). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC135763. LOC135818 (Accession XM_059804) is another VGAM2434 host target gene. LOC135818 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC135818, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC135818 BINDING SITE, designated SEQ ID:37095, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82436] Another function of VGAM2434 is therefore inhibition of LOC135818 (Accession XM_059804). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC135818. LOC143241 (Accession NM_138812) is another VGAM2434 host target gene. LOC143241 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC143241, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143241 BINDING SITE, designated SEQ ID:29035, to

the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82437] Another function of VGAM2434 is therefore inhibition of LOC143241 (Accession NM_138812). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143241. LOC145757 (Accession XM_085227) is another VGAM2434 host target gene. LOC145757 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145757, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145757 BINDING SITE, designated SEQ ID:37973, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82438] Another function of VGAM2434 is therefore inhibition of LOC145757 (Accession XM_085227). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145757. LOC146229 (Accession XM_085387) is another VGAM2434 host target gene. LOC146229 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC146229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146229 BINDING SITE, designated SEQ ID:38116, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82439] Another function of VGAM2434 is therefore inhibition of LOC146229 (Accession XM_085387). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146229. LOC146336 (Accession XM_085421) is another VGAM2434 host target gene. LOC146336 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146336, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146336 BINDING SITE, designated SEQ ID:38133, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82440] Another function of VGAM2434 is therefore inhibition of LOC146336 (Accession XM_085421). Accordingly, utilities

of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146336. LOC146346 (Accession XM_085430) is another VGAM2434 host target gene. LOC146346 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146346, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146346 BINDING SITE, designated SEQ ID:38136, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82441] Another function of VGAM2434 is therefore inhibition of LOC146346 (Accession XM_085430). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146346. LOC146455 (Accession XM_085471) is another VGAM2434 host target gene. LOC146455 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146455, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC146455 BINDING SITE, designated SEQ ID:38159, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82442] Another function of VGAM2434 is therefore inhibition of LOC146455 (Accession XM_085471). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146455. LOC146784 (Accession XM_085588) is another VGAM2434 host target gene. LOC146784 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146784, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146784 BINDING SITE, designated SEQ ID:38240, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82443] Another function of VGAM2434 is therefore inhibition of LOC146784 (Accession XM_085588). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146784. LOC146895 (Accession XM_097120) is another VGAM2434 host target gene. LOC146895 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146895, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146895 BINDING SITE, designated SEQ ID:40760, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82444] Another function of VGAM2434 is therefore inhibition of LOC146895 (Accession XM_097120). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146895. LOC146909 (Accession XM_085634) is another VGAM2434 host target gene. LOC146909 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146909, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146909 BINDING SITE, designated SEQ ID:38268, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82445] Another function of VGAM2434 is therefore inhibition of

LOC146909 (Accession XM_085634). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146909. LOC146952 (Accession XM_097138) is another VGAM2434 host target gene. LOC146952 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146952, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146952 BINDING SITE, designated SEQ ID:40769, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82446] Another function of VGAM2434 is therefore inhibition of LOC146952 (Accession XM_097138). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146952. LOC147071 (Accession XM_054031) is another VGAM2434 host target gene. LOC147071 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147071, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC147071 BINDING SITE, designated SEQ ID:36135, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82447] Another function of VGAM2434 is therefore inhibition of LOC147071 (Accession XM_054031). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147071. LOC147093 (Accession XM_097184) is another VGAM2434 host target gene. LOC147093 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147093, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147093 BINDING SITE, designated SEQ ID:40806, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82448] Another function of VGAM2434 is therefore inhibition of LOC147093 (Accession XM_097184). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147093. LOC147429 (Accession XM_085793) is an-

other VGAM2434 host target gene. LOC147429 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147429, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147429 BINDING SITE, designated SEQ ID:38338, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82449] Another function of VGAM2434 is therefore inhibition of LOC147429 (Accession XM_085793). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147429. LOC147660 (Accession XM_085825) is another VGAM2434 host target gene. LOC147660 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147660, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147660 BINDING SITE, designated SEQ ID:38350, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82450] Another function of VGAM2434 is therefore inhibition of LOC147660 (Accession XM_085825). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147660. LOC147817 (Accession XM_085903) is another VGAM2434 host target gene. LOC147817 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147817, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147817 BINDING SITE, designated SEQ ID:38389, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82451] Another function of VGAM2434 is therefore inhibition of LOC147817 (Accession XM_085903). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147817. LOC148137 (Accession NM_144692) is another VGAM2434 host target gene. LOC148137 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148137, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148137 BINDING SITE, designated SEQ ID:29519, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82452] Another function of VGAM2434 is therefore inhibition of LOC148137 (Accession NM_144692). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148137. LOC148189 (Accession XM_086087) is another VGAM2434 host target gene. LOC148189 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148189, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148189 BINDING SITE, designated SEQ ID:38486, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82453] Another function of VGAM2434 is therefore inhibition of LOC148189 (Accession XM_086087). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC148189. LOC149506 (Accession XM_097661) is another VGAM2434 host target gene. LOC149506 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149506, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149506 BINDING SITE, designated SEQ ID:41006, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82454] Another function of VGAM2434 is therefore inhibition of LOC149506 (Accession XM_097661). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149506. LOC149577 (Accession XM_097675) is another VGAM2434 host target gene. LOC149577 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149577 BINDING SITE, designated SEQ ID:41025, to the nucleotide sequence of VGAM2434 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5145.

[82455] Another function of VGAM2434 is therefore inhibition of LOC149577 (Accession XM_097675). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149577. LOC149703 (Accession XM_097719) is another VGAM2434 host target gene. LOC149703 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149703, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149703 BINDING SITE, designated SEQ ID:41064, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82456] Another function of VGAM2434 is therefore inhibition of LOC149703 (Accession XM_097719). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149703. LOC150397 (Accession XM_086907) is another VGAM2434 host target gene. LOC150397 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150397, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150397 BINDING SITE, designated SEQ ID:38962, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82457] Another function of VGAM2434 is therefore inhibition of LOC150397 (Accession XM_086907). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150397. LOC150960 (Accession XM_087059) is another VGAM2434 host target gene. LOC150960 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150960, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150960 BINDING SITE, designated SEQ ID:39031, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82458] Another function of VGAM2434 is therefore inhibition of LOC150960 (Accession XM_087059). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC150960. LOC151057 (Accession XM_097998) is another VGAM2434 host target gene. LOC151057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151057 BINDING SITE, designated SEQ ID:41293, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82459] Another function of VGAM2434 is therefore inhibition of LOC151057 (Accession XM_097998). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151057. LOC151475 (Accession XM_098063) is another VGAM2434 host target gene. LOC151475 BINDING SITE1 and LOC151475 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC151475, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151475 BINDING SITE1

and LOC151475 BINDING SITE2, designated SEQ ID:41354 and SEQ ID:41360 respectively, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82460] Another function of VGAM2434 is therefore inhibition of LOC151475 (Accession XM_098063). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151475. LOC151826 (Accession XM_087312) is another VGAM2434 host target gene. LOC151826 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151826, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151826 BINDING SITE, designated SEQ ID:39166, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82461] Another function of VGAM2434 is therefore inhibition of LOC151826 (Accession XM_087312). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151826. LOC152343 (Accession XM_087441) is an-

other VGAM2434 host target gene. LOC152343 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152343, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152343 BINDING SITE, designated SEQ ID:39264, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82462] Another function of VGAM2434 is therefore inhibition of LOC152343 (Accession XM_087441). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152343. LOC152445 (Accession XM_098231) is another VGAM2434 host target gene. LOC152445 BINDING SITE1 and LOC152445 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC152445, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152445 BINDING SITE1 and LOC152445 BINDING SITE2, designated SEQ ID:41509 and SEQ ID:41513 respectively, to the nucleotide se-

quence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82463] Another function of VGAM2434 is therefore inhibition of LOC152445 (Accession XM_098231). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152445. LOC152794 (Accession XM_087525) is another VGAM2434 host target gene. LOC152794 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152794 BINDING SITE, designated SEQ ID:39321, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82464] Another function of VGAM2434 is therefore inhibition of LOC152794 (Accession XM_087525). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152794. LOC152925 (Accession XM_087559) is another VGAM2434 host target gene. LOC152925 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC152925, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152925 BINDING SITE, designated SEQ ID:39331, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82465] Another function of VGAM2434 is therefore inhibition of LOC152925 (Accession XM_087559). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152925. LOC153077 (Accession XM_098307) is another VGAM2434 host target gene. LOC153077 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153077, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153077 BINDING SITE, designated SEQ ID:41570, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82466] Another function of VGAM2434 is therefore inhibition of LOC153077 (Accession XM_098307). Accordingly, utilities

of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153077. LOC153883 (Accession XM_087798) is another VGAM2434 host target gene. LOC153883 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153883, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153883 BINDING SITE, designated SEQ ID:39431, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82467] Another function of VGAM2434 is therefore inhibition of LOC153883 (Accession XM_087798). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153883. LOC154282 (Accession XM_098505) is another VGAM2434 host target gene. LOC154282 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154282, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC154282 BINDING SITE, designated SEQ ID:41701, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82468] Another function of VGAM2434 is therefore inhibition of LOC154282 (Accession XM_098505). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154282. LOC154726 (Accession XM_088024) is another VGAM2434 host target gene. LOC154726 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154726, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154726 BINDING SITE, designated SEQ ID:39478, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82469] Another function of VGAM2434 is therefore inhibition of LOC154726 (Accession XM_088024). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154726. LOC154877 (Accession XM_098626) is another VGAM2434 host target gene. LOC154877 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154877, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE, designated SEQ ID:41746, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82470] Another function of VGAM2434 is therefore inhibition of LOC154877 (Accession XM_098626). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154877. LOC154930 (Accession XM_088080) is another VGAM2434 host target gene. LOC154930 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154930, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154930 BINDING SITE, designated SEQ ID:39505, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82471] Another function of VGAM2434 is therefore inhibition of

LOC154930 (Accession XM_088080). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154930. LOC157798 (Accession XM_098827) is another VGAM2434 host target gene. LOC157798 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157798, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157798 BINDING SITE, designated SEQ ID:41852, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82472] Another function of VGAM2434 is therefore inhibition of LOC157798 (Accession XM_098827). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157798. LOC158549 (Accession XM_098963) is another VGAM2434 host target gene. LOC158549 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158549, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC158549 BINDING SITE, designated SEQ ID:42011, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82473] Another function of VGAM2434 is therefore inhibition of LOC158549 (Accession XM_098963). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158549. LOC158668 (Accession XM_045161) is another VGAM2434 host target gene. LOC158668 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158668, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158668 BINDING SITE, designated SEQ ID:34379, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82474] Another function of VGAM2434 is therefore inhibition of LOC158668 (Accession XM_045161). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158668. LOC158865 (Accession XM_099000) is an-

other VGAM2434 host target gene. LOC158865 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158865, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158865 BINDING SITE, designated SEQ ID:42038, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82475] Another function of VGAM2434 is therefore inhibition of LOC158865 (Accession XM_099000). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158865. LOC160646 (Accession XM_090413) is another VGAM2434 host target gene. LOC160646 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC160646, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC160646 BINDING SITE, designated SEQ ID:40005, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82476] Another function of VGAM2434 is therefore inhibition of LOC160646 (Accession XM_090413). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC160646. LOC161829 (Accession XM_091161) is another VGAM2434 host target gene. LOC161829 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC161829, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161829 BINDING SITE, designated SEQ ID:40040, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82477] Another function of VGAM2434 is therefore inhibition of LOC161829 (Accession XM_091161). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161829. LOC169611 (Accession XM_095809) is another VGAM2434 host target gene. LOC169611 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC169611, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169611 BINDING SITE, designated SEQ ID:40287, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82478] Another function of VGAM2434 is therefore inhibition of LOC169611 (Accession XM_095809). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169611. LOC196047 (Accession XM_116883) is another VGAM2434 host target gene. LOC196047 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC196047, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196047 BINDING SITE, designated SEQ ID:43147, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82479] Another function of VGAM2434 is therefore inhibition of LOC196047 (Accession XM_116883). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC196047. LOC196264 (Accession XM_113683) is another VGAM2434 host target gene. LOC196264 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196264, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196264 BINDING SITE, designated SEQ ID:42334, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82480] Another function of VGAM2434 is therefore inhibition of LOC196264 (Accession XM_113683). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196264. LOC196411 (Accession XM_113714) is another VGAM2434 host target gene. LOC196411 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196411, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196411 BINDING SITE, designated SEQ ID:42366, to the nucleotide sequence of VGAM2434 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5145.

[82481] Another function of VGAM2434 is therefore inhibition of LOC196411 (Accession XM_113714). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196411. LOC196529 (Accession XM_113746) is another VGAM2434 host target gene. LOC196529 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196529, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196529 BINDING SITE, designated SEQ ID:42411, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82482] Another function of VGAM2434 is therefore inhibition of LOC196529 (Accession XM_113746). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196529. LOC199786 (Accession XM_114021) is another VGAM2434 host target gene. LOC199786 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC199786, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199786 BINDING SITE, designated SEQ ID:42621, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82483] Another function of VGAM2434 is therefore inhibition of LOC199786 (Accession XM_114021). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199786. LOC200169 (Accession XM_117200) is another VGAM2434 host target gene. LOC200169 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200169, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200169 BINDING SITE, designated SEQ ID:43284, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82484] Another function of VGAM2434 is therefore inhibition of LOC200169 (Accession XM_117200). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC200169. LOC200310 (Accession XM_037840) is another VGAM2434 host target gene. LOC200310 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200310, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200310 BINDING SITE, designated SEQ ID:32706, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82485] Another function of VGAM2434 is therefore inhibition of LOC200310 (Accession XM_037840). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200310. LOC200314 (Accession XM_117225) is another VGAM2434 host target gene. LOC200314 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200314, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200314 BINDING SITE, designated SEQ ID:43295, to

the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82486] Another function of VGAM2434 is therefore inhibition of LOC200314 (Accession XM_117225). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200314. LOC200845 (Accession XM_114305) is another VGAM2434 host target gene. LOC200845 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC200845, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200845 BINDING SITE, designated SEQ ID:42864, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82487] Another function of VGAM2434 is therefore inhibition of LOC200845 (Accession XM_114305). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200845. LOC200860 (Accession XM_117289) is another VGAM2434 host target gene. LOC200860 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC200860, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200860 BINDING SITE, designated SEQ ID:43357, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82488] Another function of VGAM2434 is therefore inhibition of LOC200860 (Accession XM_117289). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200860. LOC201173 (Accession XM_113312) is another VGAM2434 host target gene. LOC201173 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201173, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201173 BINDING SITE, designated SEQ ID:42214, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82489] Another function of VGAM2434 is therefore inhibition of LOC201173 (Accession XM_113312). Accordingly, utilities

of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201173. LOC201220 (Accession XM_113321) is another VGAM2434 host target gene. LOC201220 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201220, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201220 BINDING SITE, designated SEQ ID:42221, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82490] Another function of VGAM2434 is therefore inhibition of LOC201220 (Accession XM_113321). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201220. LOC201294 (Accession XM_113950) is another VGAM2434 host target gene. LOC201294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC201294 BINDING SITE, designated SEQ ID:42569, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82491] Another function of VGAM2434 is therefore inhibition of LOC201294 (Accession XM_113950). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201294. LOC201411 (Accession XM_031946) is another VGAM2434 host target gene. LOC201411 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201411, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201411 BINDING SITE, designated SEQ ID:31527, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82492] Another function of VGAM2434 is therefore inhibition of LOC201411 (Accession XM_031946). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201411. LOC201696 (Accession XM_032269) is another VGAM2434 host target gene. LOC201696 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201696, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201696 BINDING SITE, designated SEQ ID:31621, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82493] Another function of VGAM2434 is therefore inhibition of LOC201696 (Accession XM_032269). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201696. LOC201702 (Accession XM_114365) is another VGAM2434 host target gene. LOC201702 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201702, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201702 BINDING SITE, designated SEQ ID:42900, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82494] Another function of VGAM2434 is therefore inhibition of

LOC201702 (Accession XM_114365). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201702. LOC202025 (Accession XM_117353) is another VGAM2434 host target gene. LOC202025 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202025, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202025 BINDING SITE, designated SEQ ID:43405, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82495] Another function of VGAM2434 is therefore inhibition of LOC202025 (Accession XM_117353). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202025. LOC202934 (Accession XM_117486) is another VGAM2434 host target gene. LOC202934 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC202934, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC202934 BINDING SITE, designated SEQ ID:43456, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82496] Another function of VGAM2434 is therefore inhibition of LOC202934 (Accession XM_117486). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202934. LOC203297 (Accession XM_059986) is another VGAM2434 host target gene. LOC203297 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC203297, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203297 BINDING SITE, designated SEQ ID:37135, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82497] Another function of VGAM2434 is therefore inhibition of LOC203297 (Accession XM_059986). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203297. LOC203339 (Accession XM_117534) is an-

other VGAM2434 host target gene. LOC203339 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203339, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203339 BINDING SITE, designated SEQ ID:43524, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82498] Another function of VGAM2434 is therefore inhibition of LOC203339 (Accession XM_117534). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203339. LOC203350 (Accession XM_117536) is another VGAM2434 host target gene. LOC203350 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203350, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203350 BINDING SITE, designated SEQ ID:43538, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82499] Another function of VGAM2434 is therefore inhibition of LOC203350 (Accession XM_117536). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203350. LOC203378 (Accession XM_117541) is another VGAM2434 host target gene. LOC203378 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203378, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203378 BINDING SITE, designated SEQ ID:43551, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82500] Another function of VGAM2434 is therefore inhibition of LOC203378 (Accession XM_117541). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203378. LOC219673 (Accession XM_167567) is another VGAM2434 host target gene. LOC219673 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219673, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219673 BINDING SITE, designated SEQ ID:44692, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82501] Another function of VGAM2434 is therefore inhibition of LOC219673 (Accession XM_167567). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219673. LOC220662 (Accession XM_165978) is another VGAM2434 host target gene. LOC220662 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC220662, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220662 BINDING SITE, designated SEQ ID:43825, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82502] Another function of VGAM2434 is therefore inhibition of LOC220662 (Accession XM_165978). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC220662. LOC221296 (Accession XM_166325) is another VGAM2434 host target gene. LOC221296 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221296, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221296 BINDING SITE, designated SEQ ID:44171, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82503] Another function of VGAM2434 is therefore inhibition of LOC221296 (Accession XM_166325). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221296. LOC221773 (Accession XM_165802) is another VGAM2434 host target gene. LOC221773 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221773, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221773 BINDING SITE, designated SEQ ID:43767, to the nucleotide sequence of VGAM2434 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5145.

[82504] Another function of VGAM2434 is therefore inhibition of LOC221773 (Accession XM_165802). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221773. LOC222031 (Accession XM_168371) is another VGAM2434 host target gene. LOC222031 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222031, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222031 BINDING SITE, designated SEQ ID:45137, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82505] Another function of VGAM2434 is therefore inhibition of LOC222031 (Accession XM_168371). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222031. LOC222070 (Accession XM_168433) is another VGAM2434 host target gene. LOC222070 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222070, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222070 BINDING SITE, designated SEQ ID:45180, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82506] Another function of VGAM2434 is therefore inhibition of LOC222070 (Accession XM_168433). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222070. LOC245771 (Accession XM_167366) is another VGAM2434 host target gene. LOC245771 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC245771, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC245771 BINDING SITE, designated SEQ ID:44634, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82507] Another function of VGAM2434 is therefore inhibition of LOC245771 (Accession XM_167366). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC245771. LOC253664 (Accession XM_170673) is another VGAM2434 host target gene. LOC253664 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253664, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253664 BINDING SITE, designated SEQ ID:45448, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82508] Another function of VGAM2434 is therefore inhibition of LOC253664 (Accession XM_170673). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253664. LOC253666 (Accession XM_170799) is another VGAM2434 host target gene. LOC253666 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253666, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253666 BINDING SITE, designated SEQ ID:45569, to

the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82509] Another function of VGAM2434 is therefore inhibition of LOC253666 (Accession XM_170799). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253666. LOC254778 (Accession XM_171193) is another VGAM2434 host target gene. LOC254778 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254778, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254778 BINDING SITE, designated SEQ ID:45979, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82510] Another function of VGAM2434 is therefore inhibition of LOC254778 (Accession XM_171193). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254778. LOC255177 (Accession XM_172941) is another VGAM2434 host target gene. LOC255177 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC255177, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255177 BINDING SITE, designated SEQ ID:46203, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82511] Another function of VGAM2434 is therefore inhibition of LOC255177 (Accession XM_172941). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255177. LOC255308 (Accession XM_170536) is another VGAM2434 host target gene. LOC255308 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255308 BINDING SITE, designated SEQ ID:45357, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82512] Another function of VGAM2434 is therefore inhibition of LOC255308 (Accession XM_170536). Accordingly, utilities

of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255308. LOC255919 (Accession XM_170794) is another VGAM2434 host target gene. LOC255919 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255919, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255919 BINDING SITE, designated SEQ ID:45555, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82513] Another function of VGAM2434 is therefore inhibition of LOC255919 (Accession XM_170794). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255919. LOC256360 (Accession XM_172918) is another VGAM2434 host target gene. LOC256360 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256360, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC256360 BINDING SITE, designated SEQ ID:46176, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82514] Another function of VGAM2434 is therefore inhibition of LOC256360 (Accession XM_172918). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256360. LOC257463 (Accession XM_048605) is another VGAM2434 host target gene. LOC257463 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257463, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257463 BINDING SITE, designated SEQ ID:35212, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82515] Another function of VGAM2434 is therefore inhibition of LOC257463 (Accession XM_048605). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257463. LOC51200 (Accession NM_016352) is another VGAM2434 host target gene. LOC51200 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51200, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51200 BINDING SITE, designated SEQ ID:18481, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82516] Another function of VGAM2434 is therefore inhibition of LOC51200 (Accession NM_016352). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51200. LOC57107 (Accession NM_020381) is another VGAM2434 host target gene. LOC57107 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57107, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57107 BINDING SITE, designated SEQ ID:21653, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82517] Another function of VGAM2434 is therefore inhibition of

LOC57107 (Accession NM_020381). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57107. LOC57146 (Accession NM_020422) is another VGAM2434 host target gene. LOC57146 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC57146, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57146 BINDING SITE, designated SEQ ID:21680, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82518] Another function of VGAM2434 is therefore inhibition of LOC57146 (Accession NM_020422). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57146. LOC63929 (Accession NM_022098) is another VGAM2434 host target gene. LOC63929 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC63929, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC63929 BINDING SITE, designated SEQ ID:22640, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82519] Another function of VGAM2434 is therefore inhibition of LOC63929 (Accession NM_022098). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC63929. LOC89932 (Accession XM_027341) is another VGAM2434 host target gene. LOC89932 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC89932, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC89932 BINDING SITE, designated SEQ ID:30494, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82520] Another function of VGAM2434 is therefore inhibition of LOC89932 (Accession XM_027341). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC89932. LOC90288 (Accession XM_030669) is another

VGAM2434 host target gene. LOC90288 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90288 BINDING SITE, designated SEQ ID:31116, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82521] Another function of VGAM2434 is therefore inhibition of LOC90288 (Accession XM_030669). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90288. LOC90333 (Accession XM_030958) is another VGAM2434 host target gene. LOC90333 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90333 BINDING SITE, designated SEQ ID:31226, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82522] Another function of VGAM2434 is therefore inhibition of LOC90333 (Accession XM_030958). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90333. LOC90371 (Accession XM_031261) is another VGAM2434 host target gene. LOC90371 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90371, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90371 BINDING SITE, designated SEQ ID:31323, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82523] Another function of VGAM2434 is therefore inhibition of LOC90371 (Accession XM_031261). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90371. LOC90408 (Accession XM_031517) is another VGAM2434 host target gene. LOC90408 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90408, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90408 BINDING SITE, designated SEQ ID:31399, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82524] Another function of VGAM2434 is therefore inhibition of LOC90408 (Accession XM_031517). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90408. LOC90485 (Accession XM_032059) is another VGAM2434 host target gene. LOC90485 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90485, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90485 BINDING SITE, designated SEQ ID:31555, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82525] Another function of VGAM2434 is therefore inhibition of LOC90485 (Accession XM_032059). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC90485. LOC91115 (Accession XM_036218) is another VGAM2434 host target gene. LOC91115 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91115, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91115 BINDING SITE, designated SEQ ID:32402, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82526] Another function of VGAM2434 is therefore inhibition of LOC91115 (Accession XM_036218). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91115. LOC91308 (Accession XM_037600) is another VGAM2434 host target gene. LOC91308 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91308 BINDING SITE, designated SEQ ID:32658, to the nucleotide sequence of VGAM2434 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5145.

[82527] Another function of VGAM2434 is therefore inhibition of LOC91308 (Accession XM_037600). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91308. LOC92267 (Accession XM_043979) is another VGAM2434 host target gene. LOC92267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92267 BINDING SITE, designated SEQ ID:34058, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82528] Another function of VGAM2434 is therefore inhibition of LOC92267 (Accession XM_043979). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92267. LOC92303 (Accession XM_044108) is another VGAM2434 host target gene. LOC92303 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92303, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92303 BINDING SITE, designated SEQ ID:34136, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82529] Another function of VGAM2434 is therefore inhibition of LOC92303 (Accession XM_044108). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92303. LOC92689 (Accession XM_046663) is another VGAM2434 host target gene. LOC92689 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92689, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92689 BINDING SITE, designated SEQ ID:34784, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82530] Another function of VGAM2434 is therefore inhibition of LOC92689 (Accession XM_046663). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC92689. LOC92697 (Accession XM_046715) is another VGAM2434 host target gene. LOC92697 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92697, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92697 BINDING SITE, designated SEQ ID:34805, to the nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82531] Another function of VGAM2434 is therefore inhibition of LOC92697 (Accession XM_046715). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92697. LOC93132 (Accession XM_049396) is another VGAM2434 host target gene. LOC93132 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93132, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93132 BINDING SITE, designated SEQ ID:35410, to the

nucleotide sequence of VGAM2434 RNA, herein designated VGAM RNA, also designated SEQ ID:5145.

[82532] Another function of VGAM2434 is therefore inhibition of LOC93132 (Accession XM_049396). Accordingly, utilities of VGAM2434 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93132. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2435 (VGAM2435) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82533] VGAM2435 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2435 was detected is described hereinabove with reference to Figs. 1-8.

[82534] VGAM2435 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus.
VGAM2435 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82535] VGAM2435 gene encodes a VGAM2435 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2435 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2435 precursor RNA is designated SEQ ID:2421, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2421 is located at position 35753 relative to the genome of Goatpox Virus.

[82536] VGAM2435 precursor RNA folds onto itself, forming VGAM2435 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82537] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2435 folded precursor RNA into VGAM2435 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 59%) nucleotide sequence of VGAM2435 RNA is designated SEQ ID:5146, and is provided hereinbelow with reference to the sequence listing part.

[82538] VGAM2435 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2435 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2435 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82539] VGAM2435 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2435 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2435 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2435 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2435 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82540] The complementary binding of VGAM2435 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2435 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2435 host target RNA into VGAM2435 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82541] It is appreciated that VGAM2435 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2435 host target genes. The mRNA of each one of this plurality of VGAM2435 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2435 RNA, herein designated VGAM RNA, and which when bound by VGAM2435 RNA causes inhibition of translation of respective one or more VGAM2435 host target proteins.

[82542] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2435 gene, herein designated VGAM GENE, on one or more VGAM2435 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82543] It is yet further appreciated that a function of VGAM2435 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2435 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2435 correlate with, and may be deduced from, the identity of the host target genes which VGAM2435 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82544] Nucleotide sequences of the VGAM2435 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2435 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2435 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2435 are further described hereinbelow with reference to Table 1.

[82545] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2435 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2435 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82546] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2435 gene, herein designated VGAM is inhibition of expression of VGAM2435 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2435 correlate with, and may be deduced from, the identity of the target genes which VGAM2435 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82547] Parkinson Disease (autosomal recessive, juvenile) 2, Parkin (PARK2, Accession NM_013987) is a VGAM2435 host target gene. PARK2 BINDING SITE1 through PARK2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PARK2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PARK2 BINDING SITE1 through PARK2 BINDING SITE3, designated SEQ ID:15150, SEQ ID:10903 and SEQ ID:15157 respectively, to the nucleotide sequence of VGAM2435 RNA, herein designated VGAM RNA, also designated SEQ

ID:5146.

[82548] A function of VGAM2435 is therefore inhibition of Parkinson Disease (autosomal recessive, juvenile) 2, Parkin (PARK2, Accession NM_013987). Accordingly, utilities of VGAM2435 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PARK2. DKFZP564G092 (Accession NM_015601) is another VGAM2435 host target gene. DKFZP564G092 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP564G092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564G092 BINDING SITE, designated SEQ ID:17875, to the nucleotide sequence of VGAM2435 RNA, herein designated VGAM RNA, also designated SEQ ID:5146.

[82549] Another function of VGAM2435 is therefore inhibition of DKFZP564G092 (Accession NM_015601). Accordingly, utilities of VGAM2435 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564G092. KIAA1271 (Accession XM_045472) is another VGAM2435 host target gene. KIAA1271 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1271 BINDING SITE, designated SEQ ID:34467, to the nucleotide sequence of VGAM2435 RNA, herein designated VGAM RNA, also designated SEQ ID:5146.

[82550] Another function of VGAM2435 is therefore inhibition of KIAA1271 (Accession XM_045472). Accordingly, utilities of VGAM2435 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1271. LOC150333 (Accession XM_097874) is another VGAM2435 host target gene. LOC150333 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150333, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150333 BINDING SITE, designated SEQ ID:41195, to the nucleotide sequence of VGAM2435 RNA, herein designated VGAM RNA, also designated SEQ ID:5146.

[82551] Another function of VGAM2435 is therefore inhibition of

LOC150333 (Accession XM_097874). Accordingly, utilities of VGAM2435 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150333. LOC254778 (Accession XM_171193) is another VGAM2435 host target gene. LOC254778 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254778, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254778 BINDING SITE, designated SEQ ID:45980, to the nucleotide sequence of VGAM2435 RNA, herein designated VGAM RNA, also designated SEQ ID:5146.

[82552] Another function of VGAM2435 is therefore inhibition of LOC254778 (Accession XM_171193). Accordingly, utilities of VGAM2435 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254778. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2436 (VGAM2436) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[82553] VGAM2436 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2436 was detected is described hereinabove with reference to Figs. 1-8.

[82554] VGAM2436 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus.
VGAM2436 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82555] VGAM2436 gene encodes a VGAM2436 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2436 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2436 precursor RNA is designated SEQ ID:2422, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2422 is located at position 79755 relative to the genome of Goatpox Virus.

[82556] VGAM2436 precursor RNA folds onto itself, forming VGAM2436 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82557] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2436 folded precursor RNA into VGAM2436 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 66%) nucleotide sequence of VGAM2436 RNA is designated SEQ ID:5147, and is provided hereinbelow with reference to the sequence listing part.

[82558] VGAM2436 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2436 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2436 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82559] VGAM2436 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2436 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2436 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2436 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2436 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82560] The complementary binding of VGAM2436 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2436 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2436 host target RNA into VGAM2436 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82561] It is appreciated that VGAM2436 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2436 host target genes. The mRNA of each one of this plurality of VGAM2436 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2436 RNA, herein designated VGAM RNA, and which when bound by VGAM2436 RNA causes inhibition of translation of respective one or more VGAM2436 host target proteins.

[82562] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2436 gene, herein designated VGAM GENE, on one or more VGAM2436 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82563] It is yet further appreciated that a function of VGAM2436 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2436 correlate with, and may be deduced from, the identity of the host target genes which VGAM2436 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82564] Nucleotide sequences of the VGAM2436 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2436 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2436 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2436 are further described hereinbelow with reference to Table 1.

[82565] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2436 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2436 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82566] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2436 gene, herein designated VGAM is inhibition of expression of VGAM2436 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2436 correlate with, and may be deduced from, the identity of the target genes which VGAM2436 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82567] Glutamate Receptor, Metabotropic 1 (GRM1, Accession NM_000838) is a VGAM2436 host target gene. GRM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRM1 BINDING SITE, designated SEQ ID:6499, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82568] A function of VGAM2436 is therefore inhibition of Gluta-

mate Receptor, Metabotropic 1 (GRM1, Accession NM_000838), a gene which promotes phosphoinositide hydrolysis. Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRM1. The function of GRM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM786.Inositol Hexaphosphate Kinase 3 (IHPK3, Accession NM_054111) is another VGAM2436 host target gene. IHPK3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IHPK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IHPK3 BINDING SITE, designated SEQ ID:27660, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82569] Another function of VGAM2436 is therefore inhibition of Inositol Hexaphosphate Kinase 3 (IHPK3, Accession NM_054111). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IHPK3. Paired-like Home-

odomain Transcription Factor 2 (PITX2, Accession NM_000325) is another VGAM2436 host target gene. PITX2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PITX2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PITX2 BINDING SITE, designated SEQ ID:5868, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82570] Another function of VGAM2436 is therefore inhibition of Paired-like Homeodomain Transcription Factor 2 (PITX2, Accession NM_000325). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PITX2. CEP3 (Accession NM_006449) is another VGAM2436 host target gene. CEP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CEP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CEP3 BINDING SITE, designated SEQ ID:13157, to the nucleotide sequence of VGAM2436 RNA,

herein designated VGAM RNA, also designated SEQ ID:5147.

[82571] Another function of VGAM2436 is therefore inhibition of CEP3 (Accession NM_006449). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CEP3. CCR4-NOT Transcription Complex, Subunit 7 (CNOT7, Accession NM_013354) is another VGAM2436 host target gene. CNOT7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNOT7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNOT7 BINDING SITE, designated SEQ ID:15000, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82572] Another function of VGAM2436 is therefore inhibition of CCR4-NOT Transcription Complex, Subunit 7 (CNOT7, Accession NM_013354). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNOT7. FLJ14440 (Accession NM_032784) is another VGAM2436

host target gene. FLJ14440 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14440, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14440 BINDING SITE, designated SEQ ID:26531, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82573] Another function of VGAM2436 is therefore inhibition of FLJ14440 (Accession NM_032784). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14440. GT650 (Accession NM_052851) is another VGAM2436 host target gene. GT650 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GT650, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GT650 BINDING SITE, designated SEQ ID:27432, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82574] Another function of VGAM2436 is therefore inhibition of GT650 (Accession NM_052851). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GT650. KIAA0332 (Accession XM_031553) is another VGAM2436 host target gene. KIAA0332 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0332, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0332 BINDING SITE, designated SEQ ID:31422, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82575] Another function of VGAM2436 is therefore inhibition of KIAA0332 (Accession XM_031553). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0332. KIAA1458 (Accession XM_044434) is another VGAM2436 host target gene. KIAA1458 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1458, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1458 BINDING SITE, designated SEQ ID:34205, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82576] Another function of VGAM2436 is therefore inhibition of KIAA1458 (Accession XM_044434). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1458. KIAA1813 (Accession XM_046743) is another VGAM2436 host target gene. KIAA1813 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1813, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1813 BINDING SITE, designated SEQ ID:34814, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82577] Another function of VGAM2436 is therefore inhibition of KIAA1813 (Accession XM_046743). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1813. MGC16703 (Accession XM_054591) is another VGAM2436 host target gene. MGC16703 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC16703, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16703 BINDING SITE, designated SEQ ID:36180, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82578] Another function of VGAM2436 is therefore inhibition of MGC16703 (Accession XM_054591). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16703. PRO0255 (Accession NM_014124) is another VGAM2436 host target gene. PRO0255 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO0255, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0255 BINDING SITE, designated SEQ ID:15383, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM

RNA, also designated SEQ ID:5147.

[82579] Another function of VGAM2436 is therefore inhibition of PRO0255 (Accession NM_014124). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0255. LOC162239 (Accession XM_091439) is another VGAM2436 host target gene. LOC162239 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC162239, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC162239 BINDING SITE, designated SEQ ID:40054, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82580] Another function of VGAM2436 is therefore inhibition of LOC162239 (Accession XM_091439). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC162239. LOC254848 (Accession XM_173133) is another VGAM2436 host target gene. LOC254848 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254848, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254848 BINDING SITE, designated SEQ ID:46383, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82581] Another function of VGAM2436 is therefore inhibition of LOC254848 (Accession XM_173133). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254848. LOC257443 (Accession XM_171072) is another VGAM2436 host target gene. LOC257443 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257443, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257443 BINDING SITE, designated SEQ ID:45873, to the nucleotide sequence of VGAM2436 RNA, herein designated VGAM RNA, also designated SEQ ID:5147.

[82582] Another function of VGAM2436 is therefore inhibition of LOC257443 (Accession XM_171072). Accordingly, utilities of VGAM2436 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC257443. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2437 (VGAM2437) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82583] VGAM2437 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2437 was detected is described hereinabove with reference to Figs. 1-8.

[82584] VGAM2437 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2437 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82585] VGAM2437 gene encodes a VGAM2437 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2437 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2437 precursor RNA is desig-

nated SEQ ID:2423, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2423 is located at position 32976 relative to the genome of Goatpox Virus.

[82586] VGAM2437 precursor RNA folds onto itself, forming VGAM2437 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82587] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2437 folded precursor RNA into VGAM2437 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2437 RNA is designated SEQ ID:5148, and is provided hereinbelow with reference to the sequence

listing part.

[82588] VGAM2437 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2437 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2437 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82589] VGAM2437 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2437 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2437 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2437 RNA, herein designated VGAM RNA, may

have a different number of host target binding sites in untranslated regions of a VGAM2437 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82590] The complementary binding of VGAM2437 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2437 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2437 host target RNA into VGAM2437 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82591] It is appreciated that VGAM2437 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2437 host target genes. The mRNA of each one of this plurality of VGAM2437 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2437 RNA, herein designated VGAM

RNA, and which when bound by VGAM2437 RNA causes inhibition of translation of respective one or more VGAM2437 host target proteins.

[82592] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2437 gene, herein designated VGAM GENE, on one or more VGAM2437 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82593] It is yet further appreciated that a function of VGAM2437 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly,

utilities of VGAM2437 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2437 correlate with, and may be deduced from, the identity of the host target genes which VGAM2437 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82594] Nucleotide sequences of the VGAM2437 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2437 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2437 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2437 are further described hereinbelow with reference to Table 1.

[82595] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2437 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2437 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82596] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2437 gene, herein designated VGAM is

inhibition of expression of VGAM2437 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2437 correlate with, and may be deduced from, the identity of the target genes which VGAM2437 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82597] FLJ23189 (Accession NM_025057) is a VGAM2437 host target gene. FLJ23189 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23189, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23189 BINDING SITE, designated SEQ ID:24658, to the nucleotide sequence of VGAM2437 RNA, herein designated VGAM RNA, also designated SEQ ID:5148.

[82598] A function of VGAM2437 is therefore inhibition of FLJ23189 (Accession NM_025057). Accordingly, utilities of VGAM2437 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23189. PC4 (Accession NM_006713) is another VGAM2437 host target gene. PC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by PC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PC4 BINDING SITE, designated SEQ ID:13540, to the nucleotide sequence of VGAM2437 RNA, herein designated VGAM RNA, also designated SEQ ID:5148.

[82599] Another function of VGAM2437 is therefore inhibition of PC4 (Accession NM_006713). Accordingly, utilities of VGAM2437 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PC4. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2438 (VGAM2438) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82600] VGAM2438 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2438 was detected is described hereinabove with reference to Figs. 1-8.

[82601] VGAM2438 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus.

VGAM2438 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82602] VGAM2438 gene encodes a VGAM2438 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2438 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2438 precursor RNA is designated SEQ ID:2424, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2424 is located at position 88305 relative to the genome of Goatpox Virus.

[82603] VGAM2438 precursor RNA folds onto itself, forming VGAM2438 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82604] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2438 folded precursor RNA into VGAM2438 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2438 RNA is designated SEQ ID:5149, and is provided hereinbelow with reference to the sequence listing part.

[82605] VGAM2438 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2438 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2438 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82606] VGAM2438 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2438 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2438 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2438 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2438 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82607] The complementary binding of VGAM2438 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2438 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2438 host target RNA into VGAM2438 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82608] It is appreciated that VGAM2438 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2438 host target genes. The mRNA of each one of this plurality of VGAM2438 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2438 RNA, herein designated VGAM RNA, and which when bound by VGAM2438 RNA causes inhibition of translation of respective one or more VGAM2438 host target proteins.

[82609] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2438 gene, herein designated VGAM GENE, on one or more VGAM2438 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82610] It is yet further appreciated that a function of VGAM2438 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2438 correlate with, and may be deduced from, the identity of the host target genes which VGAM2438 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82611] Nucleotide sequences of the VGAM2438 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2438 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2438 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2438 are further described hereinbelow with reference to Table 1.

[82612] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2438 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2438 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82613] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2438 gene, herein designated VGAM is inhibition of expression of VGAM2438 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2438 correlate with, and may be deduced from, the identity of the target genes which VGAM2438 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82614] Calcium Channel, Voltage-dependent, L Type, Alpha 1C Subunit (CACNA1C, Accession NM_000719) is a VGAM2438 host target gene. CACNA1C BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CACNA1C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

CACNA1C BINDING SITE, designated SEQ ID:6379, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82615] A function of VGAM2438 is therefore inhibition of Calcium Channel, Voltage-dependent, L Type, Alpha 1C Subunit (CACNA1C, Accession NM_000719), a gene which is alpha-1 subunit of DHP-sensitive calcium channels from cardiac muscle and the brain. Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNA1C. The function of CACNA1C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM182.CREBBP/EP300 Inhibitory Protein 1 (CRI1, Accession NM_014335) is another VGAM2438 host target gene. CRI1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRI1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRI1 BINDING SITE, designated SEQ ID:15648, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5149.

[82616] Another function of VGAM2438 is therefore inhibition of CREBBP/EP300 Inhibitory Protein 1 (CRI1, Accession NM_014335), a gene which regulates cell cycle as well as tissue-specific transcription and differentiation. Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRI1. The function of CRI1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM122.Fibroblast Growth Factor 7 (keratinocyte growth factor) (FGF7, Accession NM_002009) is another VGAM2438 host target gene. FGF7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FGF7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF7 BINDING SITE, designated SEQ ID:7749, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82617] Another function of VGAM2438 is therefore inhibition of Fibroblast Growth Factor 7 (keratinocyte growth factor)

(FGF7, Accession NM_002009), a gene which growth factor active on keratinocytes. Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF7. The function of FGF7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM678.Stearoyl-CoA Desaturase (delta-9-desaturase) (SCD, Accession NM_005063) is another VGAM2438 host target gene. SCD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCD BINDING SITE, designated SEQ ID:11488, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82618] Another function of VGAM2438 is therefore inhibition of Stearoyl-CoA Desaturase (delta-9-desaturase) (SCD, Accession NM_005063), a gene which functions in the synthesis of unsaturated fatty acids. Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with SCD. The function of SCD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM314.FLJ10508 (Accession NM_018118) is another VGAM2438 host target gene. FLJ10508 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10508, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10508 BINDING SITE, designated SEQ ID:19892, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82619] Another function of VGAM2438 is therefore inhibition of FLJ10508 (Accession NM_018118). Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10508. FLJ21106 (Accession NM_025097) is another VGAM2438 host target gene. FLJ21106 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ21106, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21106 BINDING SITE, designated SEQ ID:24735, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82620] Another function of VGAM2438 is therefore inhibition of FLJ21106 (Accession NM_025097). Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21106. KIAA0918 (Accession XM_054869) is another VGAM2438 host target gene. KIAA0918 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0918, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0918 BINDING SITE, designated SEQ ID:36197, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82621] Another function of VGAM2438 is therefore inhibition of KIAA0918 (Accession XM_054869). Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0918. KIAA1750 (Accession XM_043067) is another VGAM2438 host target gene. KIAA1750 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1750, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1750 BINDING SITE, designated SEQ ID:33872, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82622] Another function of VGAM2438 is therefore inhibition of KIAA1750 (Accession XM_043067). Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1750. PC326 (Accession NM_018442) is another VGAM2438 host target gene. PC326 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PC326, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PC326 BINDING SITE, designated SEQ ID:20513, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5149.

[82623] Another function of VGAM2438 is therefore inhibition of PC326 (Accession NM_018442). Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PC326. Signal Transducing Adaptor Molecule (SH3 domain and ITAM motif) 2 (STAM2, Accession NM_005843) is another VGAM2438 host target gene. STAM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STAM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STAM2 BINDING SITE, designated SEQ ID:12458, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82624] Another function of VGAM2438 is therefore inhibition of Signal Transducing Adaptor Molecule (SH3 domain and ITAM motif) 2 (STAM2, Accession NM_005843). Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STAM2. LOC122830 (Accession XM_058661) is another VGAM2438 host target gene. LOC122830 BIND-

ING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC122830, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122830 BINDING SITE, designated SEQ ID:36704, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82625] Another function of VGAM2438 is therefore inhibition of LOC122830 (Accession XM_058661). Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122830. LOC147649 (Accession XM_085830) is another VGAM2438 host target gene. LOC147649 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147649, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147649 BINDING SITE, designated SEQ ID:38355, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82626] Another function of VGAM2438 is therefore inhibition of

LOC147649 (Accession XM_085830). Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147649. LOC158116 (Accession XM_016240) is another VGAM2438 host target gene. LOC158116 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158116, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158116 BINDING SITE, designated SEQ ID:30252, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82627] Another function of VGAM2438 is therefore inhibition of LOC158116 (Accession XM_016240). Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158116. LOC257464 (Accession XM_116972) is another VGAM2438 host target gene. LOC257464 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257464, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC257464 BINDING SITE, designated SEQ ID:43164, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82628] Another function of VGAM2438 is therefore inhibition of LOC257464 (Accession XM_116972). Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257464. LOC90092 (Accession XM_028862) is another VGAM2438 host target gene. LOC90092 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90092 BINDING SITE, designated SEQ ID:30785, to the nucleotide sequence of VGAM2438 RNA, herein designated VGAM RNA, also designated SEQ ID:5149.

[82629] Another function of VGAM2438 is therefore inhibition of LOC90092 (Accession XM_028862). Accordingly, utilities of VGAM2438 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90092. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2439 (VGAM2439) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82630] VGAM2439 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2439 was detected is described hereinabove with reference to Figs. 1-8.

[82631] VGAM2439 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2439 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82632] VGAM2439 gene encodes a VGAM2439 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2439 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2439 precursor RNA is designated SEQ ID:2425, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2425 is located at position 129653 relative to the genome of Goatpox Virus.

[82633] VGAM2439 precursor RNA folds onto itself, forming VGAM2439 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82634] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2439 folded precursor RNA into VGAM2439 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2439 RNA is designated SEQ ID:5150, and is provided hereinbelow with reference to the sequence listing part.

[82635] VGAM2439 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2439 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2439 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82636] VGAM2439 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2439 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2439 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2439 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2439 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82637] The complementary binding of VGAM2439 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2439 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2439 host target RNA into VGAM2439 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82638] It is appreciated that VGAM2439 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2439 host target genes. The mRNA of each one of this plurality of VGAM2439 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2439 RNA, herein designated VGAM RNA, and which when bound by VGAM2439 RNA causes inhibition of translation of respective one or more

VGAM2439 host target proteins.

[82639] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2439 gene, herein designated VGAM GENE, on one or more VGAM2439 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82640] It is yet further appreciated that a function of VGAM2439 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2439 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific

functions, and accordingly utilities, of VGAM2439 correlate with, and may be deduced from, the identity of the host target genes which VGAM2439 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82641] Nucleotide sequences of the VGAM2439 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2439 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2439 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2439 are further described hereinbelow with reference to Table 1.

[82642] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2439 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2439 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82643] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2439 gene, herein designated VGAM is inhibition of expression of VGAM2439 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2439 correlate with, and may be deduced from, the identity of the target genes which VGAM2439 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82644] FK506 Binding Protein 12-rapamycin Associated Protein 1 (FRAP1, Accession NM_004958) is a VGAM2439 host target gene. FRAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FRAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FRAP1 BINDING SITE, designated SEQ ID:11405, to the nucleotide sequence of VGAM2439 RNA, herein designated VGAM RNA, also designated SEQ ID:5150.

[82645] A function of VGAM2439 is therefore inhibition of FK506 Binding Protein 12-rapamycin Associated Protein 1 (FRAP1, Accession NM_004958), a gene which acts as the target for the cell-cycle arrest and immunosuppressive effects of the fkbp12-rapamycin complex. Accordingly, utilities of VGAM2439 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FRAP1. The function of FRAP1 and its association

with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM496.Maltase-glucoamylase (alpha-glucosidase) (MGAM, Accession XM_051351) is another VGAM2439 host target gene. MGAM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGAM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGAM BINDING SITE, designated SEQ ID:35826, to the nucleotide sequence of VGAM2439 RNA, herein designated VGAM RNA, also designated SEQ ID:5150.

[82646] Another function of VGAM2439 is therefore inhibition of Maltase-glucoamylase (alpha-glucosidase) (MGAM, Accession XM_051351), a gene which plays a role in the final steps of digestion of starch. Accordingly, utilities of VGAM2439 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGAM. The function of MGAM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM791.Origin Recognition Complex, Subunit 4-like

(yeast) (ORC4L, Accession XM_030582) is another VGAM2439 host target gene. ORC4L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ORC4L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ORC4L BINDING SITE, designated SEQ ID:31090, to the nucleotide sequence of VGAM2439 RNA, herein designated VGAM RNA, also designated SEQ ID:5150.

[82647] Another function of VGAM2439 is therefore inhibition of Origin Recognition Complex, Subunit 4-like (yeast) (ORC4L, Accession XM_030582), a gene which may be required for initiation of DNA replication and has a putative nucleotide triphosphate binding motif. Accordingly, utilities of VGAM2439 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ORC4L. The function of ORC4L and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM599.6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (PFKFB4, Accession NM_004567) is another

VGAM2439 host target gene. PFKFB4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PFKFB4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PFKFB4 BINDING SITE, designated SEQ ID:10908, to the nucleotide sequence of VGAM2439 RNA, herein designated VGAM RNA, also designated SEQ ID:5150.

[82648] Another function of VGAM2439 is therefore inhibition of 6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4 (PFKFB4, Accession NM_004567), a gene which catalizes synthesis and degradation of fructose 2,6-bisphosphate. Accordingly, utilities of VGAM2439 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PFKFB4. The function of PFKFB4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1316.RIG (Accession NM_006394) is another VGAM2439 host target gene. RIG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RIG, corresponding to a HOST TARGET binding site such

as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RIG BINDING SITE, designated SEQ ID:13104, to the nucleotide sequence of VGAM2439 RNA, herein designated VGAM RNA, also designated SEQ ID:5150.

[82649] Another function of VGAM2439 is therefore inhibition of RIG (Accession NM_006394), a gene which is ribosomal protein S15. Accordingly, utilities of VGAM2439 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RIG. The function of RIG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.ATP-binding Cassette, Sub-family C (CFTR/MRP), Member 13 (ABCC13, Accession NM_138726) is another VGAM2439 host target gene. ABCC13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ABCC13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCC13 BINDING SITE, designated SEQ ID:28971, to the nucleotide sequence of VGAM2439 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5150.

[82650] Another function of VGAM2439 is therefore inhibition of ATP-binding Cassette, Sub-family C (CFTR/MRP), Member 13 (ABCC13, Accession NM_138726). Accordingly, utilities of VGAM2439 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCC13. PRO1048 (Accession NM_018497) is another VGAM2439 host target gene. PRO1048 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO1048, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1048 BINDING SITE, designated SEQ ID:20560, to the nucleotide sequence of VGAM2439 RNA, herein designated VGAM RNA, also designated SEQ ID:5150.

[82651] Another function of VGAM2439 is therefore inhibition of PRO1048 (Accession NM_018497). Accordingly, utilities of VGAM2439 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1048. LOC81537 (Accession NM_030791) is another VGAM2439 host target gene. LOC81537 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC81537, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC81537 BINDING SITE, designated SEQ ID:25088, to the nucleotide sequence of VGAM2439 RNA, herein designated VGAM RNA, also designated SEQ ID:5150.

[82652] Another function of VGAM2439 is therefore inhibition of LOC81537 (Accession NM_030791). Accordingly, utilities of VGAM2439 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC81537. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2440 (VGAM2440) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82653] VGAM2440 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2440 was detected is described hereinabove with reference to Figs. 1-8.

[82654] VGAM2440 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Goatpox Virus. VGAM2440 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82655] VGAM2440 gene encodes a VGAM2440 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2440 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2440 precursor RNA is designated SEQ ID:2426, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2426 is located at position 54822 relative to the genome of Goatpox Virus.

[82656] VGAM2440 precursor RNA folds onto itself, forming VGAM2440 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82657] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2440 folded precursor RNA into VGAM2440 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2440 RNA is designated SEQ ID:5151, and is provided hereinbelow with reference to the sequence listing part.

[82658] VGAM2440 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2440 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2440 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82659] VGAM2440 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2440 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2440 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2440 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2440 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82660] The complementary binding of VGAM2440 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2440 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2440

host target RNA into VGAM2440 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82661] It is appreciated that VGAM2440 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2440 host target genes. The mRNA of each one of this plurality of VGAM2440 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2440 RNA, herein designated VGAM RNA, and which when bound by VGAM2440 RNA causes inhibition of translation of respective one or more VGAM2440 host target proteins.

[82662] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2440 gene, herein designated VGAM GENE, on one or more VGAM2440 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82663] It is yet further appreciated that a function of VGAM2440 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2440 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2440 correlate with, and may be deduced from, the identity of the host target genes which VGAM2440 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82664] Nucleotide sequences of the VGAM2440 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2440 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2440 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2440 are further

described hereinbelow with reference to Table 1.

[82665] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2440 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2440 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82666] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2440 gene, herein designated VGAM is inhibition of expression of VGAM2440 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2440 correlate with, and may be deduced from, the identity of the target genes which VGAM2440 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82667] Kruppel-like Factor 5 (intestinal) (KLF5, Accession NM_001730) is a VGAM2440 host target gene. KLF5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KLF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KLF5

BINDING SITE, designated SEQ ID:7461, to the nucleotide sequence of VGAM2440 RNA, herein designated VGAM RNA, also designated SEQ ID:5151.

[82668] A function of VGAM2440 is therefore inhibition of Kruppel-like Factor 5 (intestinal) (KLF5, Accession NM_001730). Accordingly, utilities of VGAM2440 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KLF5. MAP Kinase-interacting Serine/threonine Kinase 1 (MKNK1, Accession NM_003684) is another VGAM2440 host target gene. MKNK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MKNK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MKNK1 BINDING SITE, designated SEQ ID:9791, to the nucleotide sequence of VGAM2440 RNA, herein designated VGAM RNA, also designated SEQ ID:5151.

[82669] Another function of VGAM2440 is therefore inhibition of MAP Kinase-interacting Serine/threonine Kinase 1 (MKNK1, Accession NM_003684). Accordingly, utilities of VGAM2440 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with MKNK1. Musculin (activated B-cell factor-1) (MSC, Accession XM_084266) is another VGAM2440 host target gene. MSC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MSC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MSC BINDING SITE, designated SEQ ID:37534, to the nucleotide sequence of VGAM2440 RNA, herein designated VGAM RNA, also designated SEQ ID:5151.

[82670] Another function of VGAM2440 is therefore inhibition of Musculin (activated B-cell factor-1) (MSC, Accession XM_084266). Accordingly, utilities of VGAM2440 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MSC. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2441 (VGAM2441) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82671] VGAM2441 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2441 was detected is described hereinabove with reference to Figs. 1-8.

[82672] VGAM2441 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2441 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82673] VGAM2441 gene encodes a VGAM2441 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2441 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2441 precursor RNA is designated SEQ ID:2427, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2427 is located at position 482 relative to the genome of Goatpox Virus.

[82674] VGAM2441 precursor RNA folds onto itself, forming VGAM2441 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82675] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2441 folded precursor RNA into VGAM2441 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2441 RNA is designated SEQ ID:5152, and is provided hereinbelow with reference to the sequence listing part.

[82676] VGAM2441 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2441 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2441 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82677] VGAM2441 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2441 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2441 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2441 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2441 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82678] The complementary binding of VGAM2441 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2441 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2441 host target RNA into VGAM2441 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82679] It is appreciated that VGAM2441 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2441 host target genes. The mRNA of each one of this plurality of VGAM2441 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2441 RNA, herein designated VGAM RNA, and which when bound by VGAM2441 RNA causes inhibition of translation of respective one or more VGAM2441 host target proteins.

[82680] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2441 gene, herein designated VGAM GENE, on one or more VGAM2441 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82681] It is yet further appreciated that a function of VGAM2441 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2441 correlate with, and may be deduced from, the identity of the host target genes which VGAM2441 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82682] Nucleotide sequences of the VGAM2441 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2441 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2441 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2441 are further described hereinbelow with reference to Table 1.

[82683] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2441 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2441 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82684] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2441 gene, herein designated VGAM is inhibition of expression of VGAM2441 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2441 correlate with, and may be deduced from, the identity of the target genes which VGAM2441 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82685] Cartilage Associated Protein (CRTAP, Accession NM_006371) is a VGAM2441 host target gene. CRTAP BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by CRTAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CRTAP BINDING SITE, designated SEQ ID:13058, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82686] A function of VGAM2441 is therefore inhibition of Cartilage Associated Protein (CRTAP, Accession NM_006371), a gene which is a novel developmentally regulated chick embryo protein. Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRTAP. The function of CRTAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.Hippocalcin-like 1 (HPCAL1, Accession NM_134421) is another VGAM2441 host target gene. HPCAL1 BINDING SITE1 and HPCAL1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HPCAL1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementar-

ity of the nucleotide sequences of HPCAL1 BINDING SITE1 and HPCAL1 BINDING SITE2, designated SEQ ID:28636 and SEQ ID:7929 respectively, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82687] Another function of VGAM2441 is therefore inhibition of Hippocalcin-like 1 (HPCAL1, Accession NM_134421). Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HPCAL1. Aminopeptidase Puromycin Sensitive (NPEPPS, Accession NM_006310) is another VGAM2441 host target gene. NPEPPS BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NPEPPS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPEPPS BINDING SITE, designated SEQ ID:13000, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82688] Another function of VGAM2441 is therefore inhibition of Aminopeptidase Puromycin Sensitive (NPEPPS, Accession NM_006310), a gene which is puromycin-sensitive

aminopeptidase and has metallopeptidase activity. Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPEPPS. The function of NPEPPS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM83.Protocadherin 9 (PCDH9, Accession XM_096054) is another VGAM2441 host target gene. PCDH9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PCDH9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH9 BINDING SITE, designated SEQ ID:40292, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82689] Another function of VGAM2441 is therefore inhibition of Protocadherin 9 (PCDH9, Accession XM_096054). Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH9. Single-minded Homolog 1 (Drosophila) (SIM1, Accession NM_005068) is another VGAM2441 host

target gene. SIM1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SIM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIM1 BINDING SITE, designated SEQ ID:11506, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82690] Another function of VGAM2441 is therefore inhibition of Single-minded Homolog 1 (Drosophila) (SIM1, Accession NM_005068), a gene which may have pleiotropic effects during embryogenesis and in the adult. Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIM1. The function of SIM1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM665.Transforming Growth Factor, Alpha (TGFA, Accession NM_003236) is another VGAM2441 host target gene. TGFA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TGFA, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TGFA BINDING SITE, designated SEQ ID:9228, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82691] Another function of VGAM2441 is therefore inhibition of Transforming Growth Factor, Alpha (TGFA, Accession NM_003236), a gene which is able to bind to the egf receptor and to act synergistically with tgf beta to promote anchorage-independent cell proliferation in soft agar. Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TGFA. The function of TGFA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM328.Zinc Finger Protein 265 (ZNF265, Accession NM_005455) is another VGAM2441 host target gene. ZNF265 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ZNF265, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of ZNF265 BINDING SITE, designated SEQ ID:11938, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82692] Another function of VGAM2441 is therefore inhibition of Zinc Finger Protein 265 (ZNF265, Accession NM_005455). Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF265. FLJ11618 (Accession NM_022452) is another VGAM2441 host target gene. FLJ11618 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11618, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11618 BINDING SITE, designated SEQ ID:22789, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82693] Another function of VGAM2441 is therefore inhibition of FLJ11618 (Accession NM_022452). Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ11618. FLJ20651 (Accession NM_017919) is another VGAM2441 host target gene. FLJ20651 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20651, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20651 BINDING SITE, designated SEQ ID:19572, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82694] Another function of VGAM2441 is therefore inhibition of FLJ20651 (Accession NM_017919). Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20651. KIAA0379 (Accession XM_042860) is another VGAM2441 host target gene. KIAA0379 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0379, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0379 BINDING SITE, designated SEQ ID:33809, to the nucleotide sequence of VGAM2441 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5152.

[82695] Another function of VGAM2441 is therefore inhibition of KIAA0379 (Accession XM_042860). Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0379. KIAA1610 (Accession XM_040622) is another VGAM2441 host target gene. KIAA1610 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1610, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1610 BINDING SITE, designated SEQ ID:33341, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82696] Another function of VGAM2441 is therefore inhibition of KIAA1610 (Accession XM_040622). Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1610. PRO1048 (Accession NM_018497) is another VGAM2441 host target gene. PRO1048 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO1048, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1048 BINDING SITE, designated SEQ ID:20555, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82697] Another function of VGAM2441 is therefore inhibition of PRO1048 (Accession NM_018497). Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1048. LOC197319 (Accession XM_113862) is another VGAM2441 host target gene. LOC197319 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC197319, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197319 BINDING SITE, designated SEQ ID:42473, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82698] Another function of VGAM2441 is therefore inhibition of LOC197319 (Accession XM_113862). Accordingly, utilities of VGAM2441 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC197319. LOC90591 (Accession XM_032811) is another VGAM2441 host target gene. LOC90591 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90591, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90591 BINDING SITE, designated SEQ ID:31757, to the nucleotide sequence of VGAM2441 RNA, herein designated VGAM RNA, also designated SEQ ID:5152.

[82699] Another function of VGAM2441 is therefore inhibition of LOC90591 (Accession XM_032811). Accordingly, utilities of VGAM2441 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90591. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2442 (VGAM2442) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82700] VGAM2442 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2442 was detected is described hereinabove with reference to Figs. 1-8.

[82701] VGAM2442 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Goatpox Virus. VGAM2442 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82702] VGAM2442 gene encodes a VGAM2442 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2442 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2442 precursor RNA is designated SEQ ID:2428, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2428 is located at position 110320 relative to the genome of Goatpox Virus.

[82703] VGAM2442 precursor RNA folds onto itself, forming VGAM2442 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82704] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2442 folded precursor RNA into VGAM2442 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2442 RNA is designated SEQ ID:5153, and is provided hereinbelow with reference to the sequence listing part.

[82705] VGAM2442 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2442 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2442 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82706] VGAM2442 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2442 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2442 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2442 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2442 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82707] The complementary binding of VGAM2442 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2442 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2442 host target RNA into VGAM2442 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82708] It is appreciated that VGAM2442 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2442 host target genes. The mRNA of each one of this plurality of VGAM2442 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2442 RNA, herein designated VGAM RNA, and which when bound by VGAM2442 RNA causes inhibition of translation of respective one or more VGAM2442 host target proteins.

[82709] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2442 gene, herein designated VGAM GENE, on one or more VGAM2442 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82710] It is yet further appreciated that a function of VGAM2442 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2442 include diagnosis, prevention and treatment of viral infection by Goatpox Virus. Specific functions, and accordingly utilities, of VGAM2442 correlate with, and may be deduced from, the identity of the host target genes which VGAM2442 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82711] Nucleotide sequences of the VGAM2442 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2442 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2442 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2442 are further described hereinbelow with reference to Table 1.

[82712] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2442 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2442 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82713] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2442 gene, herein designated VGAM is inhibition of expression of VGAM2442 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2442 correlate with, and may be deduced from, the identity of the target genes which VGAM2442 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82714] DKFZp434A2417 (Accession XM_038526) is a VGAM2442 host target gene. DKFZp434A2417 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by DKFZp434A2417, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434A2417 BINDING SITE, designated SEQ ID:32861, to the nucleotide sequence of VGAM2442 RNA, herein designated VGAM RNA, also designated SEQ ID:5153.

[82715] A function of VGAM2442 is therefore inhibition of DKFZp434A2417 (Accession XM_038526). Accordingly, utilities of VGAM2442 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434A2417. MacGAP (Accession NM_033515) is another VGAM2442 host target gene. MacGAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MacGAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MacGAP BINDING SITE, designated SEQ ID:27287, to the nucleotide sequence of VGAM2442 RNA, herein designated VGAM RNA, also designated SEQ ID:5153.

[82716] Another function of VGAM2442 is therefore inhibition of MacGAP (Accession NM_033515). Accordingly, utilities of

VGAM2442 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MacGAP. PYGO1 (Accession XM_090986) is another VGAM2442 host target gene. PYGO1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PYGO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PYGO1 BINDING SITE, designated SEQ ID:40022, to the nucleotide sequence of VGAM2442 RNA, herein designated VGAM RNA, also designated SEQ ID:5153.

[82717] Another function of VGAM2442 is therefore inhibition of PYGO1 (Accession XM_090986). Accordingly, utilities of VGAM2442 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PYGO1. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2443 (VGAM2443) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82718] VGAM2443 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2443 was detected is described hereinabove with reference to Figs. 1-8.

[82719] VGAM2443 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2443 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82720] VGAM2443 gene encodes a VGAM2443 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2443 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2443 precursor RNA is designated SEQ ID:2429, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2429 is located at position 167632 relative to the genome of Mouse Cytomegalovirus 1.

[82721] VGAM2443 precursor RNA folds onto itself, forming VGAM2443 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82722] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2443 folded precursor RNA into VGAM2443 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 70%) nucleotide sequence of VGAM2443 RNA is designated SEQ ID:5154, and is provided hereinbelow with reference to the sequence listing part.

[82723] VGAM2443 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2443 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2443 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82724] VGAM2443 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2443 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2443 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2443 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2443 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82725] The complementary binding of VGAM2443 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2443 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2443 host target RNA into VGAM2443 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82726] It is appreciated that VGAM2443 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2443 host target genes. The mRNA of each one of this plurality of VGAM2443 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2443 RNA, herein designated VGAM RNA, and which when bound by VGAM2443 RNA causes inhibition of translation of respective one or more VGAM2443 host target proteins.

[82727] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2443 gene, herein designated VGAM GENE, on one or more VGAM2443 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82728] It is yet further appreciated that a function of VGAM2443 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2443 correlate with, and may be deduced from, the identity of the host target genes which VGAM2443 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82729] Nucleotide sequences of the VGAM2443 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2443 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2443 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2443 are further described hereinbelow with reference to Table 1.

[82730] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2443 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2443 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82731] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2443 gene, herein designated VGAM is inhibition of expression of VGAM2443 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2443 correlate with, and may be deduced from, the identity of the target genes which VGAM2443 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82732] EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838) is a VGAM2443 host target gene. EGFL5 BINDING SITE is HOST TARGET binding site found in the

5` untranslated region of mRNA encoded by EGFL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGFL5 BINDING SITE, designated SEQ ID:41880, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82733] A function of VGAM2443 is therefore inhibition of EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGFL5. Eukaryotic Translation Initiation Factor 2C, 1 (EIF2C1, Accession NM_012199) is another VGAM2443 host target gene. EIF2C1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EIF2C1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EIF2C1 BINDING SITE, designated SEQ ID:14501, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82734] Another function of VGAM2443 is therefore inhibition of

Eukaryotic Translation Initiation Factor 2C, 1 (EIF2C1, Accession NM_012199), a gene which plays an important role in the eukaryotic peptide chain initiation process. Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EIF2C1. The function of EIF2C1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM118.Insulin Receptor Substrate 2 (IRS2, Accession XM_007095) is another VGAM2443 host target gene. IRS2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IRS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRS2 BINDING SITE, designated SEQ ID:30030, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82735] Another function of VGAM2443 is therefore inhibition of Insulin Receptor Substrate 2 (IRS2, Accession XM_007095), a gene which may mediate the control of various cellular processes by insulin. Accordingly, utilities

of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRS2. The function of IRS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1217.Potassium Inwardly-rectifying Channel, Subfamily J, Member 6 (KCNJ6, Accession NM_002240) is another VGAM2443 host target gene. KCNJ6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCNJ6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNJ6 BINDING SITE, designated SEQ ID:8022, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82736] Another function of VGAM2443 is therefore inhibition of Potassium Inwardly-rectifying Channel, Subfamily J, Member 6 (KCNJ6, Accession NM_002240), a gene which may be involved in the regulation of insulin secretion by glucose and/or neurotransmitters. Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNJ6.

The function of KCNJ6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2155.Mitogen-activated Protein Kinase Kinase Kinase 7 Interacting Protein 2 (MAP3K7IP2, Accession NM_015093) is another VGAM2443 host target gene. MAP3K7IP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAP3K7IP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAP3K7IP2 BINDING SITE, designated SEQ ID:17484, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82737] Another function of VGAM2443 is therefore inhibition of Mitogen-activated Protein Kinase Kinase Kinase 7 Interacting Protein 2 (MAP3K7IP2, Accession NM_015093). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAP3K7IP2. Retinoic Acid Induced 3 (RAI3, Accession NM_003979) is another VGAM2443 host target gene. RAI3 BINDING SITE is HOST TARGET binding

site found in the 3` untranslated region of mRNA encoded by RAI3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAI3 BINDING SITE, designated SEQ ID:10112, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82738] Another function of VGAM2443 is therefore inhibition of Retinoic Acid Induced 3 (RAI3, Accession NM_003979). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAI3. Stanniocalcin 1 (STC1, Accession NM_003155) is another VGAM2443 host target gene. STC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STC1 BINDING SITE, designated SEQ ID:9132, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82739] Another function of VGAM2443 is therefore inhibition of

Stanniocalcin 1 (STC1, Accession NM_003155), a gene which stimulates renal phosphate reabsorption, and could therefore prevent hypercalcemia. Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STC1. The function of STC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM623.Angiomotin (AMOT, Accession NM_133265) is another VGAM2443 host target gene. AMOT BINDING SITE1 and AMOT BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AMOT, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AMOT BINDING SITE1 and AMOT BINDING SITE2, designated SEQ ID:28408 and SEQ ID:28409 respectively, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82740] Another function of VGAM2443 is therefore inhibition of Angiomotin (AMOT, Accession NM_133265). Accordingly, utilities of VGAM2443 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with AMOT. DKFZP434J046 (Accession XM_048258) is another VGAM2443 host target gene. DKFZP434J046 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434J046, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434J046 BINDING SITE, designated SEQ ID:35151, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82741] Another function of VGAM2443 is therefore inhibition of DKFZP434J046 (Accession XM_048258). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434J046. FLJ12505 (Accession NM_024749) is another VGAM2443 host target gene. FLJ12505 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12505, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

FLJ12505 BINDING SITE, designated SEQ ID:24092, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82742] Another function of VGAM2443 is therefore inhibition of FLJ12505 (Accession NM_024749). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12505. KIAA0182 (Accession XM_050495) is another VGAM2443 host target gene. KIAA0182 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0182, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0182 BINDING SITE, designated SEQ ID:35644, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82743] Another function of VGAM2443 is therefore inhibition of KIAA0182 (Accession XM_050495). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0182. KIAA1028 (Accession XM_166324) is another VGAM2443 host target gene. KIAA1028 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1028, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1028 BINDING SITE, designated SEQ ID:44159, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82744] Another function of VGAM2443 is therefore inhibition of KIAA1028 (Accession XM_166324). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1028. KIAA1416 (Accession XM_098762) is another VGAM2443 host target gene. KIAA1416 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1416 BINDING SITE, designated SEQ ID:41800, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82745] Another function of VGAM2443 is therefore inhibition of

KIAA1416 (Accession XM_098762). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1416. Mitogen-activated Protein Kinase-activated Protein Kinase 2 (MAPKAPK2, Accession NM_004759) is another VGAM2443 host target gene. MAPKAPK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAPKAPK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPKAPK2 BINDING SITE, designated SEQ ID:11149, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82746] Another function of VGAM2443 is therefore inhibition of Mitogen-activated Protein Kinase-activated Protein Kinase 2 (MAPKAPK2, Accession NM_004759). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPKAPK2. SP329 (Accession NM_030793) is another VGAM2443 host target gene. SP329 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SP329, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SP329 BINDING SITE, designated SEQ ID:25095, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82747] Another function of VGAM2443 is therefore inhibition of SP329 (Accession NM_030793). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SP329. Three Prime Repair Exonuclease 1 (TREX1, Accession NM_033627) is another VGAM2443 host target gene. TREX1 BINDING SITE1 and TREX1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by TREX1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TREX1 BINDING SITE1 and TREX1 BINDING SITE2, designated SEQ ID:27337 and SEQ ID:27346 respectively, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82748] Another function of VGAM2443 is therefore inhibition of

Three Prime Repair Exonuclease 1 (TREX1, Accession NM_033627). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TREX1. LOC150197 (Accession XM_086801) is another VGAM2443 host target gene. LOC150197 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150197, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150197 BINDING SITE, designated SEQ ID:38865, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82749] Another function of VGAM2443 is therefore inhibition of LOC150197 (Accession XM_086801). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150197. LOC219894 (Accession XM_167782) is another VGAM2443 host target gene. LOC219894 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219894, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219894 BINDING SITE, designated SEQ ID:44795, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82750] Another function of VGAM2443 is therefore inhibition of LOC219894 (Accession XM_167782). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219894. LOC222484 (Accession XM_169424) is another VGAM2443 host target gene. LOC222484 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222484, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222484 BINDING SITE, designated SEQ ID:45298, to the nucleotide sequence of VGAM2443 RNA, herein designated VGAM RNA, also designated SEQ ID:5154.

[82751] Another function of VGAM2443 is therefore inhibition of LOC222484 (Accession XM_169424). Accordingly, utilities of VGAM2443 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC222484. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2444 (VGAM2444) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82752] VGAM2444 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2444 was detected is described hereinabove with reference to Figs. 1-8.

[82753] VGAM2444 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2444 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82754] VGAM2444 gene encodes a VGAM2444 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2444 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2444 precursor RNA is designated SEQ ID:2430, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2430 is located at position 180574 relative to the genome of Mouse Cytomegalovirus 1.

[82755] VGAM2444 precursor RNA folds onto itself, forming VGAM2444 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82756] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2444 folded precursor RNA into VGAM2444 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 64%) nucleotide sequence of VGAM2444 RNA is designated SEQ ID:5155, and is provided hereinbelow with reference to the sequence listing part.

[82757] VGAM2444 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2444 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2444 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82758] VGAM2444 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2444 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2444 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2444 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2444 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82759] The complementary binding of VGAM2444 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2444 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2444 host target RNA into VGAM2444 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82760] It is appreciated that VGAM2444 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2444 host target genes. The mRNA of each one of this plurality of VGAM2444 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2444 RNA, herein designated VGAM RNA, and which when bound by VGAM2444 RNA causes

inhibition of translation of respective one or more VGAM2444 host target proteins.

[82761] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2444 gene, herein designated VGAM GENE, on one or more VGAM2444 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82762] It is yet further appreciated that a function of VGAM2444 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2444 include diagnosis, prevention and

treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2444 correlate with, and may be deduced from, the identity of the host target genes which VGAM2444 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82763] Nucleotide sequences of the VGAM2444 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2444 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2444 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2444 are further described hereinbelow with reference to Table 1.

[82764] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2444 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2444 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82765] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2444 gene, herein designated VGAM is inhibition of expression of VGAM2444 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2444 correlate with, and may be deduced from, the identity of the target genes which VGAM2444 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82766] Dual Specificity Phosphatase 1 (DUSP1, Accession NM_004417) is a VGAM2444 host target gene. DUSP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DUSP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DUSP1 BINDING SITE, designated SEQ ID:10681, to the nucleotide sequence of VGAM2444 RNA, herein designated VGAM RNA, also designated SEQ ID:5155.

[82767] A function of VGAM2444 is therefore inhibition of Dual Specificity Phosphatase 1 (DUSP1, Accession NM_004417), a gene which is a dual specificity phosphatase . Accordingly, utilities of VGAM2444 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP1. The function of DUSP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described here-

inabove with reference to VGAM881.DKFZP572C163 (Accession XM_028314) is another VGAM2444 host target gene. DKFZP572C163 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP572C163, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP572C163 BINDING SITE, designated SEQ ID:30656, to the nucleotide sequence of VGAM2444 RNA, herein designated VGAM RNA, also designated SEQ ID:5155.

[82768] Another function of VGAM2444 is therefore inhibition of DKFZP572C163 (Accession XM_028314). Accordingly, utilities of VGAM2444 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP572C163. EFA6R (Accession NM_015310) is another VGAM2444 host target gene. EFA6R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EFA6R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFA6R BINDING SITE, designated SEQ ID:17620, to the nucleotide se-

quence of VGAM2444 RNA, herein designated VGAM RNA, also designated SEQ ID:5155.

[82769] Another function of VGAM2444 is therefore inhibition of EFA6R (Accession NM_015310). Accordingly, utilities of VGAM2444 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFA6R. ERAP140 (Accession XM_059748) is another VGAM2444 host target gene. ERAP140 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERAP140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERAP140 BINDING SITE, designated SEQ ID:37081, to the nucleotide sequence of VGAM2444 RNA, herein designated VGAM RNA, also designated SEQ ID:5155.

[82770] Another function of VGAM2444 is therefore inhibition of ERAP140 (Accession XM_059748). Accordingly, utilities of VGAM2444 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERAP140. FLJ20413 (Accession NM_017808) is another VGAM2444 host target gene. FLJ20413 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ20413, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20413 BINDING SITE, designated SEQ ID:19450, to the nucleotide sequence of VGAM2444 RNA, herein designated VGAM RNA, also designated SEQ ID:5155.

[82771] Another function of VGAM2444 is therefore inhibition of FLJ20413 (Accession NM_017808). Accordingly, utilities of VGAM2444 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20413. LOC160156 (Accession XM_090047) is another VGAM2444 host target gene. LOC160156 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC160156, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC160156 BINDING SITE, designated SEQ ID:39989, to the nucleotide sequence of VGAM2444 RNA, herein designated VGAM RNA, also designated SEQ ID:5155.

[82772] Another function of VGAM2444 is therefore inhibition of LOC160156 (Accession XM_090047). Accordingly, utilities

of VGAM2444 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC160156. LOC169966 (Accession XM_093010) is another VGAM2444 host target gene. LOC169966 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC169966, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169966 BINDING SITE, designated SEQ ID:40164, to the nucleotide sequence of VGAM2444 RNA, herein designated VGAM RNA, also designated SEQ ID:5155.

[82773] Another function of VGAM2444 is therefore inhibition of LOC169966 (Accession XM_093010). Accordingly, utilities of VGAM2444 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169966. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2445 (VGAM2445) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82774] VGAM2445 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2445 was detected is described hereinabove with reference to Figs. 1-8.

[82775] VGAM2445 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2445 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82776] VGAM2445 gene encodes a VGAM2445 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2445 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2445 precursor RNA is designated SEQ ID:2431, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2431 is located at position 13050 relative to the genome of Mouse Cytomegalovirus 1.

[82777] VGAM2445 precursor RNA folds onto itself, forming VGAM2445 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the

art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82778] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2445 folded precursor RNA into VGAM2445 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2445 RNA is designated SEQ ID:5156, and is provided hereinbelow with reference to the sequence listing part.

[82779] VGAM2445 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2445 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2445 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated

5`UTR, PROTEIN CODING and 3`UTR respectively.

[82780] VGAM2445 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2445 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2445 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2445 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2445 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82781] The complementary binding of VGAM2445 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2445 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2445 host target RNA into VGAM2445 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82782] It is appreciated that VGAM2445 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2445 host target genes. The mRNA of each one of this plurality of VGAM2445 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2445 RNA, herein designated VGAM RNA, and which when bound by VGAM2445 RNA causes inhibition of translation of respective one or more VGAM2445 host target proteins.

[82783] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2445 gene, herein designated VGAM GENE, on one or more VGAM2445 host target gene, herein designated

VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82784] It is yet further appreciated that a function of VGAM2445 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2445 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2445 correlate with, and may be deduced from, the identity of the host target genes which VGAM2445 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82785] Nucleotide sequences of the VGAM2445 precursor RNA,

herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2445 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2445 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2445 are further described hereinbelow with reference to Table 1.

[82786] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2445 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2445 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82787] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2445 gene, herein designated VGAM is inhibition of expression of VGAM2445 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2445 correlate with, and may be deduced from, the identity of the target genes which VGAM2445 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82788] RAP1A, Member of RAS Oncogene Family (RAP1A, Accession NM_002884) is a VGAM2445 host target gene. RAP1A

BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAP1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAP1A BINDING SITE, designated SEQ ID:8791, to the nucleotide sequence of VGAM2445 RNA, herein designated VGAM RNA, also designated SEQ ID:5156.

[82789] A function of VGAM2445 is therefore inhibition of RAP1A, Member of RAS Oncogene Family (RAP1A, Accession NM_002884), a gene which induces morphological reversion of a cell line transformed by a ras oncogene. Accordingly, utilities of VGAM2445 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAP1A. The function of RAP1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM993.KIAA1033 (Accession XM_035313) is another VGAM2445 host target gene. KIAA1033 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1033, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1033 BINDING SITE, designated SEQ ID:32228, to the nucleotide sequence of VGAM2445 RNA, herein designated VGAM RNA, also designated SEQ ID:5156.

[82790] Another function of VGAM2445 is therefore inhibition of KIAA1033 (Accession XM_035313). Accordingly, utilities of VGAM2445 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1033. Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840) is another VGAM2445 host target gene. PPP1R16B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP1R16B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP1R16B BINDING SITE, designated SEQ ID:30762, to the nucleotide sequence of VGAM2445 RNA, herein designated VGAM RNA, also designated SEQ ID:5156.

[82791] Another function of VGAM2445 is therefore inhibition of Protein Phosphatase 1, Regulatory (inhibitor) Subunit 16B (PPP1R16B, Accession XM_028840). Accordingly, utilities

of VGAM2445 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP1R16B. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2446 (VGAM2446) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82792] VGAM2446 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2446 was detected is described hereinabove with reference to Figs. 1-8.

[82793] VGAM2446 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2446 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82794] VGAM2446 gene encodes a VGAM2446 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2446 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2446 precursor RNA is designated SEQ ID:2432, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2432 is located at position 159425 relative to the genome of Mouse Cytomegalovirus 1.

[82795] VGAM2446 precursor RNA folds onto itself, forming VGAM2446 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82796] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2446 folded precursor RNA into VGAM2446 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 58%) nucleotide sequence of VGAM2446 RNA is designated SEQ ID:5157, and

is provided hereinbelow with reference to the sequence listing part.

[82797] VGAM2446 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2446 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2446 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82798] VGAM2446 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2446 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2446 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2446 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2446 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82799] The complementary binding of VGAM2446 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2446 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2446 host target RNA into VGAM2446 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82800] It is appreciated that VGAM2446 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2446 host target genes. The mRNA of each one of this plurality of VGAM2446 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2446 RNA, herein designated VGAM RNA, and which when bound by VGAM2446 RNA causes inhibition of translation of respective one or more VGAM2446 host target proteins.

[82801] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2446 gene, herein designated VGAM GENE, on one or more VGAM2446 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82802] It is yet further appreciated that a function of VGAM2446 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2446 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2446 correlate with, and may be deduced from, the identity of the host target genes which VGAM2446 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82803] Nucleotide sequences of the VGAM2446 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2446 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2446 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2446 are further described hereinbelow with reference to Table 1.

[82804] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2446 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2446 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82805] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2446 gene, herein designated VGAM is inhibition of expression of VGAM2446 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2446 correlate with, and may be deduced from, the identity of the target genes which VGAM2446 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82806] Contactin Associated Protein-like 2 (CNTNAP2, Accession NM_014141) is a VGAM2446 host target gene. CNTNAP2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNTNAP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNTNAP2 BINDING SITE, designated SEQ ID:15416, to the nucleotide sequence of VGAM2446 RNA, herein designated VGAM RNA, also designated SEQ ID:5157.

[82807] A function of VGAM2446 is therefore inhibition of Contactin Associated Protein-like 2 (CNTNAP2, Accession NM_014141). Accordingly, utilities of VGAM2446 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNTNAP2. DKFZP566B183

(Accession NM_015509) is another VGAM2446 host target gene. DKFZP566B183 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP566B183, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566B183 BINDING SITE, designated SEQ ID:17768, to the nucleotide sequence of VGAM2446 RNA, herein designated VGAM RNA, also designated SEQ ID:5157.

[82808] Another function of VGAM2446 is therefore inhibition of DKFZP566B183 (Accession NM_015509). Accordingly, utilities of VGAM2446 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566B183. FLJ10511 (Accession NM_018120) is another VGAM2446 host target gene. FLJ10511 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10511, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10511 BINDING SITE, designated SEQ ID:19898, to the nucleotide sequence of VGAM2446 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5157.

[82809] Another function of VGAM2446 is therefore inhibition of FLJ10511 (Accession NM_018120). Accordingly, utilities of VGAM2446 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10511. FLJ13842 (Accession NM_024645) is another VGAM2446 host target gene. FLJ13842 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13842, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13842 BINDING SITE, designated SEQ ID:23929, to the nucleotide sequence of VGAM2446 RNA, herein designated VGAM RNA, also designated SEQ ID:5157.

[82810] Another function of VGAM2446 is therefore inhibition of FLJ13842 (Accession NM_024645). Accordingly, utilities of VGAM2446 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13842. Retinoblastoma Binding Protein 7 (RBBP7, Accession XM_010272) is another VGAM2446 host target gene. RBBP7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

RBBP7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBBP7 BINDING SITE, designated SEQ ID:30150, to the nucleotide sequence of VGAM2446 RNA, herein designated VGAM RNA, also designated SEQ ID:5157.

[82811] Another function of VGAM2446 is therefore inhibition of Retinoblastoma Binding Protein 7 (RBBP7, Accession XM_010272). Accordingly, utilities of VGAM2446 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP7. LOC219654 (Accession XM_166095) is another VGAM2446 host target gene. LOC219654 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219654, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219654 BINDING SITE, designated SEQ ID:43872, to the nucleotide sequence of VGAM2446 RNA, herein designated VGAM RNA, also designated SEQ ID:5157.

[82812] Another function of VGAM2446 is therefore inhibition of

LOC219654 (Accession XM_166095). Accordingly, utilities of VGAM2446 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219654. LOC221271 (Accession XM_166307) is another VGAM2446 host target gene. LOC221271 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221271, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221271 BINDING SITE, designated SEQ ID:44126, to the nucleotide sequence of VGAM2446 RNA, herein designated VGAM RNA, also designated SEQ ID:5157.

[82813] Another function of VGAM2446 is therefore inhibition of LOC221271 (Accession XM_166307). Accordingly, utilities of VGAM2446 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221271. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2447 (VGAM2447) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes

is known in the art.

[82814] VGAM2447 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2447 was detected is described hereinabove with reference to Figs. 1-8.

[82815] VGAM2447 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2447 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82816] VGAM2447 gene encodes a VGAM2447 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2447 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2447 precursor RNA is designated SEQ ID:2433, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2433 is located at position 2867 relative to the genome of Mouse Cytomegalovirus 1.

[82817] VGAM2447 precursor RNA folds onto itself, forming VGAM2447 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-

dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82818] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2447 folded precursor RNA into VGAM2447 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 82%) nucleotide sequence of VGAM2447 RNA is designated SEQ ID:5158, and is provided hereinbelow with reference to the sequence listing part.

[82819] VGAM2447 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2447 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2447 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein cod-

ing region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82820] VGAM2447 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2447 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2447 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2447 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2447 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR

and 5`UTR regions.

[82821] The complementary binding of VGAM2447 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2447 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2447 host target RNA into VGAM2447 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82822] It is appreciated that VGAM2447 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2447 host target genes. The mRNA of each one of this plurality of VGAM2447 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2447 RNA, herein designated VGAM RNA, and which when bound by VGAM2447 RNA causes inhibition of translation of respective one or more VGAM2447 host target proteins.

[82823] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2447 gene, herein designated VGAM GENE, on one

or more VGAM2447 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82824] It is yet further appreciated that a function of VGAM2447 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2447 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2447 correlate with, and may be deduced from, the identity of the host target genes which VGAM2447 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82825] Nucleotide sequences of the VGAM2447 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2447 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2447 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2447 are further described hereinbelow with reference to Table 1.

[82826] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2447 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2447 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82827] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2447 gene, herein designated VGAM is inhibition of expression of VGAM2447 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2447 correlate with, and may be deduced from, the identity of the target genes which VGAM2447 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82828] EphB2 (EPHB2, Accession NM_004442) is a VGAM2447

host target gene. EPHB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPHB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPHB2 BINDING SITE, designated SEQ ID:10730, to the nucleotide sequence of VGAM2447 RNA, herein designated VGAM RNA, also designated SEQ ID:5158.

[82829] A function of VGAM2447 is therefore inhibition of EphB2 (EPHB2, Accession NM_004442), a gene which Eph-related receptor tyrosine kinase B2; may have a role in neurogenesis. Accordingly, utilities of VGAM2447 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPHB2. The function of EPHB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM533.G Protein-coupled Receptor 23 (GPR23, Accession XM_018505) is another VGAM2447 host target gene. GPR23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GPR23, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPR23 BINDING SITE, designated SEQ ID:30364, to the nucleotide sequence of VGAM2447 RNA, herein designated VGAM RNA, also designated SEQ ID:5158.

[82830] Another function of VGAM2447 is therefore inhibition of G Protein-coupled Receptor 23 (GPR23, Accession XM_018505), a gene which is a member of the G protein-coupled receptor family. Accordingly, utilities of VGAM2447 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPR23. The function of GPR23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1125.KIAA1209 (Accession XM_027307) is another VGAM2447 host target gene. KIAA1209 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1209, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1209 BINDING SITE, designated SEQ ID:30469, to the nucleotide sequence of VGAM2447 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5158.

[82831] Another function of VGAM2447 is therefore inhibition of KIAA1209 (Accession XM_027307). Accordingly, utilities of VGAM2447 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1209. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2448 (VGAM2448) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82832] VGAM2448 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2448 was detected is described hereinabove with reference to Figs. 1-8.

[82833] VGAM2448 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2448 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82834] VGAM2448 gene encodes a VGAM2448 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2448 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2448 precursor RNA is designated SEQ ID:2434, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2434 is located at position 134478 relative to the genome of Mouse Cytomegalovirus 1.

[82835] VGAM2448 precursor RNA folds onto itself, forming VGAM2448 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82836] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2448 folded precursor RNA into VGAM2448 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2448 RNA is designated SEQ ID:5159, and is provided hereinbelow with reference to the sequence listing part.

[82837] VGAM2448 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2448 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2448 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82838] VGAM2448 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2448 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2448 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2448 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2448 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82839] The complementary binding of VGAM2448 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2448 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2448 host target RNA into VGAM2448 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82840] It is appreciated that VGAM2448 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2448 host target genes. The mRNA of

each one of this plurality of VGAM2448 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2448 RNA, herein designated VGAM RNA, and which when bound by VGAM2448 RNA causes inhibition of translation of respective one or more VGAM2448 host target proteins.

[82841] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2448 gene, herein designated VGAM GENE, on one or more VGAM2448 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[82842] It is yet further appreciated that a function of VGAM2448 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2448 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2448 correlate with, and may be deduced from, the identity of the host target genes which VGAM2448 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82843] Nucleotide sequences of the VGAM2448 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2448 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2448 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2448 are further described hereinbelow with reference to Table 1.

[82844] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2448 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2448 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82845] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2448 gene, herein designated VGAM is inhibition of expression of VGAM2448 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2448 correlate with, and may be deduced from, the identity of the target genes which VGAM2448 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82846] Mitogen-activated Protein Kinase 4 (MAPK4, Accession NM_002747) is a VGAM2448 host target gene. MAPK4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAPK4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAPK4 BINDING SITE, designated SEQ ID:8621, to the nucleotide sequence of VGAM2448 RNA, herein designated VGAM RNA, also designated SEQ ID:5159.

[82847] A function of VGAM2448 is therefore inhibition of Mitogen-activated Protein Kinase 4 (MAPK4, Accession NM_002747), a gene which phosphorylates microtubule-

associated protein-2 may promote entry into the cell cycle. Accordingly, utilities of VGAM2448 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAPK4. The function of MAPK4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM655.FLJ10008 (Accession NM_017970) is another VGAM2448 host target gene. FLJ10008 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10008, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10008 BINDING SITE, designated SEQ ID:19691, to the nucleotide sequence of VGAM2448 RNA, herein designated VGAM RNA, also designated SEQ ID:5159.

[82848] Another function of VGAM2448 is therefore inhibition of FLJ10008 (Accession NM_017970). Accordingly, utilities of VGAM2448 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10008. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2449 (VGAM2449) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82849] VGAM2449 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2449 was detected is described hereinabove with reference to Figs. 1-8.

[82850] VGAM2449 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2449 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82851] VGAM2449 gene encodes a VGAM2449 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2449 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2449 precursor RNA is designated SEQ ID:2435, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2435 is located at position 53100 relative to the

genome of Mouse Cytomegalovirus 1.

[82852] VGAM2449 precursor RNA folds onto itself, forming VGAM2449 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82853] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2449 folded precursor RNA into VGAM2449 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2449 RNA is designated SEQ ID:5160, and is provided hereinbelow with reference to the sequence listing part.

[82854] VGAM2449 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2449 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2449 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82855] VGAM2449 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2449 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2449 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2449 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2449 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82856] The complementary binding of VGAM2449 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2449 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2449 host target RNA into VGAM2449 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82857] It is appreciated that VGAM2449 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2449 host target genes. The mRNA of each one of this plurality of VGAM2449 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2449 RNA, herein designated VGAM RNA, and which when bound by VGAM2449 RNA causes inhibition of translation of respective one or more VGAM2449 host target proteins.

[82858] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2449 gene, herein designated VGAM GENE, on one or more VGAM2449 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82859] It is yet further appreciated that a function of VGAM2449 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2449

correlate with, and may be deduced from, the identity of the host target genes which VGAM2449 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82860] Nucleotide sequences of the VGAM2449 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2449 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2449 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2449 are further described hereinbelow with reference to Table 1.

[82861] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2449 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2449 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82862] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2449 gene, herein designated VGAM is inhibition of expression of VGAM2449 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2449 correlate with, and may be deduced

from, the identity of the target genes which VGAM2449 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82863] EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838) is a VGAM2449 host target gene. EGFL5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EGFL5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGFL5 BINDING SITE, designated SEQ ID:41878, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82864] A function of VGAM2449 is therefore inhibition of EGF-like-domain, Multiple 5 (EGFL5, Accession XM_098838). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGFL5. Natriuretic Peptide Receptor A/guanylate Cyclase A (atrionatriuretic peptide receptor A) (NPR1, Accession XM_113360) is another VGAM2449 host target gene. NPR1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NPR1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NPR1 BINDING SITE, designated SEQ ID:42232, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82865] Another function of VGAM2449 is therefore inhibition of Natriuretic Peptide Receptor A/guanylate Cyclase A (atrionatriuretic peptide receptor A) (NPR1, Accession XM_113360), a gene which has guanylate cyclase activity on binding of anf. Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NPR1. The function of NPR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM719.Zinc Finger Protein 80 (pT17) (ZNF80, Accession NM_007136) is another VGAM2449 host target gene. ZNF80 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF80, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

ZNF80 BINDING SITE, designated SEQ ID:13985, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82866] Another function of VGAM2449 is therefore inhibition of Zinc Finger Protein 80 (pT17) (ZNF80, Accession NM_007136). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF80. 13CDNA73 (Accession NM_023037) is another VGAM2449 host target gene. 13CDNA73 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by 13CDNA73, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of 13CDNA73 BINDING SITE, designated SEQ ID:23320, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82867] Another function of VGAM2449 is therefore inhibition of 13CDNA73 (Accession NM_023037). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 13CDNA73. Artemin (ARTN, Accession NM_003976) is an-

other VGAM2449 host target gene. ARTN BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARTN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARTN BINDING SITE, designated SEQ ID:10109, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82868] Another function of VGAM2449 is therefore inhibition of Artemin (ARTN, Accession NM_003976). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARTN. Chromobox Homolog 6 (CBX6, Accession NM_014292) is another VGAM2449 host target gene. CBX6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CBX6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBX6 BINDING SITE, designated SEQ ID:15573, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82869] Another function of VGAM2449 is therefore inhibition of Chromobox Homolog 6 (CBX6, Accession NM_014292). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBX6. GNB4 (Accession NM_021629) is another VGAM2449 host target gene. GNB4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNB4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNB4 BINDING SITE, designated SEQ ID:22268, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82870] Another function of VGAM2449 is therefore inhibition of GNB4 (Accession NM_021629). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNB4. MAD, Mothers Against Decapentaplegic Homolog (Drosophila) Interacting Protein, Receptor Activation Anchor (MADHIP, Accession NM_007324) is another VGAM2449 host target gene. MADHIP BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by MADHIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MADHIP BINDING SITE, designated SEQ ID:14242, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82871] Another function of VGAM2449 is therefore inhibition of MAD, Mothers Against Decapentaplegic Homolog (Drosophila) Interacting Protein, Receptor Activation Anchor (MADHIP, Accession NM_007324). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MADHIP. Splicing Factor, Arginine/serine-rich 12 (SFRS12, Accession NM_139168) is another VGAM2449 host target gene. SFRS12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFRS12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFRS12 BINDING SITE, designated SEQ ID:29174, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5160.

[82872] Another function of VGAM2449 is therefore inhibition of Splicing Factor, Arginine/serine-rich 12 (SFRS12, Accession NM_139168). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFRS12. SPEC1 (Accession NM_020239) is another VGAM2449 host target gene. SPEC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPEC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPEC1 BINDING SITE, designated SEQ ID:21508, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82873] Another function of VGAM2449 is therefore inhibition of SPEC1 (Accession NM_020239). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPEC1. Testis-specific Transcript, Y-linked 9 (TTTY9, Accession NM_031927) is another VGAM2449 host target gene. TTTY9 BINDING SITE is HOST TARGET binding site found

in the 5` untranslated region of mRNA encoded by TTTY9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTTY9 BINDING SITE, designated SEQ ID:25675, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82874] Another function of VGAM2449 is therefore inhibition of Testis-specific Transcript, Y-linked 9 (TTTY9, Accession NM_031927). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTTY9. LOC126432 (Accession XM_059046) is another VGAM2449 host target gene. LOC126432 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC126432, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126432 BINDING SITE, designated SEQ ID:36839, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82875] Another function of VGAM2449 is therefore inhibition of LOC126432 (Accession XM_059046). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126432. LOC257239 (Accession XM_173125) is another VGAM2449 host target gene. LOC257239 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257239, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257239 BINDING SITE, designated SEQ ID:46373, to the nucleotide sequence of VGAM2449 RNA, herein designated VGAM RNA, also designated SEQ ID:5160.

[82876] Another function of VGAM2449 is therefore inhibition of LOC257239 (Accession XM_173125). Accordingly, utilities of VGAM2449 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257239. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2450 (VGAM2450) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[82877] VGAM2450 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2450 was detected is described hereinabove with reference to Figs. 1-8.

[82878] VGAM2450 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2450 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82879] VGAM2450 gene encodes a VGAM2450 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2450 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2450 precursor RNA is designated SEQ ID:2436, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2436 is located at position 39437 relative to the genome of Mouse Cytomegalovirus 1.

[82880] VGAM2450 precursor RNA folds onto itself, forming VGAM2450 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82881] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2450 folded precursor RNA into VGAM2450 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2450 RNA is designated SEQ ID:5161, and is provided hereinbelow with reference to the sequence listing part.

[82882] VGAM2450 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2450 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2450 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82883] VGAM2450 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2450 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2450 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2450 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2450 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82884] The complementary binding of VGAM2450 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2450 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2450 host target RNA into VGAM2450 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82885] It is appreciated that VGAM2450 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2450 host target genes. The mRNA of each one of this plurality of VGAM2450 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2450 RNA, herein designated VGAM RNA, and which when bound by VGAM2450 RNA causes inhibition of translation of respective one or more VGAM2450 host target proteins.

[82886] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2450 gene, herein designated VGAM GENE, on one or more VGAM2450 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82887] It is yet further appreciated that a function of VGAM2450 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2450 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2450 correlate with, and may be deduced from, the identity of the host target genes which VGAM2450 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[82888] Nucleotide sequences of the VGAM2450 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2450 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2450 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2450 are further described hereinbelow with reference to Table 1.

[82889] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2450 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2450 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82890] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2450 gene, herein designated VGAM is inhibition of expression of VGAM2450 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2450 correlate with, and may be deduced from, the identity of the target genes which VGAM2450 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82891] Chromosome 20 Open Reading Frame 162 (C20orf162, Accession NM_080603) is a VGAM2450 host target gene. C20orf162 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C20orf162, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf162 BINDING SITE, designated SEQ ID:27914, to the nucleotide sequence of VGAM2450 RNA, herein designated VGAM RNA, also designated SEQ ID:5161.

[82892] A function of VGAM2450 is therefore inhibition of Chromosome 20 Open Reading Frame 162 (C20orf162, Accession NM_080603). Accordingly, utilities of VGAM2450 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf162. HRIHFB2436 (Accession NM_014345) is another VGAM2450 host target gene. HRIHFB2436 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HRIHFB2436, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRIHFB2436 BINDING

SITE, designated SEQ ID:15666, to the nucleotide sequence of VGAM2450 RNA, herein designated VGAM RNA, also designated SEQ ID:5161.

[82893] Another function of VGAM2450 is therefore inhibition of HRIHFB2436 (Accession NM_014345). Accordingly, utilities of VGAM2450 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRIHFB2436. LOC145988 (Accession XM_085290) is another VGAM2450 host target gene. LOC145988 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145988, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145988 BINDING SITE, designated SEQ ID:38036, to the nucleotide sequence of VGAM2450 RNA, herein designated VGAM RNA, also designated SEQ ID:5161.

[82894] Another function of VGAM2450 is therefore inhibition of LOC145988 (Accession XM_085290). Accordingly, utilities of VGAM2450 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145988. LOC220110 (Accession XM_167882) is another VGAM2450 host target gene. LOC220110 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220110 BINDING SITE, designated SEQ ID:44893, to the nucleotide sequence of VGAM2450 RNA, herein designated VGAM RNA, also designated SEQ ID:5161.

[82895] Another function of VGAM2450 is therefore inhibition of LOC220110 (Accession XM_167882). Accordingly, utilities of VGAM2450 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220110. LOC221943 (Accession XM_168343) is another VGAM2450 host target gene. LOC221943 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221943, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221943 BINDING SITE, designated SEQ ID:45116, to the nucleotide sequence of VGAM2450 RNA, herein designated VGAM RNA, also designated SEQ ID:5161.

[82896] Another function of VGAM2450 is therefore inhibition of

LOC221943 (Accession XM_168343). Accordingly, utilities of VGAM2450 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221943. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2451 (VGAM2451) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82897] VGAM2451 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2451 was detected is described hereinabove with reference to Figs. 1-8.

[82898] VGAM2451 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2451 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82899] VGAM2451 gene encodes a VGAM2451 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2451 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2451 precursor RNA is designated SEQ ID:2437, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2437 is located at position 43825 relative to the genome of Mouse Cytomegalovirus 1.

[82900] VGAM2451 precursor RNA folds onto itself, forming VGAM2451 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82901] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2451 folded precursor RNA into VGAM2451 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide se-

quence of VGAM2451 RNA is designated SEQ ID:5162, and is provided hereinbelow with reference to the sequence listing part.

[82902] VGAM2451 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2451 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2451 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82903] VGAM2451 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2451 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2451 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2451 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2451 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82904] The complementary binding of VGAM2451 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2451 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2451 host target RNA into VGAM2451 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82905] It is appreciated that VGAM2451 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2451 host target genes. The mRNA of each one of this plurality of VGAM2451 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2451 RNA, herein designated VGAM RNA, and which when bound by VGAM2451 RNA causes inhibition of translation of respective one or more VGAM2451 host target proteins.

[82906] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2451 gene, herein designated VGAM GENE, on one or more VGAM2451 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82907] It is yet further appreciated that a function of VGAM2451

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2451 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2451 correlate with, and may be deduced from, the identity of the host target genes which VGAM2451 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82908] Nucleotide sequences of the VGAM2451 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2451 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2451 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2451 are further described hereinbelow with reference to Table 1.

[82909] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2451 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2451 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82910] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2451 gene, herein designated VGAM is inhibition of expression of VGAM2451 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2451 correlate with, and may be deduced from, the identity of the target genes which VGAM2451 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82911] KIAA1384 (Accession XM_035405) is a VGAM2451 host target gene. KIAA1384 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1384, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1384 BINDING SITE, designated SEQ ID:32258, to the nucleotide sequence of VGAM2451 RNA, herein designated VGAM RNA, also designated SEQ ID:5162.

[82912] A function of VGAM2451 is therefore inhibition of KIAA1384 (Accession XM_035405). Accordingly, utilities of VGAM2451 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1384. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2452 (VGAM2452) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82913] VGAM2452 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2452 was detected is described hereinabove with reference to Figs. 1-8.

[82914] VGAM2452 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2452 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82915] VGAM2452 gene encodes a VGAM2452 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2452 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2452 precursor RNA is designated SEQ ID:2438, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2438 is located at position 150242 relative to the genome of Mouse Cytomegalovirus 1.

[82916] VGAM2452 precursor RNA folds onto itself, forming VGAM2452 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82917] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2452 folded precursor RNA into VGAM2452 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2452 RNA is designated SEQ ID:5163, and is provided hereinbelow with reference to the sequence listing part.

[82918] VGAM2452 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2452 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2452 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82919] VGAM2452 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2452 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2452 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2452 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2452 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82920] The complementary binding of VGAM2452 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2452 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2452 host target RNA into VGAM2452 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82921] It is appreciated that VGAM2452 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2452 host target genes. The mRNA of each one of this plurality of VGAM2452 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2452 RNA, herein designated VGAM RNA, and which when bound by VGAM2452 RNA causes inhibition of translation of respective one or more

VGAM2452 host target proteins.

[82922] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2452 gene, herein designated VGAM GENE, on one or more VGAM2452 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82923] It is yet further appreciated that a function of VGAM2452 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1.

Specific functions, and accordingly utilities, of VGAM2452 correlate with, and may be deduced from, the identity of the host target genes which VGAM2452 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82924] Nucleotide sequences of the VGAM2452 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2452 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2452 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2452 are further described hereinbelow with reference to Table 1.

[82925] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2452 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2452 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82926] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2452 gene, herein designated VGAM is inhibition of expression of VGAM2452 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2452 correlate with, and may be deduced from, the identity of the target genes which VGAM2452 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82927] Flavin Containing Monooxygenase 4 (FMO4, Accession NM_002022) is a VGAM2452 host target gene. FMO4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FMO4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FMO4 BINDING SITE, designated SEQ ID:7768, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82928] A function of VGAM2452 is therefore inhibition of Flavin Containing Monooxygenase 4 (FMO4, Accession NM_002022). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FMO4. Jerky Homolog (mouse) (JRK, Accession XM_098818) is another VGAM2452 host target gene. JRK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by JRK, corresponding to a HOST TAR-

GET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JRK BINDING SITE, designated SEQ ID:41836, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82929] Another function of VGAM2452 is therefore inhibition of Jerky Homolog (mouse) (JRK, Accession XM_098818), a gene which might function as a DNA-binding protein. Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JRK. The function of JRK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM210.Melanoma Antigen, Family A, 3 (MAGEA3, Accession NM_005362) is another VGAM2452 host target gene. MAGEA3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAGEA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAGEA3 BINDING SITE, designated SEQ ID:11839, to the nucleotide

sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82930] Another function of VGAM2452 is therefore inhibition of Melanoma Antigen, Family A, 3 (MAGEA3, Accession NM_005362), a gene which may play a role in embryonal development and tumor transformation or aspects of tumor progression. antigen recognized on a melanoma by autologous cytolytic t lymphocytes. Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAGEA3. The function of MAGEA3 has been established by previous studies. Genes of the MAGE family direct the expression of tumor antigens that are recognized on a human melanoma by autologous cytolytic T lymphocytes. Family A (see OMIM Ref. No. 300016) is clustered at Xq28 and family B is clustered at Xp21.3 (see OMIM Ref. No. 300097). De Plaen et al. (1994) identified 12 family A MAGE genes. MAGE3 cDNA was cloned from a melanoma cell cDNA library. The MAGE3 gene comprises 3 exons, with the last exon containing the entire coding sequence. The gene encodes a 314-amino acid polypeptide. RT-PCR revealed that MAGE2 is expressed in a variety of cancer cell lines, but among normal tissues only in testis and

placenta. De Plaen et al. (1994) used human/rodent cell hybrids to map the MAGE family A cluster to Xq26-qter. Rogner et al. (1995) refined the mapping of the MAGE family A cluster to Xq28. The 12 genes are arranged in 3 clusters within 3.5 Mb.

[82931] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[82932] De Plaen, E.; Arden, K.; Traversari, C.; Gaforio, J. J.; Szikora, J.-P.; De Smet, C.; Brasseur, F.; van der Bruggen, P.; Lethe, B.; Lurquin, C.; Brasseur, R.; Chomez, P.; De Backer, O.; Cavenee, W.; Boon, T. : Structure, chromosomal localization, and expression of 12 genes of the MAGE family. Immunogenetics 40: 360-369, 1994. ; and

[82933] Rogner, U. C.; Wilke, K.; Steck, E.; Korn, B.; Poustka, A. : The melanoma antigen gene (MAGE) family is clustered in the chromosomal band Xq28. Genomics 29: 725-731, 1995.

[82934] Further studies establishing the function and utilities of MAGEA3 are found in John Hopkins OMIM database record ID 300174, and in sited publications numbered 7228-7229 listed in the bibliography section hereinbelow, which are also hereby incorporated by refer-

ence.Chromosome 5 Open Reading Frame 4 (C5orf4, Accession NM_032385) is another VGAM2452 host target gene. C5orf4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C5orf4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5orf4 BINDING SITE, designated SEQ ID:26185, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82935] Another function of VGAM2452 is therefore inhibition of Chromosome 5 Open Reading Frame 4 (C5orf4, Accession NM_032385). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf4. Cleavage and Polyadenylation Specific Factor 2, 100kDa (CPSF2, Accession XM_029311) is another VGAM2452 host target gene. CPSF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CPSF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide se-

quences of CPSF2 BINDING SITE, designated SEQ ID:30864, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82936] Another function of VGAM2452 is therefore inhibition of Cleavage and Polyadenylation Specific Factor 2, 100kDa (CPSF2, Accession XM_029311). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPSF2. KIAA1024 (Accession XM_044580) is another VGAM2452 host target gene. KIAA1024 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1024, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1024 BINDING SITE, designated SEQ ID:34234, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82937] Another function of VGAM2452 is therefore inhibition of KIAA1024 (Accession XM_044580). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1024. MAGE-E1 (Accession NM_030801) is another VGAM2452 host target gene. MAGE-E1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAGE-E1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAGE-E1 BINDING SITE, designated SEQ ID:25106, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82938] Another function of VGAM2452 is therefore inhibition of MAGE-E1 (Accession NM_030801). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAGE-E1. LOC128259 (Accession XM_059228) is another VGAM2452 host target gene. LOC128259 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC128259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC128259 BINDING SITE, designated SEQ ID:36920, to the nucleotide sequence of VGAM2452 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5163.

[82939] Another function of VGAM2452 is therefore inhibition of LOC128259 (Accession XM_059228). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128259. LOC155036 (Accession XM_098651) is another VGAM2452 host target gene. LOC155036 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC155036, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155036 BINDING SITE, designated SEQ ID:41752, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82940] Another function of VGAM2452 is therefore inhibition of LOC155036 (Accession XM_098651). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155036. LOC158510 (Accession XM_088592) is another VGAM2452 host target gene. LOC158510 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158510, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158510 BINDING SITE, designated SEQ ID:39858, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82941] Another function of VGAM2452 is therefore inhibition of LOC158510 (Accession XM_088592). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158510. LOC199991 (Accession XM_117169) is another VGAM2452 host target gene. LOC199991 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC199991, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199991 BINDING SITE, designated SEQ ID:43275, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82942] Another function of VGAM2452 is therefore inhibition of LOC199991 (Accession XM_117169). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC199991. LOC201229 (Accession XM_113925) is another VGAM2452 host target gene. LOC201229 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201229, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201229 BINDING SITE, designated SEQ ID:42541, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82943] Another function of VGAM2452 is therefore inhibition of LOC201229 (Accession XM_113925). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201229. LOC222681 (Accession XM_167116) is another VGAM2452 host target gene. LOC222681 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222681, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222681 BINDING SITE, designated SEQ ID:44617, to

the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82944] Another function of VGAM2452 is therefore inhibition of LOC222681 (Accession XM_167116). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222681. LOC257507 (Accession XM_175204) is another VGAM2452 host target gene. LOC257507 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC257507, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257507 BINDING SITE, designated SEQ ID:46683, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82945] Another function of VGAM2452 is therefore inhibition of LOC257507 (Accession XM_175204). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257507. LOC257625 (Accession XM_175267) is another VGAM2452 host target gene. LOC257625 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC257625, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257625 BINDING SITE, designated SEQ ID:46739, to the nucleotide sequence of VGAM2452 RNA, herein designated VGAM RNA, also designated SEQ ID:5163.

[82946] Another function of VGAM2452 is therefore inhibition of LOC257625 (Accession XM_175267). Accordingly, utilities of VGAM2452 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257625. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2453 (VGAM2453) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82947] VGAM2453 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2453 was detected is described hereinabove with reference to Figs. 1-8.

[82948] VGAM2453 gene, herein designated VGAM GENE, is a viral

gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2453 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[82949] VGAM2453 gene encodes a VGAM2453 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2453 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2453 precursor RNA is designated SEQ ID:2439, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2439 is located at position 45147 relative to the genome of Mouse Cytomegalovirus 1.

[82950] VGAM2453 precursor RNA folds onto itself, forming VGAM2453 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82951] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2453 folded precursor RNA into VGAM2453 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 50%) nucleotide sequence of VGAM2453 RNA is designated SEQ ID:5164, and is provided hereinbelow with reference to the sequence listing part.

[82952] VGAM2453 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2453 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2453 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82953] VGAM2453 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2453 host target RNA, herein designated VGAM HOST TARGET RNA. This

complementary binding is due to the fact that the nucleotide sequence of VGAM2453 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2453 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2453 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82954] The complementary binding of VGAM2453 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2453 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2453

host target RNA into VGAM2453 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82955] It is appreciated that VGAM2453 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2453 host target genes. The mRNA of each one of this plurality of VGAM2453 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2453 RNA, herein designated VGAM RNA, and which when bound by VGAM2453 RNA causes inhibition of translation of respective one or more VGAM2453 host target proteins.

[82956] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2453 gene, herein designated VGAM GENE, on one or more VGAM2453 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4

and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82957] It is yet further appreciated that a function of VGAM2453 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2453 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2453 correlate with, and may be deduced from, the identity of the host target genes which VGAM2453 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82958] Nucleotide sequences of the VGAM2453 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2453 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2453 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2453 are further

described hereinbelow with reference to Table 1.

[82959] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2453 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2453 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82960] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2453 gene, herein designated VGAM is inhibition of expression of VGAM2453 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2453 correlate with, and may be deduced from, the identity of the target genes which VGAM2453 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82961] Chromosome 20 Open Reading Frame 44 (C20orf44, Accession NM_018244) is a VGAM2453 host target gene. C20orf44 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C20orf44, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of C20orf44 BINDING SITE, designated SEQ ID:20208, to the nucleotide sequence of VGAM2453 RNA, herein designated VGAM RNA, also designated SEQ ID:5164.

[82962] A function of VGAM2453 is therefore inhibition of Chromosome 20 Open Reading Frame 44 (C20orf44, Accession NM_018244). Accordingly, utilities of VGAM2453 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf44. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2454 (VGAM2454) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[82963] VGAM2454 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2454 was detected is described hereinabove with reference to Figs. 1-8.

[82964] VGAM2454 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2454 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[82965] VGAM2454 gene encodes a VGAM2454 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2454 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2454 precursor RNA is designated SEQ ID:2440, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2440 is located at position 170592 relative to the genome of Mouse Cytomegalovirus 1.

[82966] VGAM2454 precursor RNA folds onto itself, forming VGAM2454 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[82967] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2454 folded precursor RNA into VGAM2454 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2454 RNA is designated SEQ ID:5165, and is provided hereinbelow with reference to the sequence listing part.

[82968] VGAM2454 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2454 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2454 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[82969] VGAM2454 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2454 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2454 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2454 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2454 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[82970] The complementary binding of VGAM2454 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2454 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2454 host target RNA into VGAM2454 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[82971] It is appreciated that VGAM2454 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2454 host target genes. The mRNA of each one of this plurality of VGAM2454 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2454 RNA, herein designated VGAM RNA, and which when bound by VGAM2454 RNA causes inhibition of translation of respective one or more VGAM2454 host target proteins.

[82972] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2454 gene, herein designated VGAM GENE, on one or more VGAM2454 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[82973] It is yet further appreciated that a function of VGAM2454 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2454 correlate with, and may be deduced from, the identity of the host target genes which VGAM2454 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[82974] Nucleotide sequences of the VGAM2454 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2454 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2454 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2454 are further described hereinbelow with reference to Table 1.

[82975] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2454 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2454 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[82976] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2454 gene, herein designated VGAM is inhibition of expression of VGAM2454 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2454 correlate with, and may be deduced from, the identity of the target genes which VGAM2454 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[82977] Actinin, Alpha 2 (ACTN2, Accession NM_001103) is a VGAM2454 host target gene. ACTN2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ACTN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACTN2 BINDING SITE, designated SEQ ID:6756, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82978] A function of VGAM2454 is therefore inhibition of Actinin, Alpha 2 (ACTN2, Accession NM_001103), a gene which an actin-binding protein with multiple roles in different cell types. Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACTN2. The function of ACTN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM88.Rho Guanine Nucleotide Exchange Factor (GEF) 7 (ARHGEF7, Accession NM_003899) is another VGAM2454 host target gene. ARHGEF7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHGEF7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGEF7 BINDING SITE, designated SEQ ID:9985, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82979] Another function of VGAM2454 is therefore inhibition of Rho Guanine Nucleotide Exchange Factor (GEF) 7 (ARHGEF7, Accession NM_003899), a gene which acts as a

rac1 guanine nucleotide exchange factor (gef) and can induce membrane ruffling. Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF7. The function of ARHGEF7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM297.Brain-specific Angiogenesis Inhibitor 2 (BAI2, Accession NM_001703) is another VGAM2454 host target gene. BAI2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BAI2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BAI2 BINDING SITE, designated SEQ ID:7426, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82980] Another function of VGAM2454 is therefore inhibition of Brain-specific Angiogenesis Inhibitor 2 (BAI2, Accession NM_001703). Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BAI2. Core-binding Factor,

Runt Domain, Alpha Subunit 2; Translocated To, 3 (CBFA2T3, Accession NM_005187) is another VGAM2454 host target gene. CBFA2T3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CBFA2T3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBFA2T3 BINDING SITE, designated SEQ ID:11687, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82981] Another function of VGAM2454 is therefore inhibition of Core-binding Factor, Runt Domain, Alpha Subunit 2; Translocated To, 3 (CBFA2T3, Accession NM_005187). Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBFA2T3. Filamin A, Alpha (actin binding protein 280) (FLNA, Accession NM_001456) is another VGAM2454 host target gene. FLNA BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLNA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of FLNA BINDING SITE, designated SEQ ID:7192, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82982] Another function of VGAM2454 is therefore inhibition of Filamin A, Alpha (actin binding protein 280) (FLNA, Accession NM_001456), a gene which promotes orthogonal branching of actin filaments and links actin filaments to membrane glycoproteins. Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLNA. The function of FLNA has been established by previous studies. Actin-binding protein, or filamin, is a 280-kD protein that crosslinks actin filaments into orthogonal networks in cortical cytoplasm and participates in the anchoring of membrane proteins for the actin cytoskeleton. By analysis of the native ABP protein and cloning of the human endothelial ABP cDNA, Gorlin et al. (1990) demonstrated that ABP is a 2,647-amino acid protein with 3 functional domains: an N-terminal filamentous actin-binding domain, a C-terminal self-association domain, and a membrane glycoprotein-binding domain. The N-terminal actin-binding domain of ABP280 displays strong

structural and functional similarity to the N-terminal domains of dystrophin (OMIM Ref. No. 300377), alpha-actinin (OMIM Ref. No. 102575), and beta-spectrin (OMIM Ref. No. 182870). Periventricular heterotopia (OMIM Ref. No. 300049) is an X-linked dominant disorder in which many neurons fail to migrate to the cerebral cortex and persist as nodules lining the ventricular surface. Heterozygous females with the disorder present with epilepsy and other signs, including patent ductus arteriosus and coagulopathy, whereas hemizygous affected males die embryonically. Fox et al. (1998) identified the cause as mutations in the FLN1 gene, which is required for locomotion of many cell types. They demonstrated a previously unrecognized high level of expression of FLN1 in the developing cortex. Their studies demonstrated that FLN1 is required for neuronal migration to the cortex and is essential for embryogenesis. In identifying filamin-1 as the gene mutant in periventricular heterotopia, Fox et al. (1998) first narrowed the map location to an interval approximately 1 cM between marker DXS15 and the pseudoautosomal region of Xq28 by the study of additional markers. Subsequent analysis of a large duplication of Xq28 in a male patient with periventricular heterotopia

(Fink et al., 1997) with a severe, albeit nonlethal, phenotype allowed the candidate interval to be refined even further. They defined the exact centromeric boundary of the duplicated segment of Xq28 as base 3377 of 3,395 bases in intron 1 of the isocitrate dehydrogenase gene (IDH3G; 300089), approximately 600 kb distal to DXS15. However, none of the genes identified at the breakpoints or insertion site of the duplication harbored independent mutations in other patients with periventricular heterotopia. Therefore, Fox et al. (1998) concluded that the duplication itself was responsible for the disorder in this patient. Fox et al. (1998) studied the pattern of X inactivation in females with FLN1 mutations in nucleated peripheral blood cells. No evidence of preferential lyonization in these cells was found, suggesting that FLN1 is not required in a cell-autonomous fashion for survival of mixed peripheral white blood cells. However, an essential cell-autonomous role for FLN1 in a subset of nucleated cells or nonnucleated cells (e.g., platelets) could not be excluded. Sheen et al. (2001) performed SSCP analysis of FLN1 throughout its entire coding region in 6 periventricular heterotopia pedigrees, 31 sporadic female patients, and 24 sporadic male periventricular heterotopia patients. The authors detected

FLN1 mutations in 83% of periventricular heterotopia pedigrees and 19% of sporadic females with periventricular heterotopia. Moreover, 0 of 7 females with periventricular heterotopia with atypical radiographic features showed FLN1 mutations, suggesting that other genes may cause atypical periventricular heterotopia. Two of 24 males analyzed with periventricular heterotopia (9%) also carried FLN1 mutations. Whereas FLN1 mutations in periventricular heterotopia pedigrees caused severe predicted loss of FLN1 protein function, both male FLN1 mutations were consistent with partial loss of function of the protein. Moreover, sporadic female FLN1 mutations associated with periventricular heterotopia appear to cause either severe or partial loss of function. In the largest reported pedigree with periventricular heterotopia (OMIM Ref. No. 300049) (Huttenlocher et al., 1994), Fox et al. (1998) found a C-to-T substitution in exon 3 of the FLN1 gene, which converted a CAG (gln) to a TAG (stop) codon and truncated the FLN1 protein at amino acid residue 182 of the 2,647 total amino acids in the normal protein.

[82983] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[82984] Sheen, V. L.; Dixon, P. H.; Fox, J. W.; Hong, S. E.; Kinton, L.; Sisodiya, S. M.; Duncan, J. S.; Dubeau, F.; Scheffer, I. E.; Schachter, S. C.; Wilner, A.; Henchy, R.; and 18 others : Mutations in the X-linked filamin 1 gene cause periventricular nodular heterotopia in males as well as in females. Hum. Molec. Genet. 10: 1775-1783, 2001. ; and

[82985] Fox, J. W.; Lamperti, E. D.; Eksioglu, Y. Z.; Hong, S. E.; Feng, Y.; Graham, D. A.; Scheffer, I. E.; Dobyns, W. B.; Hirsch, B. A.; Radtke, R. A.; Berkovic, S. F.; Huttenlocher, P. R.; W.

[82986] Further studies establishing the function and utilities of FLNA are found in John Hopkins OMIM database record ID 300017, and in sited publications numbered 7230-7233, 7255-726 and 9435-7264 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.V-maf Musculoaponeurotic Fibrosarcoma Oncogene Homolog (avian) (MAF, Accession NM_005360) is another VGAM2454 host target gene. MAF BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAF BINDING

SITE, designated SEQ ID:11836, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82987] Another function of VGAM2454 is therefore inhibition of V-maf Musculoaponeurotic Fibrosarcoma Oncogene Homolog (avian) (MAF, Accession NM_005360), a gene which is a transcription factor; contains a leucine zipper motif. Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAF. The function of MAF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM822.MYC-associated Zinc Finger Protein (purine-binding transcription factor) (MAZ, Accession XM_055771) is another VGAM2454 host target gene. MAZ BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAZ BINDING SITE, designated SEQ ID:36324, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ

ID:5165.

[82988] Another function of VGAM2454 is therefore inhibition of MYC-associated Zinc Finger Protein (purine-binding transcription factor) (MAZ, Accession XM_055771). Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAZ. Regulating Synaptic Membrane Exocytosis 1 (RIMS1, Accession XM_052206) is another VGAM2454 host target gene. RIMS1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RIMS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RIMS1 BINDING SITE, designated SEQ ID:35956, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82989] Another function of VGAM2454 is therefore inhibition of Regulating Synaptic Membrane Exocytosis 1 (RIMS1, Accession XM_052206), a gene which may have a regulatory role in the membrane interactions during trafficking of synaptic vesicles. Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and

clinical conditions associated with RIMS1. The function of RIMS1 has been established by previous studies. Coppola et al. (2001) obtained 6 isoforms of human RIM that differ from each other in the distance between their 2 C2 domains. Binding analysis showed that the C2 domains of RIM interact in a calcium-independent manner with N-type calcium channels. They also interact weakly with SNAP25 (OMIM Ref. No. 600322) and strongly with synaptotagmin-1 (SYT1; 185605). In the presence of calcium, the interaction with SYT1 increases and that with SNAP25 decreases. Coppola et al. (2001) concluded that RIM1 is a scaffold protein that interacts with multiple binding partners and coordinates different stages of the secretory process. Animal model experiments lend further support to the function of RIMS1. Long-term potentiation (LTP) is involved in learning and memory. One form of LTP requires activation of postsynaptic NMDA receptors (e.g., GRIN2B; 138252), while the other form, mossy fiber LTP (mfLTP), occurs in the presynaptic areas and requires Rab3a and activation of protein kinase A (PKA; OMIM Ref. No. 176911). RIM1 is a PKA substrate. Castillo et al. (2002) showed that in Rim1-deficient mice, mfLTP was abolished in the hippocampus and cerebellum. They lo-

calized the expression of mfLTP to the interface between synaptic vesicles and the active zone and showed that the vesicle protein Rab3a and the active zone protein Rim1 are required.

[82990] It is appreciated that the abovementioned animal model for RIMS1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[82991] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[82992] Coppola, T.; Magnin-Luthi, S.; Perret-Menoud, V.; Gattesco, S.; Schiavo, G.; Regazzi, R. : Direct interaction of the Rab3 effector RIM with Ca(2+) channels, SNAP-25, and synaptotagmin. J. Biol. Chem. 276: 32756-32762, 2001. ; and

[82993] Castillo, P. E.; Schoch, S.; Schmitz, F.; Sudhof, T. C.; Malenka, R. C. : RIM1-alpha is required for presynaptic long-term potentiation. Nature 415: 327-330, 2002.

[82994] Further studies establishing the function and utilities of RIMS1 are found in John Hopkins OMIM database record ID 606629, and in sited publications numbered 6113-6115, 95 and 6116-6117 listed in the bibliography section

hereinbelow, which are also hereby incorporated by reference.Complexin 1 (CPLX1, Accession NM_006651) is another VGAM2454 host target gene. CPLX1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CPLX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CPLX1 BINDING SITE, designated SEQ ID:13448, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82995] Another function of VGAM2454 is therefore inhibition of Complexin 1 (CPLX1, Accession NM_006651). Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CPLX1. GC20 (Accession XM_044184) is another VGAM2454 host target gene. GC20 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GC20, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GC20 BINDING SITE, designated SEQ ID:34167, to the nucleotide sequence of

VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82996] Another function of VGAM2454 is therefore inhibition of GC20 (Accession XM_044184). Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GC20. MGC14386 (Accession NM_033544) is another VGAM2454 host target gene. MGC14386 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC14386, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC14386 BINDING SITE, designated SEQ ID:27306, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82997] Another function of VGAM2454 is therefore inhibition of MGC14386 (Accession NM_033544). Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14386. PRO1048 (Accession NM_018497) is another VGAM2454 host target gene. PRO1048 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by PRO1048, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1048 BINDING SITE, designated SEQ ID:20563, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82998] Another function of VGAM2454 is therefore inhibition of PRO1048 (Accession NM_018497). Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1048. Regulator of G-protein Signalling 19 (RGS19, Accession NM_005873) is another VGAM2454 host target gene. RGS19 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RGS19, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RGS19 BINDING SITE, designated SEQ ID:12491, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[82999] Another function of VGAM2454 is therefore inhibition of

Regulator of G-protein Signalling 19 (RGS19, Accession NM_005873). Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RGS19. SCYD1 (Accession XM_165650) is another VGAM2454 host target gene. SCYD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCYD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCYD1 BINDING SITE, designated SEQ ID:43709, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[83000] Another function of VGAM2454 is therefore inhibition of SCYD1 (Accession XM_165650). Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCYD1. LOC128977 (Accession XM_059313) is another VGAM2454 host target gene. LOC128977 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC128977, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC128977 BINDING SITE, designated SEQ ID:36949, to the nucleotide sequence of VGAM2454 RNA, herein designated VGAM RNA, also designated SEQ ID:5165.

[83001] Another function of VGAM2454 is therefore inhibition of LOC128977 (Accession XM_059313). Accordingly, utilities of VGAM2454 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128977. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2455 (VGAM2455) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83002] VGAM2455 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2455 was detected is described hereinabove with reference to Figs. 1-8.

[83003] VGAM2455 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2455 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[83004] VGAM2455 gene encodes a VGAM2455 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2455 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2455 precursor RNA is designated SEQ ID:2441, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2441 is located at position 3102 relative to the genome of Mouse Cytomegalovirus 1.

[83005] VGAM2455 precursor RNA folds onto itself, forming VGAM2455 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83006] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2455 folded precursor RNA into VGAM2455

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2455 RNA is designated SEQ ID:5166, and is provided hereinbelow with reference to the sequence listing part.

[83007] VGAM2455 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2455 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2455 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83008] VGAM2455 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2455 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2455 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2455 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2455 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83009] The complementary binding of VGAM2455 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2455 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2455 host target RNA into VGAM2455 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[83010] It is appreciated that VGAM2455 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2455 host target genes. The mRNA of each one of this plurality of VGAM2455 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2455 RNA, herein designated VGAM RNA, and which when bound by VGAM2455 RNA causes inhibition of translation of respective one or more VGAM2455 host target proteins.

[83011] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2455 gene, herein designated VGAM GENE, on one or more VGAM2455 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83012] It is yet further appreciated that a function of VGAM2455 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2455 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2455 correlate with, and may be deduced from, the identity of the host target genes which VGAM2455 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83013] Nucleotide sequences of the VGAM2455 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2455 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2455 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2455 are further described hereinbelow with reference to Table 1.

[83014] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2455 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2455 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83015] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2455 gene, herein designated VGAM is inhibition of expression of VGAM2455 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2455 correlate with, and may be deduced from, the identity of the target genes which VGAM2455 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83016] DKFZP434J214 (Accession XM_027639) is a VGAM2455 host target gene. DKFZP434J214 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434J214, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434J214 BINDING SITE, designated SEQ ID:30549, to the nucleotide sequence of VGAM2455 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5166.

[83017] A function of VGAM2455 is therefore inhibition of DKFZP434J214 (Accession XM_027639). Accordingly, utilities of VGAM2455 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434J214. KIAA1708 (Accession XM_040211) is another VGAM2455 host target gene. KIAA1708 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1708, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1708 BINDING SITE, designated SEQ ID:33274, to the nucleotide sequence of VGAM2455 RNA, herein designated VGAM RNA, also designated SEQ ID:5166.

[83018] Another function of VGAM2455 is therefore inhibition of KIAA1708 (Accession XM_040211). Accordingly, utilities of VGAM2455 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1708. MGC20235 (Accession NM_145041) is another VGAM2455 host target gene. MGC20235 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC20235, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC20235 BINDING SITE, designated SEQ ID:29669, to the nucleotide sequence of VGAM2455 RNA, herein designated VGAM RNA, also designated SEQ ID:5166.

[83019] Another function of VGAM2455 is therefore inhibition of MGC20235 (Accession NM_145041). Accordingly, utilities of VGAM2455 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC20235. LOC147949 (Accession XM_085973) is another VGAM2455 host target gene. LOC147949 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147949, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147949 BINDING SITE, designated SEQ ID:38423, to the nucleotide sequence of VGAM2455 RNA, herein designated VGAM RNA, also designated SEQ ID:5166.

[83020] Another function of VGAM2455 is therefore inhibition of LOC147949 (Accession XM_085973). Accordingly, utilities of VGAM2455 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC147949. LOC147990 (Accession XM_097358) is another VGAM2455 host target gene. LOC147990 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147990, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147990 BINDING SITE, designated SEQ ID:40864, to the nucleotide sequence of VGAM2455 RNA, herein designated VGAM RNA, also designated SEQ ID:5166.

[83021] Another function of VGAM2455 is therefore inhibition of LOC147990 (Accession XM_097358). Accordingly, utilities of VGAM2455 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147990. LOC163115 (Accession XM_092010) is another VGAM2455 host target gene. LOC163115 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC163115, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163115 BINDING SITE, designated SEQ ID:40089, to

the nucleotide sequence of VGAM2455 RNA, herein designated VGAM RNA, also designated SEQ ID:5166.

[83022] Another function of VGAM2455 is therefore inhibition of LOC163115 (Accession XM_092010). Accordingly, utilities of VGAM2455 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163115. LOC92697 (Accession XM_046715) is another VGAM2455 host target gene. LOC92697 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92697, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92697 BINDING SITE, designated SEQ ID:34799, to the nucleotide sequence of VGAM2455 RNA, herein designated VGAM RNA, also designated SEQ ID:5166.

[83023] Another function of VGAM2455 is therefore inhibition of LOC92697 (Accession XM_046715). Accordingly, utilities of VGAM2455 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92697. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2456 (VGAM2456) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83024] VGAM2456 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2456 was detected is described hereinabove with reference to Figs. 1-8.

[83025] VGAM2456 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2456 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83026] VGAM2456 gene encodes a VGAM2456 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2456 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2456 precursor RNA is designated SEQ ID:2442, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2442 is located at position 166990 relative to the genome of Mouse Cytomegalovirus 1.

[83027] VGAM2456 precursor RNA folds onto itself, forming VGAM2456 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83028] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2456 folded precursor RNA into VGAM2456 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2456 RNA is designated SEQ ID:5167, and is provided hereinbelow with reference to the sequence listing part.

[83029] VGAM2456 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2456 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2456 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83030] VGAM2456 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2456 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2456 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2456 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2456 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83031] The complementary binding of VGAM2456 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2456 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2456 host target RNA into VGAM2456 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83032] It is appreciated that VGAM2456 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2456 host target genes. The mRNA of each one of this plurality of VGAM2456 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2456 RNA, herein designated VGAM RNA, and which when bound by VGAM2456 RNA causes inhibition of translation of respective one or more VGAM2456 host target proteins.

[83033] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2456 gene, herein designated VGAM GENE, on one or more VGAM2456 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83034] It is yet further appreciated that a function of VGAM2456 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2456 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2456 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2456 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83035] Nucleotide sequences of the VGAM2456 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2456 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2456 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2456 are further described hereinbelow with reference to Table 1.

[83036] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2456 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2456 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83037] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2456 gene, herein designated VGAM is inhibition of expression of VGAM2456 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2456 correlate with, and may be deduced from, the identity of the target genes which VGAM2456

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83038] Caspase Recruitment Domain Family, Member 4 (CARD4, Accession NM_006092) is a VGAM2456 host target gene. CARD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CARD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CARD4 BINDING SITE, designated SEQ ID:12739, to the nucleotide sequence of VGAM2456 RNA, herein designated VGAM RNA, also designated SEQ ID:5167.

[83039] A function of VGAM2456 is therefore inhibition of Caspase Recruitment Domain Family, Member 4 (CARD4, Accession NM_006092), a gene which Activates CASP9 to induce apoptosis, regulates activation of NF-kappaB. Accordingly, utilities of VGAM2456 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARD4. The function of CARD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM492.Fig. 1 further pro-

vides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2457 (VGAM2457) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83040] VGAM2457 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2457 was detected is described hereinabove with reference to Figs. 1-8.

[83041] VGAM2457 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2457 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83042] VGAM2457 gene encodes a VGAM2457 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2457 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2457 precursor RNA is designated SEQ ID:2443, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2443 is located at position 49086 relative to the genome of Mouse Cytomegalovirus 1.

[83043] VGAM2457 precursor RNA folds onto itself, forming VGAM2457 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83044] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2457 folded precursor RNA into VGAM2457 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2457 RNA is designated SEQ ID:5168, and is provided hereinbelow with reference to the sequence listing part.

[83045] VGAM2457 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2457 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2457 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83046] VGAM2457 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2457 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2457 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2457 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2457 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83047] The complementary binding of VGAM2457 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2457 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2457 host target RNA into VGAM2457 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83048] It is appreciated that VGAM2457 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2457 host target genes. The mRNA of each one of this plurality of VGAM2457 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2457 RNA, herein designated VGAM RNA, and which when bound by VGAM2457 RNA causes inhibition of translation of respective one or more

VGAM2457 host target proteins.

[83049] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2457 gene, herein designated VGAM GENE, on one or more VGAM2457 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83050] It is yet further appreciated that a function of VGAM2457 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1.

Specific functions, and accordingly utilities, of VGAM2457 correlate with, and may be deduced from, the identity of the host target genes which VGAM2457 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83051] Nucleotide sequences of the VGAM2457 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2457 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2457 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2457 are further described hereinbelow with reference to Table 1.

[83052] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2457 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2457 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83053] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2457 gene, herein designated VGAM is inhibition of expression of VGAM2457 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2457 correlate with, and may be deduced from, the identity of the target genes which VGAM2457 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83054] APM1 (Accession NM_004797) is a VGAM2457 host target gene. APM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by APM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of APM1 BINDING SITE, designated SEQ ID:11210, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83055] A function of VGAM2457 is therefore inhibition of APM1 (Accession NM_004797). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with APM1. ATPase, Aminophospholipid Transporter-like, Class I, Type 8A, Member 2 (ATP8A2, Accession XM_167916) is another VGAM2457 host target gene. ATP8A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP8A2, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP8A2 BINDING SITE, designated SEQ ID:44913, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83056] Another function of VGAM2457 is therefore inhibition of ATPase, Aminophospholipid Transporter-like, Class I, Type 8A, Member 2 (ATP8A2, Accession XM_167916). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP8A2. Chromosome 14 Open Reading Frame 1 (C14orf1, Accession NM_007176) is another VGAM2457 host target gene. C14orf1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C14orf1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C14orf1 BINDING SITE, designated SEQ ID:14029, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83057] Another function of VGAM2457 is therefore inhibition of Chromosome 14 Open Reading Frame 1 (C14orf1, Acces-

sion NM_007176). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C14orf1. EphA8 (EPHA8, Accession NM_020526) is another VGAM2457 host target gene. EPHA8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPHA8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPHA8 BINDING SITE, designated SEQ ID:21741, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83058] Another function of VGAM2457 is therefore inhibition of EphA8 (EPHA8, Accession NM_020526), a gene which Eph-related receptor tyrosine kinase A8. Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPHA8. The function of EPHA8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM494.Ellis Van Creveld Syndrome (EVC, Accession NM_014556) is another VGAM2457 host

target gene. EVC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EVC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EVC BINDING SITE, designated SEQ ID:15884, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83059] Another function of VGAM2457 is therefore inhibition of Ellis Van Creveld Syndrome (EVC, Accession NM_014556). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EVC. Fanconi Anemia, Complementation Group F (FANCF, Accession NM_022725) is another VGAM2457 host target gene. FANCF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FANCF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FANCF BINDING SITE, designated SEQ ID:22923, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5168.

[83060] Another function of VGAM2457 is therefore inhibition of Fanconi Anemia, Complementation Group F (FANCF, Accession NM_022725). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCF. IMP (inosine monophosphate) Dehydrogenase 1 (IMPDH1, Accession NM_000883) is another VGAM2457 host target gene. IMPDH1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by IMPDH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IMPDH1 BINDING SITE, designated SEQ ID:6579, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83061] Another function of VGAM2457 is therefore inhibition of IMP (inosine monophosphate) Dehydrogenase 1 (IMPDH1, Accession NM_000883). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IMPDH1. Tripartite Motif-containing 9 (TRIM9, Accession

NM_015163) is another VGAM2457 host target gene. TRIM9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TRIM9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TRIM9 BINDING SITE, designated SEQ ID:17517, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83062] Another function of VGAM2457 is therefore inhibition of Tripartite Motif-containing 9 (TRIM9, Accession NM_015163), a gene which may function as a positive regulator for mannosylphosphate transferase and is required to mediate mannosylphosphate transfer in both the core and outer chain portions of n-linked. oligosaccharides. Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TRIM9. The function of TRIM9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.Ankyrin Repeat and SOCS Box-containing 16 (ASB16, Accession

XM_046024) is another VGAM2457 host target gene. ASB16 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ASB16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ASB16 BINDING SITE, designated SEQ ID:34653, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83063] Another function of VGAM2457 is therefore inhibition of Ankyrin Repeat and SOCS Box-containing 16 (ASB16, Accession XM_046024). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASB16. FLJ20897 (Accession NM_032378) is another VGAM2457 host target gene. FLJ20897 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20897, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20897 BINDING SITE, designated SEQ ID:26173, to the nucleotide sequence of VGAM2457

RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83064] Another function of VGAM2457 is therefore inhibition of FLJ20897 (Accession NM_032378). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20897. KIAA0441 (Accession NM_014797) is another VGAM2457 host target gene. KIAA0441 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0441, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0441 BINDING SITE, designated SEQ ID:16710, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83065] Another function of VGAM2457 is therefore inhibition of KIAA0441 (Accession NM_014797). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0441. MGC14697 (Accession NM_032747) is another VGAM2457 host target gene. MGC14697 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by MGC14697, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC14697 BINDING SITE, designated SEQ ID:26484, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83066] Another function of VGAM2457 is therefore inhibition of MGC14697 (Accession NM_032747). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC14697. Sideroflexin 2 (SFXN2, Accession XM_058359) is another VGAM2457 host target gene. SFXN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFXN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFXN2 BINDING SITE, designated SEQ ID:36603, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83067] Another function of VGAM2457 is therefore inhibition of Sideroflexin 2 (SFXN2, Accession XM_058359). Accord-

ingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFXN2. SKRP1 (Accession NM_080876) is another VGAM2457 host target gene. SKRP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SKRP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SKRP1 BINDING SITE, designated SEQ ID:28120, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83068] Another function of VGAM2457 is therefore inhibition of SKRP1 (Accession NM_080876). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SKRP1. Syntaxin 4A (placental) (STX4A, Accession NM_004604) is another VGAM2457 host target gene. STX4A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by STX4A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STX4A BIND-

ING SITE, designated SEQ ID:10947, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83069] Another function of VGAM2457 is therefore inhibition of Syntaxin 4A (placental) (STX4A, Accession NM_004604). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STX4A. Vacuolar Protein Sorting 4A (yeast) (VPS4A, Accession NM_013245) is another VGAM2457 host target gene. VPS4A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VPS4A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VPS4A BINDING SITE, designated SEQ ID:14906, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83070] Another function of VGAM2457 is therefore inhibition of Vacuolar Protein Sorting 4A (yeast) (VPS4A, Accession NM_013245). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VPS4A. LOC160646

(Accession XM_090413) is another VGAM2457 host target gene. LOC160646 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC160646, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC160646 BINDING SITE, designated SEQ ID:40002, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83071] Another function of VGAM2457 is therefore inhibition of LOC160646 (Accession XM_090413). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC160646. LOC221296 (Accession XM_166325) is another VGAM2457 host target gene. LOC221296 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221296, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221296 BINDING SITE, designated SEQ ID:44169, to the nucleotide sequence of VGAM2457 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5168.

[83072] Another function of VGAM2457 is therefore inhibition of LOC221296 (Accession XM_166325). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221296. LOC255308 (Accession XM_170536) is another VGAM2457 host target gene. LOC255308 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255308, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255308 BINDING SITE, designated SEQ ID:45355, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83073] Another function of VGAM2457 is therefore inhibition of LOC255308 (Accession XM_170536). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255308. LOC56963 (Accession XM_049372) is another VGAM2457 host target gene. LOC56963 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC56963, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC56963 BINDING SITE, designated SEQ ID:35399, to the nucleotide sequence of VGAM2457 RNA, herein designated VGAM RNA, also designated SEQ ID:5168.

[83074] Another function of VGAM2457 is therefore inhibition of LOC56963 (Accession XM_049372). Accordingly, utilities of VGAM2457 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC56963. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2458 (VGAM2458) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83075] VGAM2458 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2458 was detected is described hereinabove with reference to Figs. 1-8.

[83076] VGAM2458 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus

1. VGAM2458 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83077] VGAM2458 gene encodes a VGAM2458 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2458 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2458 precursor RNA is designated SEQ ID:2444, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2444 is located at position 183475 relative to the genome of Mouse Cytomegalovirus 1.

[83078] VGAM2458 precursor RNA folds onto itself, forming VGAM2458 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83079] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2458 folded precursor RNA into VGAM2458 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 65%) nucleotide sequence of VGAM2458 RNA is designated SEQ ID:5169, and is provided hereinbelow with reference to the sequence listing part.

[83080] VGAM2458 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2458 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2458 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83081] VGAM2458 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2458 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2458 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2458 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2458 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83082] The complementary binding of VGAM2458 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2458 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2458 host target RNA into VGAM2458 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83083] It is appreciated that VGAM2458 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2458 host target genes. The mRNA of each one of this plurality of VGAM2458 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2458 RNA, herein designated VGAM RNA, and which when bound by VGAM2458 RNA causes inhibition of translation of respective one or more VGAM2458 host target proteins.

[83084] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2458 gene, herein designated VGAM GENE, on one or more VGAM2458 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83085] It is yet further appreciated that a function of VGAM2458 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2458 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2458 correlate with, and may be deduced from, the identity of the host target genes which VGAM2458 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83086] Nucleotide sequences of the VGAM2458 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2458 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2458 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2458 are further described hereinbelow with reference to Table 1.

[83087] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2458 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2458 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83088] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2458 gene, herein designated VGAM is inhibition of expression of VGAM2458 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2458 correlate with, and may be deduced from, the identity of the target genes which VGAM2458 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83089] Male Germ Cell-associated Kinase (MAK, Accession NM_005906) is a VGAM2458 host target gene. MAK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MAK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAK BINDING SITE, designated SEQ ID:12528, to the nucleotide

sequence of VGAM2458 RNA, herein designated VGAM RNA, also designated SEQ ID:5169.

[83090] A function of VGAM2458 is therefore inhibition of Male Germ Cell-associated Kinase (MAK, Accession NM_005906), a gene which plays an important role in spermatogenesis. Accordingly, utilities of VGAM2458 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAK. The function of MAK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1322.Prominin-like 1 (mouse) (PROML1, Accession NM_006017) is another VGAM2458 host target gene. PROML1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PROML1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PROML1 BINDING SITE, designated SEQ ID:12636, to the nucleotide sequence of VGAM2458 RNA, herein designated VGAM RNA, also designated SEQ ID:5169.

[83091] Another function of VGAM2458 is therefore inhibition of

Prominin-like 1 (mouse) (PROML1, Accession NM_006017), a gene which is a Transmembrane protein. Accordingly, utilities of VGAM2458 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PROML1. The function of PROML1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM905.RAD9 Homolog (S. pombe) (RAD9, Accession NM_004584) is another VGAM2458 host target gene. RAD9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAD9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD9 BINDING SITE, designated SEQ ID:10931, to the nucleotide sequence of VGAM2458 RNA, herein designated VGAM RNA, also designated SEQ ID:5169.

[83092] Another function of VGAM2458 is therefore inhibition of RAD9 Homolog (S. pombe) (RAD9, Accession NM_004584), a gene which may function as a cell cycle checkpoint protein. Accordingly, utilities of VGAM2458 include diagnosis, prevention and treatment of diseases

and clinical conditions associated with RAD9. The function of RAD9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.DKFZp434J0617 (Accession NM_032246) is another VGAM2458 host target gene. DKFZp434J0617 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZp434J0617, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp434J0617 BINDING SITE, designated SEQ ID:25981, to the nucleotide sequence of VGAM2458 RNA, herein designated VGAM RNA, also designated SEQ ID:5169.

[83093] Another function of VGAM2458 is therefore inhibition of DKFZp434J0617 (Accession NM_032246). Accordingly, utilities of VGAM2458 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp434J0617. HT012 (Accession NM_018473) is another VGAM2458 host target gene. HT012 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HT012, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HT012 BINDING SITE, designated SEQ ID:20540, to the nucleotide sequence of VGAM2458 RNA, herein designated VGAM RNA, also designated SEQ ID:5169.

[83094] Another function of VGAM2458 is therefore inhibition of HT012 (Accession NM_018473). Accordingly, utilities of VGAM2458 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HT012. KIAA0945 (Accession NM_014952) is another VGAM2458 host target gene. KIAA0945 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0945, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0945 BINDING SITE, designated SEQ ID:17288, to the nucleotide sequence of VGAM2458 RNA, herein designated VGAM RNA, also designated SEQ ID:5169.

[83095] Another function of VGAM2458 is therefore inhibition of KIAA0945 (Accession NM_014952). Accordingly, utilities of VGAM2458 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0945. Signal-regulatory Protein Beta 1 (SIRPB1, Accession NM_006065) is another VGAM2458 host target gene. SIRPB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SIRPB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIRPB1 BINDING SITE, designated SEQ ID:12707, to the nucleotide sequence of VGAM2458 RNA, herein designated VGAM RNA, also designated SEQ ID:5169.

[83096] Another function of VGAM2458 is therefore inhibition of Signal-regulatory Protein Beta 1 (SIRPB1, Accession NM_006065). Accordingly, utilities of VGAM2458 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIRPB1. LOC154834 (Accession XM_098621) is another VGAM2458 host target gene. LOC154834 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154834, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of LOC154834 BINDING SITE, designated SEQ ID:41731, to the nucleotide sequence of VGAM2458 RNA, herein designated VGAM RNA, also designated SEQ ID:5169.

[83097] Another function of VGAM2458 is therefore inhibition of LOC154834 (Accession XM_098621). Accordingly, utilities of VGAM2458 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154834. LOC51094 (Accession NM_015999) is another VGAM2458 host target gene. LOC51094 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51094, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51094 BINDING SITE, designated SEQ ID:18089, to the nucleotide sequence of VGAM2458 RNA, herein designated VGAM RNA, also designated SEQ ID:5169.

[83098] Another function of VGAM2458 is therefore inhibition of LOC51094 (Accession NM_015999). Accordingly, utilities of VGAM2458 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51094. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2459 (VGAM2459) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83099] VGAM2459 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2459 was detected is described hereinabove with reference to Figs. 1-8.

[83100] VGAM2459 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2459 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83101] VGAM2459 gene encodes a VGAM2459 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2459 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2459 precursor RNA is designated SEQ ID:2445, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2445 is located at position 121309 relative to the genome of Mouse Cytomegalovirus 1.

[83102] VGAM2459 precursor RNA folds onto itself, forming VGAM2459 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83103] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2459 folded precursor RNA into VGAM2459 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide sequence of VGAM2459 RNA is designated SEQ ID:5170, and is provided hereinbelow with reference to the sequence listing part.

[83104] VGAM2459 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2459 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2459 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83105] VGAM2459 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2459 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2459 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2459 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2459 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83106] The complementary binding of VGAM2459 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2459 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2459 host target RNA into VGAM2459 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83107] It is appreciated that VGAM2459 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2459 host target genes. The mRNA of each one of this plurality of VGAM2459 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2459 RNA, herein designated VGAM RNA, and which when bound by VGAM2459 RNA causes inhibition of translation of respective one or more

VGAM2459 host target proteins.

[83108] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2459 gene, herein designated VGAM GENE, on one or more VGAM2459 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83109] It is yet further appreciated that a function of VGAM2459 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1.

Specific functions, and accordingly utilities, of VGAM2459 correlate with, and may be deduced from, the identity of the host target genes which VGAM2459 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83110] Nucleotide sequences of the VGAM2459 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2459 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2459 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2459 are further described hereinbelow with reference to Table 1.

[83111] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2459 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2459 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83112] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2459 gene, herein designated VGAM is inhibition of expression of VGAM2459 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2459 correlate with, and may be deduced from, the identity of the target genes which VGAM2459 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83113] Gamma-glutamyltransferase 2 (GGT2, Accession XM_057166) is a VGAM2459 host target gene. GGT2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GGT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GGT2 BINDING SITE, designated SEQ ID:36489, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83114] A function of VGAM2459 is therefore inhibition of Gamma-glutamyltransferase 2 (GGT2, Accession XM_057166). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GGT2. Interleukin-1 Receptor-associated Kinase 4 (IRAK4, Accession XM_028349) is another VGAM2459 host target gene. IRAK4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IRAK4, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRAK4 BINDING SITE, designated SEQ ID:30692, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83115] Another function of VGAM2459 is therefore inhibition of Interleukin-1 Receptor-associated Kinase 4 (IRAK4, Accession XM_028349), a gene which may function as an IRAK1 kinase, triggering a cascade of phosphorylation events. Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRAK4. The function of IRAK4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1291.Potassium Intermediate/small Conductance Calcium-activated Channel, Subfamily N, Member 4 (KCNN4, Accession NM_002250) is another VGAM2459 host target gene. KCNN4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KCNN4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCNN4 BINDING SITE, designated SEQ ID:8038, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83116] Another function of VGAM2459 is therefore inhibition of Potassium Intermediate/small Conductance Calcium-activated Channel, Subfamily N, Member 4 (KCNN4, Accession NM_002250), a gene which forms a voltage-independent potassium channel that is activated by intracellular calcium. Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNN4. The function of KCNN4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM152.Paired Box Gene 7 (PAX7, Accession NM_002584) is another VGAM2459 host target gene. PAX7 BINDING SITE1 and PAX7 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PAX7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of PAX7 BINDING SITE1 and PAX7 BINDING SITE2, designated SEQ ID:8446 and SEQ ID:15134 respectively, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83117] Another function of VGAM2459 is therefore inhibition of Paired Box Gene 7 (PAX7, Accession NM_002584), a gene which involves in myogenesis. Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAX7. The function of PAX7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM304.Ribosomal Protein S6 Kinase, 90kDa, Polypeptide 1 (RPS6KA1, Accession XM_001416) is another VGAM2459 host target gene. RPS6KA1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RPS6KA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RPS6KA1 BINDING SITE, designated SEQ ID:29836, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM

RNA, also designated SEQ ID:5170.

[83118] Another function of VGAM2459 is therefore inhibition of Ribosomal Protein S6 Kinase, 90kDa, Polypeptide 1 (RPS6KA1, Accession XM_001416). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RPS6KA1. ARS2 (Accession NM_015908) is another VGAM2459 host target gene. ARS2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARS2 BINDING SITE, designated SEQ ID:18045, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83119] Another function of VGAM2459 is therefore inhibition of ARS2 (Accession NM_015908). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARS2. Cerebellin 1 Precursor (CBLN1, Accession NM_004352) is another VGAM2459 host target gene. CBLN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by CBLN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBLN1 BINDING SITE, designated SEQ ID:10557, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83120] Another function of VGAM2459 is therefore inhibition of Cerebellin 1 Precursor (CBLN1, Accession NM_004352). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBLN1. DKFZP566F2124 (Accession NM_015630) is another VGAM2459 host target gene. DKFZP566F2124 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP566F2124, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566F2124 BINDING SITE, designated SEQ ID:17887, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83121] Another function of VGAM2459 is therefore inhibition of

DKFZP566F2124 (Accession NM_015630). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566F2124. FLJ11712 (Accession NM_024570) is another VGAM2459 host target gene. FLJ11712 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ11712, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11712 BINDING SITE, designated SEQ ID:23796, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83122] Another function of VGAM2459 is therefore inhibition of FLJ11712 (Accession NM_024570). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11712. FLJ32468 (Accession NM_145115) is another VGAM2459 host target gene. FLJ32468 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ32468, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ32468 BINDING SITE, designated SEQ ID:29721, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83123] Another function of VGAM2459 is therefore inhibition of FLJ32468 (Accession NM_145115). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32468. KIAA0469 (Accession NM_014851) is another VGAM2459 host target gene. KIAA0469 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0469, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0469 BINDING SITE, designated SEQ ID:16893, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83124] Another function of VGAM2459 is therefore inhibition of KIAA0469 (Accession NM_014851). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0469. KIAA0662 (Accession XM_088539) is another

VGAM2459 host target gene. KIAA0662 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0662, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0662 BINDING SITE, designated SEQ ID:39803, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83125] Another function of VGAM2459 is therefore inhibition of KIAA0662 (Accession XM_088539). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0662. KIAA1530 (Accession XM_042661) is another VGAM2459 host target gene. KIAA1530 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1530, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1530 BINDING SITE, designated SEQ ID:33733, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83126] Another function of VGAM2459 is therefore inhibition of KIAA1530 (Accession XM_042661). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1530. LOC161635 (Accession XM_172921) is another VGAM2459 host target gene. LOC161635 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC161635, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC161635 BINDING SITE, designated SEQ ID:46184, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83127] Another function of VGAM2459 is therefore inhibition of LOC161635 (Accession XM_172921). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC161635. LOC254057 (Accession XM_173085) is another VGAM2459 host target gene. LOC254057 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254057, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254057 BINDING SITE, designated SEQ ID:46347, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83128] Another function of VGAM2459 is therefore inhibition of LOC254057 (Accession XM_173085). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254057. LOC83693 (Accession NM_031463) is another VGAM2459 host target gene. LOC83693 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC83693, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC83693 BINDING SITE, designated SEQ ID:25495, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83129] Another function of VGAM2459 is therefore inhibition of LOC83693 (Accession NM_031463). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC83693. LOC90288 (Accession XM_030669) is another VGAM2459 host target gene. LOC90288 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90288 BINDING SITE, designated SEQ ID:31105, to the nucleotide sequence of VGAM2459 RNA, herein designated VGAM RNA, also designated SEQ ID:5170.

[83130] Another function of VGAM2459 is therefore inhibition of LOC90288 (Accession XM_030669). Accordingly, utilities of VGAM2459 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90288. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2460 (VGAM2460) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83131] VGAM2460 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2460 was detected is described hereinabove with reference to Figs. 1-8.

[83132] VGAM2460 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2460 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83133] VGAM2460 gene encodes a VGAM2460 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2460 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2460 precursor RNA is designated SEQ ID:2446, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2446 is located at position 17895 relative to the genome of Mouse Cytomegalovirus 1.

[83134] VGAM2460 precursor RNA folds onto itself, forming VGAM2460 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83135] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2460 folded precursor RNA into VGAM2460 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2460 RNA is designated SEQ ID:5171, and is provided hereinbelow with reference to the sequence listing part.

[83136] VGAM2460 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2460 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2460 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83137] VGAM2460 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2460 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2460 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2460 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2460 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83138] The complementary binding of VGAM2460 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2460 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2460 host target RNA into VGAM2460 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83139] It is appreciated that VGAM2460 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2460 host target genes. The mRNA of each one of this plurality of VGAM2460 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2460 RNA, herein designated VGAM RNA, and which when bound by VGAM2460 RNA causes inhibition of translation of respective one or more VGAM2460 host target proteins.

[83140] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2460 gene, herein designated VGAM GENE, on one or more VGAM2460 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83141] It is yet further appreciated that a function of VGAM2460 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2460 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2460 correlate with, and may be deduced from, the identity of the host target genes which VGAM2460 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83142] Nucleotide sequences of the VGAM2460 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2460 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2460 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2460 are further described hereinbelow with reference to Table 1.

[83143] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2460 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2460 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83144] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2460 gene, herein designated VGAM is inhibition of expression of VGAM2460 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2460 correlate with, and may be deduced from, the identity of the target genes which VGAM2460 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83145] CAP350 (Accession NM_014810) is a VGAM2460 host target gene. CAP350 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CAP350, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAP350 BINDING SITE, designated SEQ ID:16771, to the nucleotide sequence of VGAM2460 RNA, herein designated VGAM RNA, also designated SEQ ID:5171.

[83146] A function of VGAM2460 is therefore inhibition of CAP350 (Accession NM_014810). Accordingly, utilities of VGAM2460 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAP350. KIAA0350 (Accession XM_028332) is another VGAM2460 host target gene. KIAA0350 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0350, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0350 BINDING SITE, designated SEQ ID:30663, to the nucleotide sequence of VGAM2460 RNA, herein designated VGAM RNA, also designated SEQ ID:5171.

[83147] Another function of VGAM2460 is therefore inhibition of KIAA0350 (Accession XM_028332). Accordingly, utilities of VGAM2460 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA0350. KIAA1944 (Accession XM_062545) is another VGAM2460 host target gene. KIAA1944 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1944, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1944 BINDING SITE, designated SEQ ID:37229, to the nucleotide sequence of VGAM2460 RNA, herein designated VGAM RNA, also designated SEQ ID:5171.

[83148] Another function of VGAM2460 is therefore inhibition of KIAA1944 (Accession XM_062545). Accordingly, utilities of VGAM2460 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1944. LOC152579 (Accession XM_087489) is another VGAM2460 host target gene. LOC152579 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152579, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152579 BINDING SITE, designated SEQ ID:39290, to

the nucleotide sequence of VGAM2460 RNA, herein designated VGAM RNA, also designated SEQ ID:5171.

[83149] Another function of VGAM2460 is therefore inhibition of LOC152579 (Accession XM_087489). Accordingly, utilities of VGAM2460 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152579. LOC158654 (Accession XM_088632) is another VGAM2460 host target gene. LOC158654 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158654, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158654 BINDING SITE, designated SEQ ID:39876, to the nucleotide sequence of VGAM2460 RNA, herein designated VGAM RNA, also designated SEQ ID:5171.

[83150] Another function of VGAM2460 is therefore inhibition of LOC158654 (Accession XM_088632). Accordingly, utilities of VGAM2460 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158654. LOC200448 (Accession XM_114234) is another VGAM2460 host target gene. LOC200448 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by LOC200448, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200448 BINDING SITE, designated SEQ ID:42816, to the nucleotide sequence of VGAM2460 RNA, herein designated VGAM RNA, also designated SEQ ID:5171.

[83151] Another function of VGAM2460 is therefore inhibition of LOC200448 (Accession XM_114234). Accordingly, utilities of VGAM2460 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200448. LOC222166 (Accession XM_168425) is another VGAM2460 host target gene. LOC222166 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222166, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222166 BINDING SITE, designated SEQ ID:45150, to the nucleotide sequence of VGAM2460 RNA, herein designated VGAM RNA, also designated SEQ ID:5171.

[83152] Another function of VGAM2460 is therefore inhibition of LOC222166 (Accession XM_168425). Accordingly, utilities

of VGAM2460 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222166. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2461 (VGAM2461) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83153] VGAM2461 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2461 was detected is described hereinabove with reference to Figs. 1-8.

[83154] VGAM2461 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2461 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83155] VGAM2461 gene encodes a VGAM2461 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2461 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2461 precursor RNA is designated SEQ ID:2447, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2447 is located at position 219567 relative to the genome of Mouse Cytomegalovirus 1.

[83156] VGAM2461 precursor RNA folds onto itself, forming VGAM2461 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83157] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2461 folded precursor RNA into VGAM2461 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2461 RNA is designated SEQ ID:5172, and

is provided hereinbelow with reference to the sequence listing part.

[83158] VGAM2461 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2461 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2461 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83159] VGAM2461 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2461 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2461 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2461 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2461 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83160] The complementary binding of VGAM2461 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2461 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2461 host target RNA into VGAM2461 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83161] It is appreciated that VGAM2461 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2461 host target genes. The mRNA of each one of this plurality of VGAM2461 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2461 RNA, herein designated VGAM RNA, and which when bound by VGAM2461 RNA causes inhibition of translation of respective one or more VGAM2461 host target proteins.

[83162] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2461 gene, herein designated VGAM GENE, on one or more VGAM2461 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83163] It is yet further appreciated that a function of VGAM2461 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2461 correlate with, and may be deduced from, the identity of the host target genes which VGAM2461 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83164] Nucleotide sequences of the VGAM2461 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2461 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2461 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2461 are further described hereinbelow with reference to Table 1.

[83165] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2461 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2461 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83166] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2461 gene, herein designated VGAM is inhibition of expression of VGAM2461 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2461 correlate with, and may be deduced from, the identity of the target genes which VGAM2461 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83167] Cyclin-dependent Kinase 2 (CDK2, Accession NM_001798) is a VGAM2461 host target gene. CDK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDK2 BINDING SITE, designated SEQ ID:7552, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83168] A function of VGAM2461 is therefore inhibition of Cyclin-dependent Kinase 2 (CDK2, Accession NM_001798), a gene which plays a unique role in cell cycle regulation of vertebrate cells. Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDK2. The function of

CDK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1467.Cytochrome P450, Subfamily VIIIB (sterol 12-alpha-hydroxylase), Polypeptide 1 (CYP8B1, Accession NM_004391) is another VGAM2461 host target gene. CYP8B1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP8B1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP8B1 BINDING SITE, designated SEQ ID:10625, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83169] Another function of VGAM2461 is therefore inhibition of Cytochrome P450, Subfamily VIIIB (sterol 12-alpha-hydroxylase), Polypeptide 1 (CYP8B1, Accession NM_004391), a gene which functions in bile acid biosynthesis. Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP8B1. The function of CYP8B1 and its association with various diseases and clin-

ical conditions, has been established by previous studies, as described hereinabove with reference to VGAM923.High-mobility Group Nucleosomal Binding Domain 2 (HMGN2, Accession NM_005517) is another VGAM2461 host target gene. HMGN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HMGN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMGN2 BINDING SITE, designated SEQ ID:12040, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83170] Another function of VGAM2461 is therefore inhibition of High-mobility Group Nucleosomal Binding Domain 2 (HMGN2, Accession NM_005517), a gene which binds HMG proteins and may confer specific conformations to transcriptionally active regions of chromatin. Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HMGN2. The function of HMGN2 has been established by previous studies. Chromosomal proteins HMG-17 and HMG-14 are among the most abundant, ubiqui-

tous, and evolutionarily conserved nonhistone proteins found in the nuclei of higher eukaryotes. The large number of retropseudogenes are scattered over several chromosomes. Landsman and Bustin (1986) showed that the nonhistone chromosomal proteins HMG-14 (OMIM Ref. No. 163920) and HMG-17 are encoded by distinct genes, each of which is part of a separate multigene family. These families may have evolved independently from similar genetic elements or from a shared ancestral gene in which the nucleotide sequence coding for the DNA-binding domain of the protein is the most conserved region. The structural differences between the molecules and the differences in their DNA-binding domains suggest that the proteins may be involved in distinguishable cellular functions. They may confer specific conformations to transcriptionally active regions of chromatin. (HMG stands for 'high mobility group.') Landsman and Bustin (1986) and Landsman et al. (1986) isolated and sequenced full-length cDNAs for human HMG-14 and HMG-17. The sequences indicate that these are both functional genes. Porkka et al. (2002) reported a cDNA that encodes a fragment of HMG17 (referred to as HMGN2 by them), a highly conserved nucleosomal protein thought to be involved in

unfolding higher-order chromatin structure and facilitating the transcriptional activation of mammalian genes (Bustin, 1999). Porkka et al. (2002) derived a 31-amino acid synthetic peptide from this HMG17 fragment which, when injected intravenously, accumulates in the nuclei of tumor endothelial cells and tumor cells, carrying a payload to a tumor and into the cell nuclei in the tumor. They suggested that the peptide may be suitable for targeting cytotoxic drugs and gene therapy vectors into tumors.

[83171] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83172] Landsman, D.; Bustin, M. : Chromosomal proteins HMG-14 and HMG-17: distinct multigene families coding for similar types of transcripts. J. Biol. Chem. 261: 16087-16091, 1986. ; and

[83173] Porkka, K.; Laakkonen, P.; Hoffman, J. A.; Bernasconi, M.; Ruoslahti, E. : A fragment of the HMGN2 protein homes to the nuclei of tumor cells and tumor endothelial cells in vivo. Proc. N.

[83174] Further studies establishing the function and utilities of HMGN2 are found in John Hopkins OMIM database record ID 163910, and in sited publications numbered

3011-3018 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.RAD1 Homolog (S. pombe) (RAD1, Accession NM_133377) is another VGAM2461 host target gene. RAD1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RAD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAD1 BINDING SITE, designated SEQ ID:28500, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83175] Another function of VGAM2461 is therefore inhibition of RAD1 Homolog (S. pombe) (RAD1, Accession NM_133377), a gene which has important roles in DNA damage-activated mitotic and meiotic cell cycle checkpoints. Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAD1. The function of RAD1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM922.RNA (guanine-7-) Methyltransferase (RNMT, Accession

NM_003799) is another VGAM2461 host target gene. RNMT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNMT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNMT BINDING SITE, designated SEQ ID:9888, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83176] Another function of VGAM2461 is therefore inhibition of RNA (guanine-7-) Methyltransferase (RNMT, Accession NM_003799), a gene which catalyzes the methylation of GpppN- at the guanine N7 position. Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNMT. The function of RNMT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM178.WW45 (Accession NM_021818) is another VGAM2461 host target gene. WW45 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WW45, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WW45 BINDING SITE, designated SEQ ID:22397, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83177] Another function of VGAM2461 is therefore inhibition of WW45 (Accession NM_021818), a gene which is required for ubiquitination and therefore degradation of several cell surface proteins like gap1, fur4, mal61 and ste2. also acts on rbp1. Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WW45. The function of WW45 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1646.CXYorf1 (Accession XM_088704) is another VGAM2461 host target gene. CXYorf1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CXYorf1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CXYorf1 BINDING SITE, designated SEQ ID:39910, to the nucleotide

sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83178] Another function of VGAM2461 is therefore inhibition of CXYorf1 (Accession XM_088704). Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXY-orf1. KIAA1393 (Accession XM_050793) is another VGAM2461 host target gene. KIAA1393 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1393, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1393 BINDING SITE, designated SEQ ID:35684, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83179] Another function of VGAM2461 is therefore inhibition of KIAA1393 (Accession XM_050793). Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1393. PRO0902 (Accession NM_053057) is another VGAM2461 host target gene. PRO0902 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by PRO0902, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0902 BINDING SITE, designated SEQ ID:27606, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83180] Another function of VGAM2461 is therefore inhibition of PRO0902 (Accession NM_053057). Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0902. TU3A (Accession NM_007177) is another VGAM2461 host target gene. TU3A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TU3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TU3A BINDING SITE, designated SEQ ID:14034, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83181] Another function of VGAM2461 is therefore inhibition of TU3A (Accession NM_007177). Accordingly, utilities of

VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TU3A. LOC152267 (Accession XM_017070) is another VGAM2461 host target gene. LOC152267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152267 BINDING SITE, designated SEQ ID:30294, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83182] Another function of VGAM2461 is therefore inhibition of LOC152267 (Accession XM_017070). Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152267. LOC200093 (Accession XM_032184) is another VGAM2461 host target gene. LOC200093 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200093, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC200093 BINDING SITE, designated SEQ ID:31602, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83183] Another function of VGAM2461 is therefore inhibition of LOC200093 (Accession XM_032184). Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200093. LOC204084 (Accession XM_115181) is another VGAM2461 host target gene. LOC204084 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC204084, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC204084 BINDING SITE, designated SEQ ID:43086, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83184] Another function of VGAM2461 is therefore inhibition of LOC204084 (Accession XM_115181). Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC204084. LOC221463 (Accession XM_166374) is another VGAM2461 host target gene. LOC221463 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221463, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221463 BINDING SITE, designated SEQ ID:44202, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83185] Another function of VGAM2461 is therefore inhibition of LOC221463 (Accession XM_166374). Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221463. LOC91040 (Accession XM_035641) is another VGAM2461 host target gene. LOC91040 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91040 BINDING SITE, designated SEQ ID:32319, to the nucleotide sequence of VGAM2461 RNA, herein designated VGAM RNA, also designated SEQ ID:5172.

[83186] Another function of VGAM2461 is therefore inhibition of

LOC91040 (Accession XM_035641). Accordingly, utilities of VGAM2461 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91040. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2462 (VGAM2462) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83187] VGAM2462 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2462 was detected is described hereinabove with reference to Figs. 1-8.

[83188] VGAM2462 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2462 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83189] VGAM2462 gene encodes a VGAM2462 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2462 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2462 precursor RNA is designated SEQ ID:2448, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2448 is located at position 164 relative to the genome of Mouse Cytomegalovirus 1.

[83190] VGAM2462 precursor RNA folds onto itself, forming VGAM2462 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83191] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2462 folded precursor RNA into VGAM2462 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 48%) nucleotide se-

quence of VGAM2462 RNA is designated SEQ ID:5173, and is provided hereinbelow with reference to the sequence listing part.

[83192] VGAM2462 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2462 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2462 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83193] VGAM2462 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2462 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2462 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2462 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2462 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83194] The complementary binding of VGAM2462 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2462 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2462 host target RNA into VGAM2462 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83195] It is appreciated that VGAM2462 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2462 host target genes. The mRNA of each one of this plurality of VGAM2462 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2462 RNA, herein designated VGAM RNA, and which when bound by VGAM2462 RNA causes inhibition of translation of respective one or more VGAM2462 host target proteins.

[83196] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2462 gene, herein designated VGAM GENE, on one or more VGAM2462 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83197] It is yet further appreciated that a function of VGAM2462

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2462 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2462 correlate with, and may be deduced from, the identity of the host target genes which VGAM2462 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83198] Nucleotide sequences of the VGAM2462 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2462 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2462 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2462 are further described hereinbelow with reference to Table 1.

[83199] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2462 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2462 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83200] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2462 gene, herein designated VGAM is inhibition of expression of VGAM2462 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2462 correlate with, and may be deduced from, the identity of the target genes which VGAM2462 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83201] CARPX (Accession NM_020178) is a VGAM2462 host target gene. CARPX BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CARPX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CARPX BINDING SITE, designated SEQ ID:21397, to the nucleotide sequence of VGAM2462 RNA, herein designated VGAM RNA, also designated SEQ ID:5173.

[83202] A function of VGAM2462 is therefore inhibition of CARPX (Accession NM_020178), a gene which is alpha-carbonic anhydrases-related protein. Accordingly, utilities of VGAM2462 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CARPX.

The function of CARPX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM904.Neural Retina Leucine Zipper (NRL, Accession NM_006177) is another VGAM2462 host target gene. NRL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NRL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NRL BINDING SITE, designated SEQ ID:12837, to the nucleotide sequence of VGAM2462 RNA, herein designated VGAM RNA, also designated SEQ ID:5173.

[83203] Another function of VGAM2462 is therefore inhibition of Neural Retina Leucine Zipper (NRL, Accession NM_006177), a gene which has a basic motif and a leucine zipper domain similar to jun and fos. Accordingly, utilities of VGAM2462 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRL. The function of NRL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM419.Retinoic Acid Receptor, Beta (RARB, Acces-

sion NM_016152) is another VGAM2462 host target gene. RARB BINDING SITE1 and RARB BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RARB, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RARB BINDING SITE1 and RARB BINDING SITE2, designated SEQ ID:18235 and SEQ ID:6691 respectively, to the nucleotide sequence of VGAM2462 RNA, herein designated VGAM RNA, also designated SEQ ID:5173.

[83204] Another function of VGAM2462 is therefore inhibition of Retinoic Acid Receptor, Beta (RARB, Accession NM_016152), a gene which is one member of the steroid/thyroid hormone receptor family of ligand-activated transcription factors. Accordingly, utilities of VGAM2462 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RARB. The function of RARB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM179.TEM7 (Accession NM_020405) is another VGAM2462 host target gene. TEM7 BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by TEM7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TEM7 BINDING SITE, designated SEQ ID:21673, to the nucleotide sequence of VGAM2462 RNA, herein designated VGAM RNA, also designated SEQ ID:5173.

[83205] Another function of VGAM2462 is therefore inhibition of TEM7 (Accession NM_020405), a gene which involves in angiogenesis. Accordingly, utilities of VGAM2462 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TEM7. The function of TEM7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM23.KIAA1340 (Accession XM_044836) is another VGAM2462 host target gene. KIAA1340 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1340, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1340 BINDING SITE, designated SEQ ID:34299, to the

nucleotide sequence of VGAM2462 RNA, herein designated VGAM RNA, also designated SEQ ID:5173.

[83206] Another function of VGAM2462 is therefore inhibition of KIAA1340 (Accession XM_044836). Accordingly, utilities of VGAM2462 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1340. PRO1331 (Accession NM_030778) is another VGAM2462 host target gene. PRO1331 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRO1331, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1331 BINDING SITE, designated SEQ ID:25066, to the nucleotide sequence of VGAM2462 RNA, herein designated VGAM RNA, also designated SEQ ID:5173.

[83207] Another function of VGAM2462 is therefore inhibition of PRO1331 (Accession NM_030778). Accordingly, utilities of VGAM2462 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1331. LOC201696 (Accession XM_032269) is another VGAM2462 host target gene. LOC201696 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by LOC201696, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201696 BINDING SITE, designated SEQ ID:31625, to the nucleotide sequence of VGAM2462 RNA, herein designated VGAM RNA, also designated SEQ ID:5173.

[83208] Another function of VGAM2462 is therefore inhibition of LOC201696 (Accession XM_032269). Accordingly, utilities of VGAM2462 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201696. LOC221092 (Accession XM_167749) is another VGAM2462 host target gene. LOC221092 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221092, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221092 BINDING SITE, designated SEQ ID:44774, to the nucleotide sequence of VGAM2462 RNA, herein designated VGAM RNA, also designated SEQ ID:5173.

[83209] Another function of VGAM2462 is therefore inhibition of LOC221092 (Accession XM_167749). Accordingly, utilities

of VGAM2462 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221092. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2463 (VGAM2463) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83210] VGAM2463 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2463 was detected is described hereinabove with reference to Figs. 1-8.

[83211] VGAM2463 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2463 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83212] VGAM2463 gene encodes a VGAM2463 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2463 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nu-

cleotide sequence of VGAM2463 precursor RNA is designated SEQ ID:2449, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2449 is located at position 225478 relative to the genome of Mouse Cytomegalovirus 1.

[83213] VGAM2463 precursor RNA folds onto itself, forming VGAM2463 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83214] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2463 folded precursor RNA into VGAM2463 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2463 RNA is designated SEQ ID:5174, and

is provided hereinbelow with reference to the sequence listing part.

[83215] VGAM2463 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2463 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2463 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83216] VGAM2463 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2463 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2463 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limit-

ing - VGAM2463 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2463 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83217] The complementary binding of VGAM2463 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2463 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2463 host target RNA into VGAM2463 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83218] It is appreciated that VGAM2463 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2463 host target genes. The mRNA of each one of this plurality of VGAM2463 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly com-

plementary to VGAM2463 RNA, herein designated VGAM RNA, and which when bound by VGAM2463 RNA causes inhibition of translation of respective one or more VGAM2463 host target proteins.

[83219] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2463 gene, herein designated VGAM GENE, on one or more VGAM2463 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83220] It is yet further appreciated that a function of VGAM2463 is inhibition of expression of host target genes, as part of

a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2463 correlate with, and may be deduced from, the identity of the host target genes which VGAM2463 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83221] Nucleotide sequences of the VGAM2463 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2463 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2463 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2463 are further described hereinbelow with reference to Table 1.

[83222] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2463 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2463 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83223] As mentioned hereinabove with reference to Fig. 1, a

function of VGAM2463 gene, herein designated VGAM is inhibition of expression of VGAM2463 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2463 correlate with, and may be deduced from, the identity of the target genes which VGAM2463 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83224] Active BCR-related Gene (ABR, Accession NM_001092) is a VGAM2463 host target gene. ABR BINDING SITE1 and ABR BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ABR, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABR BINDING SITE1 and ABR BINDING SITE2, designated SEQ ID:6750 and SEQ ID:22495 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83225] A function of VGAM2463 is therefore inhibition of Active BCR-related Gene (ABR, Accession NM_001092), a gene which gtpase-activating protein for rac and cdc42. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions

associated with ABR. The function of ABR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM489.ADP-ribosylation Factor 3 (ARF3, Accession NM_001659) is another VGAM2463 host target gene. ARF3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARF3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARF3 BINDING SITE, designated SEQ ID:7379, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83226] Another function of VGAM2463 is therefore inhibition of ADP-ribosylation Factor 3 (ARF3, Accession NM_001659). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARF3. Asialoglycoprotein Receptor 2 (ASGR2, Accession NM_001181) is another VGAM2463 host target gene. ASGR2 BINDING SITE1 through ASGR2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ASGR2, corre-

sponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ASGR2 BINDING SITE1 through ASGR2 BINDING SITE3, designated SEQ ID:6852, SEQ ID:28132 and SEQ ID:28131 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83227] Another function of VGAM2463 is therefore inhibition of Asialoglycoprotein Receptor 2 (ASGR2, Accession NM_001181). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ASGR2. B-cell CLL/lymphoma 9 (BCL9, Accession NM_004326) is another VGAM2463 host target gene. BCL9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL9 BINDING SITE, designated SEQ ID:10523, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83228] Another function of VGAM2463 is therefore inhibition of B-cell CLL/lymphoma 9 (BCL9, Accession NM_004326), a gene which recruits of PYGO to the nuclear beta-catenin-TCF complex in Wnt/Wingless signaling. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL9. The function of BCL9 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM74.BRIP1 (Accession NM_032043) is another VGAM2463 host target gene. BRIP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BRIP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BRIP1 BINDING SITE, designated SEQ ID:25755, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83229] Another function of VGAM2463 is therefore inhibition of BRIP1 (Accession NM_032043). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BRIP1.

Calcium Channel, Voltage-dependent, Gamma Subunit 7 (CACNG7, Accession NM_031896) is another VGAM2463 host target gene. CACNG7 BINDING SITE1 and CACNG7 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CACNG7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CACNG7 BINDING SITE1 and CACNG7 BINDING SITE2, designated SEQ ID:25639 and SEQ ID:25640 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83230] Another function of VGAM2463 is therefore inhibition of Calcium Channel, Voltage-dependent, Gamma Subunit 7 (CACNG7, Accession NM_031896), a gene which may stabilize the calcium channel in an inactivated (closed) state. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CACNG7. The function of CACNG7 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2228.Cholinergic Receptor, Nicotinic, Alpha

Polypeptide 5 (CHRNA5, Accession XM_007577) is another VGAM2463 host target gene. CHRNA5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CHRNA5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHRNA5 BINDING SITE, designated SEQ ID:30058, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83231] Another function of VGAM2463 is therefore inhibition of Cholinergic Receptor, Nicotinic, Alpha Polypeptide 5 (CHRNA5, Accession XM_007577). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRNA5. Cholinergic Receptor, Nicotinic, Beta Polypeptide 1 (muscle) (CHRNB1, Accession XM_018451) is another VGAM2463 host target gene. CHRNB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHRNB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHRNB1

BINDING SITE, designated SEQ ID:30359, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83232] Another function of VGAM2463 is therefore inhibition of Cholinergic Receptor, Nicotinic, Beta Polypeptide 1 (muscle) (CHRNB1, Accession XM_018451). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHRNB1. Ceroid-lipofuscinosis, Neuronal 6, Late Infantile, Variant (CLN6, Accession NM_017882) is another VGAM2463 host target gene. CLN6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CLN6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLN6 BINDING SITE, designated SEQ ID:19550, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83233] Another function of VGAM2463 is therefore inhibition of Ceroid-lipofuscinosis, Neuronal 6, Late Infantile, Variant (CLN6, Accession NM_017882). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with CLN6. Collagen, Type I, Alpha 1 (COL1A1, Accession NM_000088) is another VGAM2463 host target gene. COL1A1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL1A1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL1A1 BINDING SITE, designated SEQ ID:5538, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83234] Another function of VGAM2463 is therefore inhibition of Collagen, Type I, Alpha 1 (COL1A1, Accession NM_000088). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL1A1. Corticotropin Releasing Hormone Receptor 2 (CRHR2, Accession NM_001883) is another VGAM2463 host target gene. CRHR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CRHR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of CRHR2 BINDING SITE, designated SEQ ID:7612, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83235] Another function of VGAM2463 is therefore inhibition of Corticotropin Releasing Hormone Receptor 2 (CRHR2, Accession NM_001883), a gene which is a corticotropin releasing factor receptor type II. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CRHR2. The function of CRHR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM737.Cytochrome B-561 (CYB561, Accession NM_001915) is another VGAM2463 host target gene. CYB561 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CYB561, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYB561 BINDING SITE, designated SEQ ID:7630, to the nucleotide sequence of VGAM2463 RNA,

herein designated VGAM RNA, also designated SEQ ID:5174.

[83236] Another function of VGAM2463 is therefore inhibition of Cytochrome B-561 (CYB561, Accession NM_001915), a gene which is a secretory vesicle-specific electron transport protein. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYB561. The function of CYB561 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1929.Damage-specific DNA Binding Protein 1, 127kDa (DDB1, Accession NM_001923) is another VGAM2463 host target gene. DDB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DDB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDB1 BINDING SITE, designated SEQ ID:7639, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83237] Another function of VGAM2463 is therefore inhibition of

Damage-specific DNA Binding Protein 1, 127kDa (DDB1, Accession NM_001923). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDB1. Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST, Accession NM_001933) is another VGAM2463 host target gene. DLST BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DLST, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLST BINDING SITE, designated SEQ ID:7643, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83238] Another function of VGAM2463 is therefore inhibition of Dihydrolipoamide S-succinyltransferase (E2 component of 2-oxo-glutarate complex) (DLST, Accession NM_001933), a gene which catalyzes the oxidative decarboxylation of alpha-keto acids. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLST. The function of DLST and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to VGAM656.Ectodermal Dysplasia 1, Anhidrotic (ED1, Accession NM_001399) is another VGAM2463 host target gene. ED1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ED1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ED1 BINDING SITE, designated SEQ ID:7097, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83239] Another function of VGAM2463 is therefore inhibition of Ectodermal Dysplasia 1, Anhidrotic (ED1, Accession NM_001399). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ED1. EH-domain Containing 3 (EHD3, Accession NM_014600) is another VGAM2463 host target gene. EHD3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EHD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of EHD3 BINDING SITE, designated SEQ ID:15957, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83240] Another function of VGAM2463 is therefore inhibition of EH-domain Containing 3 (EHD3, Accession NM_014600). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EHD3. Empty Spiracles Homolog 2 (Drosophila) (EMX2, Accession XM_113640) is another VGAM2463 host target gene. EMX2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EMX2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EMX2 BINDING SITE, designated SEQ ID:42316, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83241] Another function of VGAM2463 is therefore inhibition of Empty Spiracles Homolog 2 (Drosophila) (EMX2, Accession XM_113640), a gene which may function in combinations with otx1/2 to specify cell fates in the developing central

nervous system. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMX2. The function of EMX2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM510.Eyes Absent Homolog 4 (Drosophila) (EYA4, Accession NM_004100) is another VGAM2463 host target gene. EYA4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EYA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EYA4 BINDING SITE, designated SEQ ID:10309, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83242] Another function of VGAM2463 is therefore inhibition of Eyes Absent Homolog 4 (Drosophila) (EYA4, Accession NM_004100), a gene which may be involved in development of the eye (by similarity). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EYA4. The function of EYA4 and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM707.Fanconi Anemia, Complementation Group C (FANCC, Accession XM_047190) is another VGAM2463 host target gene. FANCC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FANCC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FANCC BINDING SITE, designated SEQ ID:34906, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83243] Another function of VGAM2463 is therefore inhibition of Fanconi Anemia, Complementation Group C (FANCC, Accession XM_047190). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCC. F-box and Leucine-rich Repeat Protein 4 (FBXL4, Accession NM_012160) is another VGAM2463 host target gene. FBXL4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FBXL4, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXL4 BINDING SITE, designated SEQ ID:14459, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83244] Another function of VGAM2463 is therefore inhibition of F-box and Leucine-rich Repeat Protein 4 (FBXL4, Accession NM_012160), a gene which may degrade regulatory proteins by recruiting them for ubiquitin conjugating enzymes. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXL4. The function of FBXL4 has been established by previous studies. The F box, named after cyclin F (CCNF; 600227), in which it was originally observed, is an approximately 40-amino acid motif that binds SKP1 (OMIM Ref. No. 601434). F-box proteins are components of modular E3 ubiquitin protein ligases called SCFs (SKP1, OMIM Ref. No. 603134), F-box proteins), which function in phosphorylation-dependent ubiquitination. Using a yeast 2-hybrid screen with SKP1 as bait, followed by searching sequence databases, Winston et al. (1999) and Cenciarelli et al. (1999) identified 33

mammalian and 26 human F-box proteins, respectively. These contained C termini with leucine-rich repeats (FBXLs, e.g., SKP2 (OMIM Ref. No. 601436)), WD40 domains (FBXWs, e.g., BTRCP (OMIM Ref. No. 603482)), or no recognizable motifs (FBXOs, e.g., CCNF). Using RT-PCR analysis, Winston et al. (1999) detected FBXL4 expression in heart, kidney, liver, lung, pancreas, and placenta, but not in skeletal muscle. Immunofluorescence microscopy demonstrated both nuclear and cytoplasmic expression. By searching sequence databases, Ilyin et al. (2000) identified a cDNA encoding FBXL4, which they referred to as FBL5. The deduced 621-amino acid protein contains at least 9 leucine-rich repeats. Based on its inclusion within a mapped clone, Ilyin et al. (2000) mapped the FBXL4 gene to 6q16.1-q16.3.

[83245] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83246] Cenciarelli, C.; Chiaur, D. S.; Guardavaccaro, D.; Parks, W.; Vidal, M.; Pagano, M. : Identification of a family of human F-box proteins. Curr. Biol. 9: 1177-1179, 1999. ; and

[83247] Ilyin, G. P.; Rialland, M.; Pigeon, C.; Guguen-Guillouzo, C. : cDNA cloning and expression analysis of new members

of the mammalian F-box protein family. Genomics 67: 40-47, 2000.

[83248] Further studies establishing the function and utilities of FBXL4 are found in John Hopkins OMIM database record ID 605654, and in sited publications numbered 40 and 8278 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Fragile Histidine Triad Gene (FHIT, Accession NM_002012) is another VGAM2463 host target gene. FHIT BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FHIT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FHIT BINDING SITE, designated SEQ ID:7753, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83249] Another function of VGAM2463 is therefore inhibition of Fragile Histidine Triad Gene (FHIT, Accession NM_002012), a gene which cleaves a-5'-ppp-5'a to yield amp and adp. possible tumor suppressor for specific tissues. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical con-

ditions associated with FHIT. The function of FHIT has been established by previous studies. Cohen et al. (1979) observed a constitutional reciprocal t(3;8) translocation associated with early onset, bilateral, and multifocal clear cell renal carcinoma (OMIM Ref. No. 144700). Wang and Perkins (1984) demonstrated that the site of the break on chromosome 3 is at 3p14.2. Another cytogenetic landmark in the 3p14.2 region is the most common of the constitutive aphidicolin-inducible fragile sites, FRA3B (Markkanen et al., 1982). A 200 to 300 kb region of 3p14.2, including the fragile site locus FRA3B, is homozygously deleted in multiple tumor-derived cell lines. By exon amplification from cosmids covering this deleted region, Ohta et al. (1996) identified a human gene they designated FHIT for 'fragile histidine triad' gene. The FHIT gene, a member of the histidine triad gene family, encodes a protein similar to the aph1 gene in S. pombe. The gene is composed of 10 exons distributed over at least 500 kb, with three 5-prime untranslated exons centromeric to the renal carcinoma-associated 3p14.2 breakpoint, the remaining exons telomeric to this translocation breakpoint, and exon 5 within the homozygously deleted fragile region. Aberrant transcripts of the FHIT locus were

found in approximately 50% of esophageal, stomach, and colon carcinomas. Sozzi et al. (1996) analyzed the FHIT gene structure and transcription in a large series of lung cancers of the small cell (SCLC) and nonsmall cell (NSCLC) type. FHIT transcripts from tumors and normal tissues were studied by RT-PCR. In 11 of 14 SCLC tumors, abnormal-sized transcripts were found. Both normal- and abnormal-sized transcripts were present in 9 of these cases. In 18 of 25 NSCLC tumors, abnormal transcripts were found; in these tumors, there were 1 or 2 abnormal-sized bands which were always accompanied by a normal-sized transcript. The authors postulated that the normal-sized transcripts reflected the presence of normal cells within the tumors. Sozzi et al. (1996) reported loss of heterozygosity for microsatellite markers internal to and flanking the FHIT locus. Eleven of 12 informative tumors that exhibited abnormal FHIT transcripts showed allelic loss at one or more of the loci tested. The authors postulated that in these tumors inactivation of the FHIT gene occurred by a mechanism of loss of one allele and altered expression of the remaining allele. They further postulated that loss of function of the FHIT gene could result in the constitutive accumulation of high levels of intracellular

diadenosine tetraphosphate and the stimulation of DNA synthesis and proliferation. Sozzi et al. (1996) proposed that breakage in a fragile site-containing gene may occur as a consequence of physical, chemical, and biologic agents. Virgilio et al. (1996) noted that head and neck cancers (HNSCC; 601400) represent 3% of all cancer in Western countries. In some geographic areas such as India, the proportion of cancer represented by these cancers is as high as 45%; 90 to 95% of head and neck cancers are of the squamous cell type. Tobacco and alcohol have been recognized as etiologic factors in these carcinomas. Several regions of loss of heterozygosity (LOH) have been identified in HNSCC. The 9p region presents the highest rate of genetic alteration (75%) and LOH has been related to the CDKN2 (OMIM Ref. No. 600160) tumor suppressor gene. The second most frequent alteration involves 3p (45 to 55%). Virgilio et al. (1996) examined 26 HNSCC cell lines for deletions within the FHIT locus by Southern analysis, for allelic loss of specific exons of FHIT by fluorescence in situ hybridization, and for integrity of FHIT transcripts. Three of the 26 cell lines exhibited homozygous deletions within the FHIT gene, 55% (15 of 25) showed aberrant transcripts, and 65% (13 of 20) showed multiple

cell populations with losses of different portions of the FHIT alleles. When the data were combined, 22 of 26 cell lines showed alterations of at least 1 allele of the FHIT gene. Thus, Virgilio et al. (1996) concluded that loss of FHIT function may be important in the development and/or progression of head and neck cancers. Animal model experiments lend further support to the function of FHIT. To investigate the role of the Fhit gene in carcinogen induction of neoplasia, Fong et al. (2000) inactivated 1 Fhit allele in mouse embryonic stem cells to produce F1 mice with an inactivated Fhit allele (+/−). Fhit +/+ and +/− mice were treated intragastrically with nitrosomethylbenzylamine and observed for 10 weeks posttreatment. In 25% of the +/+ mice, adenoma or papilloma of the forestomach developed, whereas 100% of the +/− mice developed multiple tumors that were a mixture of adenomas, squamous papillomas, and invasive carcinomas of the forestomach, as well as tumors of sebaceous glands. The visceral and sebaceous tumors, which lacked Fhit protein, were similar to those characteristic of the Muir-Torre familial cancer syndrome (OMIM Ref. No. 158320).

[83250] It is appreciated that the abovementioned animal model for FHIT is acknowledged by those skilled in the art as a

scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[83251] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83252] Sozzi, G.; Veronese, M. L.; Negrini, M.; Baffa, R.; Cotticelli, M. G.; Inoue, H.; Tornielli, S.; Pilotti, S.; De Gregorio, L.; Pastorino, U.; Pierotti, M. A.; Ohta, M.; Huebner, K.; Croce, C. M. : The FHIT gene at 3p14.2 is abnormal in lung cancer. Cell 85: 17-26, 1996. ; and

[83253] Virgilio, L.; Shuster, M.; Gollin, S. M.; Veronese, M. L.; Ohta, M.; Huebner, K.; Croce, C. M. : FHIT gene alterations in head and neck squamous cell carcinomas. Proc. Nat. Acad. Sci. 9.

[83254] Further studies establishing the function and utilities of FHIT are found in John Hopkins OMIM database record ID 601153, and in sited publications numbered 7544-7545, 12515, 11542, 12516, 2857, 7857-7859, 2858, 9369-9375, 169 and 9376-9378 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.FK506 Binding Protein 1A, 12kDa (FKBP1A, Accession NM_000801) is another VGAM2463 host target gene. FKBP1A BINDING SITE is HOST TARGET

binding site found in the 3` untranslated region of mRNA encoded by FKBP1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FKBP1A BINDING SITE, designated SEQ ID:6474, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83255] Another function of VGAM2463 is therefore inhibition of FK506 Binding Protein 1A, 12kDa (FKBP1A, Accession NM_000801), a gene which FK506-binding protein 1A. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FKBP1A. The function of FKBP1A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM57.Fibronectin 1 (FN1, Accession NM_002026) is another VGAM2463 host target gene. FN1 BINDING SITE1 and FN1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FN1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of FN1 BINDING SITE1 and FN1 BINDING SITE2, designated SEQ ID:7779 and SEQ ID:27645 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83256] Another function of VGAM2463 is therefore inhibition of Fibronectin 1 (FN1, Accession NM_002026), a gene which binds cell surfaces and various compounds including collagen, fibrin, heparin, dna, and actin. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FN1. The function of FN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1063.FXYD Domain Containing Ion Transport Regulator 6 (FXYD6, Accession NM_022003) is another VGAM2463 host target gene. FXYD6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FXYD6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FXYD6 BINDING SITE, designated SEQ ID:22552, to the nucleotide sequence of

VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83257] Another function of VGAM2463 is therefore inhibition of FXYD Domain Containing Ion Transport Regulator 6 (FXYD6, Accession NM_022003). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FXYD6. Frizzled Homolog 7 (Drosophila) (FZD7, Accession NM_003507) is another VGAM2463 host target gene. FZD7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FZD7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FZD7 BINDING SITE, designated SEQ ID:9600, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83258] Another function of VGAM2463 is therefore inhibition of Frizzled Homolog 7 (Drosophila) (FZD7, Accession NM_003507), a gene which enhances beta-catenin mediated signaling. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FZD7. The function of FZD7

and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1063.UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) (GALNT2, Accession NM_004481) is another VGAM2463 host target gene. GALNT2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GALNT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALNT2 BINDING SITE, designated SEQ ID:10799, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83259] Another function of VGAM2463 is therefore inhibition of UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 2 (GalNAc-T2) (GALNT2, Accession NM_004481), a gene which catalyzes the initial reaction in o-linked oligosaccharide biosynthesis. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNT2. The function of GALNT2 and its asso-

ciation with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM187.UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7, Accession NM_054110) is another VGAM2463 host target gene. GALNT7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GALNT7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALNT7 BINDING SITE, designated SEQ ID:27651, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83260] Another function of VGAM2463 is therefore inhibition of UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetylgalactosaminyltransferase 7 (GalNAc-T7) (GALNT7, Accession NM_054110). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALNT7. Glial Fibrillary Acidic Protein (GFAP, Accession NM_002055) is another VGAM2463 host target gene.

GFAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GFAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GFAP BINDING SITE, designated SEQ ID:7815, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83261] Another function of VGAM2463 is therefore inhibition of Glial Fibrillary Acidic Protein (GFAP, Accession NM_002055). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GFAP. Guanine Nucleotide Binding Protein (G protein), Alpha 11 (Gq class) (GNA11, Accession XM_072009) is another VGAM2463 host target gene. GNA11 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GNA11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNA11 BINDING SITE, designated SEQ ID:37454, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ

ID:5174.

[83262] Another function of VGAM2463 is therefore inhibition of Guanine Nucleotide Binding Protein (G protein), Alpha 11 (Gq class) (GNA11, Accession XM_072009), a gene which acts as an activator of phospholipase c. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNA11. The function of GNA11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1956.Guanine Nucleotide Binding Protein (G protein), Alpha Activating Activity Polypeptide O (GNAO1, Accession XM_165653) is another VGAM2463 host target gene. GNAO1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GNAO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNAO1 BINDING SITE, designated SEQ ID:43721, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83263] Another function of VGAM2463 is therefore inhibition of

Guanine Nucleotide Binding Protein (G protein), Alpha Activating Activity Polypeptide O (GNAO1, Accession XM_165653), a gene which functions as modulators or transducers in various transmembrane signaling systems. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNAO1. The function of GNAO1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM665.GNAS Complex Locus (GNAS, Accession NM_016592) is another VGAM2463 host target gene. GNAS BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GNAS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GNAS BINDING SITE, designated SEQ ID:18679, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83264] Another function of VGAM2463 is therefore inhibition of GNAS Complex Locus (GNAS, Accession NM_016592), a gene which transduces signals from G protein-coupled

receptors and activates adenylyl cyclase. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GNAS. The function of GNAS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1205.Glutamate Receptor, Metabotropic 4 (GRM4, Accession NM_000841) is another VGAM2463 host target gene. GRM4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GRM4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRM4 BINDING SITE, designated SEQ ID:6504, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83265] Another function of VGAM2463 is therefore inhibition of Glutamate Receptor, Metabotropic 4 (GRM4, Accession NM_000841), a gene which is mediated by a g-protein that inhibits adenylate cyclase activity. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with GRM4. The function of GRM4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1052.Glutamate Receptor, Metabotropic 6 (GRM6, Accession NM_000843) is another VGAM2463 host target gene. GRM6 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GRM6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRM6 BINDING SITE, designated SEQ ID:6508, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83266] Another function of VGAM2463 is therefore inhibition of Glutamate Receptor, Metabotropic 6 (GRM6, Accession NM_000843). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRM6. GTF2I Repeat Domain Containing 1 (GTF2IRD1, Accession NM_016328) is another VGAM2463 host target gene. GTF2IRD1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GTF2IRD1, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GTF2IRD1 BINDING SITE, designated SEQ ID:18452, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83267] Another function of VGAM2463 is therefore inhibition of GTF2I Repeat Domain Containing 1 (GTF2IRD1, Accession NM_016328). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GTF2IRD1. Huntingtin-associated Protein 1 (neuroan 1) (HAP1, Accession NM_003949) is another VGAM2463 host target gene. HAP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HAP1 BINDING SITE, designated SEQ ID:10076, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83268] Another function of VGAM2463 is therefore inhibition of Huntingtin-associated Protein 1 (neuroan 1) (HAP1, Ac-

cession NM_003949), a gene which functions as an adaptor protein using coiled coils to mediate interactions among cytoskeletal, vascular, and motor proteins. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HAP1. The function of HAP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM126.Host Cell Factor C1 (VP16-accessory protein) (HCFC1, Accession XM_048390) is another VGAM2463 host target gene. HCFC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HCFC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCFC1 BINDING SITE, designated SEQ ID:35157, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83269] Another function of VGAM2463 is therefore inhibition of Host Cell Factor C1 (VP16-accessory protein) (HCFC1, Accession XM_048390), a gene which is a host cell factor, has a role in cell proliferation and can form a complex

with HSV VP16. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCFC1. The function of HCFC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM341.High Mobility Group AT-hook 2 (HMGA2, Accession NM_003483) is another VGAM2463 host target gene. HMGA2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HMGA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HMGA2 BINDING SITE, designated SEQ ID:9572, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83270] Another function of VGAM2463 is therefore inhibition of High Mobility Group AT-hook 2 (HMGA2, Accession NM_003483), a gene which may affect transcription and cell differentiation; shares common DNA-binding motif with other HMG HMG I/Y family members. Accordingly, utilities of VGAM2463 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with HMGA2. The function of HMGA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM552.HTRA3 (Accession XM_114416) is another VGAM2463 host target gene. HTRA3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HTRA3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HTRA3 BINDING SITE, designated SEQ ID:42940, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83271] Another function of VGAM2463 is therefore inhibition of HTRA3 (Accession XM_114416). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTRA3. Inositol 1,4,5-trisphosphate 3-kinase B (ITPKB, Accession NM_002221) is another VGAM2463 host target gene. ITPKB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITPKB,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITPKB BINDING SITE, designated SEQ ID:7982, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83272] Another function of VGAM2463 is therefore inhibition of Inositol 1,4,5-trisphosphate 3-kinase B (ITPKB, Accession NM_002221), a gene which is a type B inositol 1,4,5-triphosphate 3 kinase. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITPKB. The function of ITPKB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1252.Potassium Voltage-gated Channel, Shaker-related Subfamily, Beta Member 2 (KCNAB2, Accession NM_003636) is another VGAM2463 host target gene. KCNAB2 BINDING SITE1 and KCNAB2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KCNAB2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the comple-

mentarity of the nucleotide sequences of KCNAB2 BINDING SITE1 and KCNAB2 BINDING SITE2, designated SEQ ID:9707 and SEQ ID:9708 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83273] Another function of VGAM2463 is therefore inhibition of Potassium Voltage-gated Channel, Shaker-related Subfamily, Beta Member 2 (KCNAB2, Accession NM_003636), a gene which is the beta subunit of shaker voltage-gated potassium channels. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCNAB2. The function of KCNAB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM659.LIM Domain Kinase 1 (LIMK1, Accession NM_016735) is another VGAM2463 host target gene. LIMK1 BINDING SITE1 through LIMK1 BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LIMK1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LIMK1 BINDING SITE1

through LIMK1 BINDING SITE4, designated SEQ ID:18801, SEQ ID:18803, SEQ ID:8125 and SEQ ID:8126 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83274] Another function of VGAM2463 is therefore inhibition of LIM Domain Kinase 1 (LIMK1, Accession NM_016735). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LIMK1. V-maf Musculoaponeurotic Fibrosarcoma Oncogene Homolog (avian) (MAF, Accession NM_005360) is another VGAM2463 host target gene. MAF BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MAF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MAF BINDING SITE, designated SEQ ID:11837, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83275] Another function of VGAM2463 is therefore inhibition of V-maf Musculoaponeurotic Fibrosarcoma Oncogene Homolog (avian) (MAF, Accession NM_005360), a gene which is a transcription factor; contains a leucine zipper motif.

Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MAF. The function of MAF and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM822.MAP/microtubule Affinity-regulating Kinase 3 (MARK3, Accession NM_002376) is another VGAM2463 host target gene. MARK3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MARK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MARK3 BINDING SITE, designated SEQ ID:8190, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83276] Another function of VGAM2463 is therefore inhibition of MAP/microtubule Affinity-regulating Kinase 3 (MARK3, Accession NM_002376), a gene which may be involved in cell cycle regulation. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MARK3. The func-

tion of MARK3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM964.Meningioma (disrupted in balanced translocation) 1 (MN1, Accession NM_002430) is another VGAM2463 host target gene. MN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MN1 BINDING SITE, designated SEQ ID:8273, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83277] Another function of VGAM2463 is therefore inhibition of Meningioma (disrupted in balanced translocation) 1 (MN1, Accession NM_002430). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MN1. MAX Binding Protein (MNT, Accession NM_020310) is another VGAM2463 host target gene. MNT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MNT, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MNT BINDING SITE, designated SEQ ID:21563, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83278] Another function of VGAM2463 is therefore inhibition of MAX Binding Protein (MNT, Accession NM_020310). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MNT. NESH (Accession NM_016428) is another VGAM2463 host target gene. NESH BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NESH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NESH BINDING SITE, designated SEQ ID:18548, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83279] Another function of VGAM2463 is therefore inhibition of NESH (Accession NM_016428), a gene which plays a role in cell growth signalling. Accordingly, utilities of

VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NESH. The function of NESH has been established by previous studies. By screening a hepatocellular cDNA library using PCR with degenerate primers corresponding to p53 (OMIM Ref. No. 191170)/p73 (OMIM Ref. No. 601990) exon domains, followed by probing a placenta cDNA library, Miyazaki et al. (2000) obtained a cDNA encoding an SH3-containing protein they designated NESH (new molecule including SH3). SH3 domains contain about 50 amino acids that bind to proline-rich sequences and often play a role in cell growth signalling. Sequence analysis predicted that the 366-amino acid NESH protein, which is most homologous to SSH3BP1 (OMIM Ref. No. 603050), has a central serine-rich region followed by a proline-rich region and a C-terminal SH3 domain. RT-PCR analysis detected variable expression of NESH in all tissues tested. Miyazaki et al. (2000) suggested that the similarity of NESH to SSH3BP1, an EPS8 (OMIM Ref. No. 600206)-binding protein, indicates that its SH3 domain may interact with other proteins in signal transduction. GENE FUNCTION Using the yeast 2-hybrid system, Matsuda et al. (2001) identified TARSH (OMIM Ref. No.

606279) as a binding partner of NESH.

[83280] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83281] Matsuda, S.; Iriyama, C.; Yokozaki, S.; Ichigotani, Y.; Shirafuji, N.; Yamaki, K.; Hayakawa, T.; Hamaguchi, M. : Cloning and sequencing of a novel human gene that encodes a putative target protein of Nesh-SH3. J. Hum. Genet. 46: 483-486, 2001. ; and

[83282] Miyazaki, K.; Matsuda, S.; Ichigotani, Y.; Takenouchi, Y.; Hayashi, K.; Fukuda, Y.; Nimura, Y.; Hamaguchi, M. : Isolation and characterization of a novel human gene (NESH) which encode.

[83283] Further studies establishing the function and utilities of NESH are found in John Hopkins OMIM database record ID 606363, and in sited publications numbered 451 and 6175 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Nitric Oxide Synthase 1 (neuronal) (NOS1, Accession NM_000620) is another VGAM2463 host target gene. NOS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NOS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NOS1 BINDING SITE, designated SEQ ID:6231, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83284] Another function of VGAM2463 is therefore inhibition of Nitric Oxide Synthase 1 (neuronal) (NOS1, Accession NM_000620), a gene which produces nitric oxide (no) which is a messenger molecule with diverse functions throughout the body. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOS1. The function of NOS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM323.Neurexin 1 (NRXN1, Accession NM_138735) is another VGAM2463 host target gene. NRXN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NRXN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NRXN1 BINDING SITE, designated SEQ ID:28996, to the

nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83285] Another function of VGAM2463 is therefore inhibition of Neurexin 1 (NRXN1, Accession NM_138735), a gene which may be involved in cell recognition, cell adhesion, and mediate intracellular signaling. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRXN1. The function of NRXN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM191.Occludin (OCLN, Accession NM_002538) is another VGAM2463 host target gene. OCLN BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by OCLN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OCLN BINDING SITE, designated SEQ ID:8381, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83286] Another function of VGAM2463 is therefore inhibition of Occludin (OCLN, Accession NM_002538). Accordingly,

utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OCLN. Paired Box Gene 2 (PAX2, Accession NM_003987) is another VGAM2463 host target gene. PAX2 BINDING SITE1 through PAX2 BINDING SITE6 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PAX2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAX2 BINDING SITE1 through PAX2 BINDING SITE6, designated SEQ ID:10138, SEQ ID:10140, SEQ ID:10141, SEQ ID:10144, SEQ ID:10146 and SEQ ID:10147 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83287] Another function of VGAM2463 is therefore inhibition of Paired Box Gene 2 (PAX2, Accession NM_003987), a gene which involves in kidney cell differentiation. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAX2. The function of PAX2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to VGAM407.Polycystic Kidney Disease 2-like 1 (PKD2L1, Accession NM_016112) is another VGAM2463 host target gene. PKD2L1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PKD2L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PKD2L1 BINDING SITE, designated SEQ ID:18192, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83288] Another function of VGAM2463 is therefore inhibition of Polycystic Kidney Disease 2-like 1 (PKD2L1, Accession NM_016112). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PKD2L1. Pleckstrin (PLEK, Accession NM_002664) is another VGAM2463 host target gene. PLEK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PLEK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLEK BINDING SITE, designated SEQ ID:8534,

to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83289] Another function of VGAM2463 is therefore inhibition of Pleckstrin (PLEK, Accession NM_002664), a gene which is the major protein kinase c substrate of platelets. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLEK. The function of PLEK and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Paired Mesoderm Homeo Box 1 (PMX1, Accession NM_022716) is another VGAM2463 host target gene. PMX1 BINDING SITE1 and PMX1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PMX1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PMX1 BINDING SITE1 and PMX1 BINDING SITE2, designated SEQ ID:22916 and SEQ ID:13781 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83290] Another function of VGAM2463 is therefore inhibition of

Paired Mesoderm Homeo Box 1 (PMX1, Accession NM_022716), a gene which acts as a transcriptional regulator of muscle creatine kinase. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PMX1. The function of PMX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Protein Phosphatase 2A, Regulatory Subunit B' (PR 53) (PPP2R4, Accession XM_026944) is another VGAM2463 host target gene. PPP2R4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PPP2R4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP2R4 BINDING SITE, designated SEQ ID:30376, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83291] Another function of VGAM2463 is therefore inhibition of Protein Phosphatase 2A, Regulatory Subunit B' (PR 53) (PPP2R4, Accession XM_026944), a gene which is a regulatory subunit of protein phosphatase 2A. Accordingly,

utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP2R4. The function of PPP2R4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM435.Periaxin (PRX, Accession NM_020956) is another VGAM2463 host target gene. PRX BINDING SITE1 and PRX BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PRX, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRX BINDING SITE1 and PRX BINDING SITE2, designated SEQ ID:21935 and SEQ ID:21940 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83292] Another function of VGAM2463 is therefore inhibition of Periaxin (PRX, Accession NM_020956), a gene which seems to be required for maintenance of peripheral nerve myelin sheath. may have a role in axon-glial interactions, possibly by interacting with the cytoplasmic domains of integral membrane proteins such as myelin-associated

glycoprotein in the periaxonal regions of the schwann cell plasma membrane. may have a role in the early phases of myelin deposition. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRX. The function of PRX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM476.Prostaglandin-endoperoxide Synthase 1 (prostaglandin G/H synthase and cyclooxygenase) (PTGS1, Accession NM_000962) is another VGAM2463 host target gene. PTGS1 BINDING SITE1 and PTGS1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTGS1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTGS1 BINDING SITE1 and PTGS1 BINDING SITE2, designated SEQ ID:6673 and SEQ ID:8744 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83293] Another function of VGAM2463 is therefore inhibition of Prostaglandin-endoperoxide Synthase 1 (prostaglandin G/

H synthase and cyclooxygenase) (PTGS1, Accession NM_000962), a gene which may play an important role in regulating or promoting cell proliferation in some normal and neoplastically transformed cells. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTGS1. The function of PTGS1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1224.Protein Tyrosine Phosphatase, Receptor Type, S (PTPRS, Accession NM_130853) is another VGAM2463 host target gene. PTPRS BINDING SITE1 through PTPRS BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PTPRS, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPRS BINDING SITE1 through PTPRS BINDING SITE4, designated SEQ ID:28390, SEQ ID:28391, SEQ ID:8767 and SEQ ID:12130 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83294] Another function of VGAM2463 is therefore inhibition of

Protein Tyrosine Phosphatase, Receptor Type, S (PTPRS, Accession NM_130853), a gene which controls motor axon guidance and may be a cell adhesion receptor. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPRS. The function of PTPRS has been established by previous studies. Protein-tyrosine phosphatase sigma (PTPRS) is a receptor type protein-tyrosine phosphatase that has been cloned and identified in mouse, in rat, and in human (Pulido et al., 1995). PTPRS is a member of a subfamily of receptor type PTPases that includes LAR (OMIM Ref. No. 179590) and PTP-delta. Wagner et al. (1996) noted that this subfamily of cell surface glycoproteins is characterized by the presence of an extracellular cell adhesion molecule-like motif and 2 intracellular phosphatase domains. Transcripts of these genes are subject to RNA processing, resulting in several distinct isoforms. These proteins share a high overall degree of sequence similarity, especially in the second intracellular catalytic domain, which is thought to interact with the same molecule. Analysis of the expression pattern of PTPRS suggests that it may be involved in the development of the nervous system. Batt et al. (2002) examined the

role of PTP on pituitary, pancreas, and enteroendocrine cytodifferentiation, hormone production, and development. The adenohypophyses of PTPRS-null mice were small and exhibited reduced GH (see OMIM Ref. No. 139250) and PRL (OMIM Ref. No. 176760) immunoreactivity. Cells containing TSH (see OMIM Ref. No. 188530), LH (see OMIM Ref. No. 152780), FSH (see OMIM Ref. No. 136530), ACTH, pituitary-specific POU homeodomain factor (Pit1; 173110), estrogen receptor (see OMIM Ref. No. 133430), and steroidogenic factor-1 (OMIM Ref. No. 184757) were found in normal proportions and distributions. The diminished expression of GH and PRL was not associated with apoptosis of somatotrophs or lactotrophs. In the knockout mice, pancreatic islets were hypoplastic with reduced insulin immunoreactivity, and there was also variable expression of gut hormones. Functionally, the GH deficiency was associated with hypoglycemia and death in the PTPRS-null neonates, and accordingly, intraperitoneal administration of GH rescued the PTPRS-null neonates and normalized the blood glucose. The authors concluded that PTP-sigma plays a major role in differentiation and development of the neuroendocrine system. Animal model experiments lend further support to the function of PT-

PRS. On the basis of its expression and homology with the Drosophila melanogaster orthologs, which have roles in the targeting of axonal growth cones, Elchebly et al. (1999) hypothesized that PTP-sigma may also have a modulating function in cell-cell interactions, as well as in axon guidance during mammalian embryogenesis. To investigate its function in vivo, they generated Ptprs-deficient mice. The resulting Ptprs -/- animals displayed retarded growth, increased neonatal mortality, hyposmia, and hypofecundity. Anatomic and histologic analyses showed a decrease in overall brain size with severe depletion of luteinizing hormone-releasing hormone (OMIM Ref. No. 152760)-immunoreactive cells in the hypothalamus of the Ptprs -/- mice. These mice also had an enlarged intermediate pituitary lobe, but smaller anterior and posterior lobes. These results suggested that tyrosine phosphorylation-dependent signaling pathways regulated by PTP-sigma influence the proliferation and/or adhesiveness of various cell types in the developing hypothalamopituitary axis.

[83295] It is appreciated that the abovementioned animal model for PTPRS is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appre-

ciated from the publications sited hereinbelow.

[83296] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83297] Batt, J.; Asa, S.; Fladd, C.; Rotin, D. : Pituitary, pancreatic and gut neuroendocrine defects in protein tyrosine phosphatase-sigma-deficient mice. Molec. Endocr. 16: 155-169, 2002. ; and

[83298] Elchebly, M.; Wagner, J.; Kennedy, T. E.; Lanctot, C.; Michaliszyn, E.; Itie, A.; Drouin, J.; Tremblay, M. L. : Neuroendocrine dysplasia in mice lacking protein tyrosine phosphatase sig.

[83299] Further studies establishing the function and utilities of PTPRS are found in John Hopkins OMIM database record ID 601576, and in sited publications numbered 6677-6681 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Radical Fringe Homolog (Drosophila) (RFNG, Accession XM_113942) is another VGAM2463 host target gene. RFNG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RFNG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of RFNG BINDING SITE, designated SEQ ID:42558, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83300] Another function of VGAM2463 is therefore inhibition of Radical Fringe Homolog (Drosophila) (RFNG, Accession XM_113942), a gene which controls activation of the Notch signal transduction pathway;. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFNG. The function of RFNG has been established by previous studies. Fringe proteins can positively and negatively modulate the ability of Notch ligands to activate the Notch receptor. Moloney et al. (2000) established the biochemical mechanism of Fringe action. Drosophila and mammalian Fringe proteins possess a fucose-specific beta-1,3 N-acetylglucosaminyltransferase activity that initiates elongation of O-linked fucose residues attached to epidermal growth factor (EGF; 131530)-like sequence repeats of Notch. They obtained biologic evidence that Fringe-dependent elongation of O-linked fucose on Notch modulates Notch signaling by using coculture assays in mammalian cells and by expression of an enzymatically

inactive Fringe mutant in Drosophila. Bruckner et al. (2000) showed that Fringe acts in the Golgi as a glycosyltransferase enzyme that modifies the EGF modules of Notch and alters the ability of Notch to bind its ligand Delta (OMIM Ref. No. 602768). The authors demonstrated that Fringe catalyzes the addition of N-acetylglucosamine to fucose, which is consistent with a role in the elongation of O-linked fucose O-glycosylation that is associated with EGF repeats. Vertebrate limb outgrowth requires a structure called the apical ectodermal ridge (AER), formation of which relies on the previous establishment of the dorsoventral limb axis. The AER of the vertebrate limb bud lies at the junction of the dorsal and ventral ectoderm and directs patterning of the growing limb outgrowth. Rfng is expressed in the dorsal ectoderm before the ridge appears, and is repressed by Engrailed-1 (OMIM Ref. No. 131290), which is expressed in the ventral ectoderm. Rodriguez-Esteban et al. (1997) found that misexpression of these genes results in a ridge being formed wherever there is a boundary between cells expressing and not expressing Rfng. Thus, as in Drosophila, Rfng positions the ridge at the dorsoventral limb boundary. The results of Laufer et al. (1997) supported the hypothesis that the AER

forms at the juxtaposition of Rfng-expressing and nonexpressing cells, and furthermore dissociate the molecular control of AER formation from that of dorsoventral tissue specification. Laufer et al. (1997) also found that Rfng expression in chick limb dorsal ectoderm is established in part through repression by Engrailed-1 in the ventral ectoderm.

[83301] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83302] Moloney, D. J.; Panin, V. M.; Johnston, S. H.; Chen, J.; Shao, L.; Wilson, R.; Wang, Y.; Stanley, P.; Irvine, K. D.; Haltiwanger, R. S.; Vogt, T. F. : Fringe is a glycosyltransferase that modifies Notch. Nature 406: 369-375, 2000. ; and

[83303] Laufer, E.; Dahn, R.; Orozco, O. E.; Yeo, C.-Y.; Pisenti, J.; Henrique, D.; Abbott, U. K.; Fallon, J. F.; Tabin, C. : Expression of Radical fringe in limb-bud ectoderm regulates apical.

[83304] Further studies establishing the function and utilities of RFNG are found in John Hopkins OMIM database record ID 602578, and in sited publications numbered 5746, 7964, 7966, 1235 and 7967 listed in the bibliography section hereinbelow, which are also hereby incorporated by refer-

ence.Ret Finger Protein (RFP, Accession NM_006510) is another VGAM2463 host target gene. RFP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RFP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RFP BINDING SITE, designated SEQ ID:13260, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83305] Another function of VGAM2463 is therefore inhibition of Ret Finger Protein (RFP, Accession NM_006510), a gene which involvels in transcriptional regulation and may act in male germ cell development . Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFP. The function of RFP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM302.Retinoschisis (X-linked, juvenile) 1 (RS1, Accession NM_000330) is another VGAM2463 host target gene. RS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

RS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RS1 BINDING SITE, designated SEQ ID:5878, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83306] Another function of VGAM2463 is therefore inhibition of Retinoschisis (X-linked, juvenile) 1 (RS1, Accession NM_000330). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RS1. Retinoid X Receptor, Alpha (RXRA, Accession NM_002957) is another VGAM2463 host target gene. RXRA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RXRA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RXRA BINDING SITE, designated SEQ ID:8869, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83307] Another function of VGAM2463 is therefore inhibition of Retinoid X Receptor, Alpha (RXRA, Accession NM_002957),

a gene which activates genes required for vitamin A metabolism, binds 9-cis retinoic acid. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RXRA. The function of RXRA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM349.Syndecan 4 (amphiglycan, ryudocan) (SDC4, Accession NM_002999) is another VGAM2463 host target gene. SDC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SDC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SDC4 BINDING SITE, designated SEQ ID:8891, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83308] Another function of VGAM2463 is therefore inhibition of Syndecan 4 (amphiglycan, ryudocan) (SDC4, Accession NM_002999), a gene which is a cell surface proteoglycan. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with SDC4. The function of SDC4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM552.SET7 (Accession NM_030648) is another VGAM2463 host target gene. SET7 BINDING SITE1 and SET7 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SET7, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SET7 BINDING SITE1 and SET7 BINDING SITE2, designated SEQ ID:24981 and SEQ ID:24982 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83309] Another function of VGAM2463 is therefore inhibition of SET7 (Accession NM_030648). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SET7. Sine Oculis Homeobox Homolog 3 (Drosophila) (SIX3, Accession NM_005413) is another VGAM2463 host target gene. SIX3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

SIX3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SIX3 BINDING SITE, designated SEQ ID:11882, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83310] Another function of VGAM2463 is therefore inhibition of Sine Oculis Homeobox Homolog 3 (Drosophila) (SIX3, Accession NM_005413), a gene which may be involved in visual system development. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SIX3. The function of SIX3 has been established by previous studies. Holoprosencephaly (HPE) is a common, severe malformation of the brain that involves separation of the central nervous system into left and right halves. Mild HPE can consist of signs such as a single central incisor, hypotelorism, microcephaly, or other craniofacial findings that can be present with or without associated brain malformations. The etiology of HPE is highly heterogeneous, with the proposed participation of a minimum of 12 HPE-associated genetic loci as well as the causal involvement of specific teratogens acting at the earliest stages of neu-

rulation (Roessler and Muenke, 1998). Schell et al. (1996) mapped the HPE2 (OMIM Ref. No. 157170) locus to a 1-Mb interval on 2p21 and defined a minimal critical region by a set of 6 overlapping deletions and 3 clustered translocations in HPE patients. Wallis et al. (1999) described the isolation and characterization of the homeo box-containing SIX3 gene from the HPE2 minimal critical region. They showed that at least 2 of the HPE-associated translocation breakpoints in 2p21 are less than 200 kb from the 5-prime end of SIX3. Mutational analysis identified 4 different mutations in the homeodomain of SIX3 that were predicted to interfere with transcriptional activation and were associated with HPE. Wallis et al. (1999) proposed that SIX3 is the HPE2 gene, essential for the development of the anterior neural plate and eyes in humans.

[83311] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83312] Roessler, E.; Muenke, M. : Holoprosencephaly: a paradigm for the complex genetics of brain development. J. Inherit. Metab. Dis. 21: 481-497, 1998. ; and

[83313] Wallis, D. E.; Roessler, E.; Hehr, U.; Nanni, L.; Wiltshire, T.;

Richieri-Costa, A.; Gillessen-Kaesbach, G.; Zackai, E. H.; Rommens, J.; Muenke, M. : Mutations in the homeodomain of t.

[83314] Further studies establishing the function and utilities of SIX3 are found in John Hopkins OMIM database record ID 603714, and in sited publications numbered 5287-529 and 11447 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Solute Carrier Family 16 (monocarboxylic acid transporters), Member 2 (putative transporter) (SLC16A2, Accession NM_006517) is another VGAM2463 host target gene. SLC16A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC16A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC16A2 BINDING SITE, designated SEQ ID:13269, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83315] Another function of VGAM2463 is therefore inhibition of Solute Carrier Family 16 (monocarboxylic acid transporters), Member 2 (putative transporter) (SLC16A2, Ac-

cession NM_006517). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC16A2. Solute Carrier Family 6 (neurotransmitter transporter, creatine), Member 8 (SLC6A8, Accession NM_005629) is another VGAM2463 host target gene. SLC6A8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC6A8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC6A8 BINDING SITE, designated SEQ ID:12150, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83316] Another function of VGAM2463 is therefore inhibition of Solute Carrier Family 6 (neurotransmitter transporter, creatine), Member 8 (SLC6A8, Accession NM_005629). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A8. Solute Carrier Family 9 (sodium/hydrogen exchanger), Isoform 5 (SLC9A5, Accession NM_004594) is another VGAM2463 host target gene. SLC9A5 BINDING SITE1 and SLC9A5 BINDING SITE2 are

HOST TARGET binding sites found in untranslated regions of mRNA encoded by SLC9A5, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC9A5 BINDING SITE1 and SLC9A5 BINDING SITE2, designated SEQ ID:10936 and SEQ ID:30065 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83317] Another function of VGAM2463 is therefore inhibition of Solute Carrier Family 9 (sodium/hydrogen exchanger), Isoform 5 (SLC9A5, Accession NM_004594). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC9A5. Stanniocalcin 1 (STC1, Accession NM_003155) is another VGAM2463 host target gene. STC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STC1 BINDING SITE, designated SEQ ID:9134, to the nucleotide sequence of VGAM2463 RNA, herein

designated VGAM RNA, also designated SEQ ID:5174.

[83318] Another function of VGAM2463 is therefore inhibition of Stanniocalcin 1 (STC1, Accession NM_003155), a gene which stimulates renal phosphate reabsorption, and could therefore prevent hypercalcemia. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STC1. The function of STC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM623.Serine/threonine Kinase 13 (aurora/IPL1-like) (STK13, Accession NM_003160) is another VGAM2463 host target gene. STK13 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by STK13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STK13 BINDING SITE, designated SEQ ID:9139, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83319] Another function of VGAM2463 is therefore inhibition of Serine/threonine Kinase 13 (aurora/IPL1-like) (STK13, Ac-

cession NM_003160), a gene which is a testis-specific serine/threonine kinase. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with STK13. The function of STK13 has been established by previous studies. The Drosophila 'Aurora' and S. cerevisiae Ipl1 protein kinases are involved in mitotic events such as centrosome separation and chromosome segregation. By screening a human placenta library with Xenopus Eg2 (an Aurora/Ipl1-related kinase) cDNA, Bernard et al. (1998) isolated a partial STK13 cDNA. They obtained a full-length cDNA using RACE on testis mRNA. The catalytic domain of the predicted 275-amino acid protein shares 80% and 68% identity with those of AURORA2 (OMIM Ref. No. 603072) and AIK (OMIM Ref. No. 602687), respectively. Independently, Tseng et al. (1998) isolated cDNAs encoding 2 novel protein kinases, mouse Aie1 (Aurora/Ipl1/EG2-1) and human STK13, which they designated AIE2. Both Aie1 and AIE2 contain a central serine/threonine kinase domain. The authors reported that AIE2 contains 309 amino acids. Northern blot analysis detected expression of a 1.35-kb AIE2 mRNA only in testis. Full-grown Xenopus oocytes arrest at the G2/M border of meiosis I. Proges-

terone breaks this arrest, leading to the resumption of the meiotic cell cycles and maturation of the oocyte into a fertilizable egg. In these oocytes, progesterone interacts with an unidentified surface-associated receptor, which induces a nontranscriptional signaling pathway that stimulates the translation of dormant c-mos mRNA. The translational recruitment of c-mos and several other mRNAs is regulated by cytoplasmic polyadenylation, a process that requires two 3-prime untranslated regions, the cytoplasmic polyadenylation element (CPE) and the polyadenylation hexanucleotide AAUAAA. Mendez et al. (2000) demonstrated that an early site-specific phosphorylation of CPEB (the CPE binding factor) is essential for the polyadenylation of c-mos mRNA and its subsequent translation, and for oocyte maturation. In addition, they showed that this selective, early phosphorylation of CPEB is catalyzed by Eg2.

[83320] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83321] Bernard, M.; Sanseau, P.; Henry, C.; Couturier, A.; Prigent, C. : Cloning of STK13, a third human protein kinase related to Drosophila Aurora and budding yeast Ipl1 that

maps on chromosome 19q13.3-ter. Genomics 53: 406-409, 1998. ; and

[83322] Mendez, R.; Hake, L. E.; Andresson, T.; Littlepage, L. E.; Ruderman, J. V.; Richter, J. D. : Phosphorylation of CPE binding factor by Eg2 regulates translation of c-mos mRNA. Nature 404.

[83323] Further studies establishing the function and utilities of STK13 are found in John Hopkins OMIM database record ID 603495, and in sited publications numbered 851 and 10269 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Suppressor of Fused Homolog (Drosophila) (SUFU, Accession NM_016169) is another VGAM2463 host target gene. SUFU BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SUFU, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SUFU BINDING SITE, designated SEQ ID:18257, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83324] Another function of VGAM2463 is therefore inhibition of Suppressor of Fused Homolog (Drosophila) (SUFU, Acces-

sion NM_016169). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUFU. Suppressor of Ty 6 Homolog (S. cerevisiae) (SUPT6H, Accession XM_017037) is another VGAM2463 host target gene. SUPT6H BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SUPT6H, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SUPT6H BINDING SITE, designated SEQ ID:30292, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83325] Another function of VGAM2463 is therefore inhibition of Suppressor of Ty 6 Homolog (S. cerevisiae) (SUPT6H, Accession XM_017037), a gene which may normally act to repress transcription at a variety of loci, and also plays a role in chromatin structure or assembly. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SUPT6H. The function of SUPT6H and its association with various diseases and clinical conditions, has been es-

tablished by previous studies, as described hereinabove with reference to VGAM1959.Transforming, Acidic Coiled-coil Containing Protein 1 (TACC1, Accession NM_006283) is another VGAM2463 host target gene. TACC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TACC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TACC1 BINDING SITE, designated SEQ ID:12964, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83326] Another function of VGAM2463 is therefore inhibition of Transforming, Acidic Coiled-coil Containing Protein 1 (TACC1, Accession NM_006283). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TACC1. Tafazzin (cardiomyopathy, dilated 3A (X-linked); Endocardial Fibroelastosis 2; Barth Syndrome) (TAZ, Accession NM_000116) is another VGAM2463 host target gene. TAZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAZ, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAZ BINDING SITE, designated SEQ ID:5585, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83327] Another function of VGAM2463 is therefore inhibition of Tafazzin (cardiomyopathy, dilated 3A (X-linked); Endocardial Fibroelastosis 2; Barth Syndrome) (TAZ, Accession NM_000116). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TAZ. Telomeric Repeat Binding Factor 2 (TERF2, Accession NM_005652) is another VGAM2463 host target gene. TERF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TERF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TERF2 BINDING SITE, designated SEQ ID:12189, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83328] Another function of VGAM2463 is therefore inhibition of Telomeric Repeat Binding Factor 2 (TERF2, Accession

NM_005652), a gene which plays a key role in the protective activity of telomeres. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TERF2. The function of TERF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1689.TIRAP (Accession NM_052887) is another VGAM2463 host target gene. TIRAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIRAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIRAP BINDING SITE, designated SEQ ID:27477, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83329] Another function of VGAM2463 is therefore inhibition of TIRAP (Accession NM_052887), a gene which is a adapter involved in theTLR4 signaling pathway in the innate immune response. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIRAP. The function of

TIRAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM189.Thiopurine S-methyltransferase (TPMT, Accession NM_000367) is another VGAM2463 host target gene. TPMT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TPMT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TPMT BINDING SITE, designated SEQ ID:5939, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83330] Another function of VGAM2463 is therefore inhibition of Thiopurine S-methyltransferase (TPMT, Accession NM_000367), a gene which catalyzes the s-methylation of thiopurine drugs such as 6-mercaptopurine. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TPMT. The function of TPMT and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM682.Unc-5 Homolog B (C. elegans)

(UNC5C, Accession NM_003728) is another VGAM2463 host target gene. UNC5C BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by UNC5C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UNC5C BINDING SITE, designated SEQ ID:9819, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83331] Another function of VGAM2463 is therefore inhibition of Unc-5 Homolog B (C. elegans) (UNC5C, Accession NM_003728), a gene which is a putative receptor for netrin, which is involved in axon guidance. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UNC5C. The function of UNC5C and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM298.Vasodilator-stimulated Phosphoprotein (VASP, Accession NM_003370) is another VGAM2463 host target gene. VASP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by VASP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VASP BINDING SITE, designated SEQ ID:9397, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83332] Another function of VGAM2463 is therefore inhibition of Vasodilator-stimulated Phosphoprotein (VASP, Accession NM_003370), a gene which may act in concert with profilin to convey signal transduction to actin filament production. Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VASP. The function of VASP has been established by previous studies. Human platelet activation is inhibited by agents such as prostaglandins and NO donors, which elevate cAMP or cGMP levels. The vasodilator-stimulated phosphoprotein (VASP) is phosphorylated in human platelets in response to both cAMP- and cGMP-elevating agents, and its phosphorylation correlates with platelet inhibition. Haffner et al. (1995) cloned the VASP gene from human and canine cells and showed that VASP is a 380-amino acid protein with a predicted molec-

ular mass of 39.8 kD. Brindle et al. (1996) showed that VASP binds to the proline-rich domain of vinculin (OMIM Ref. No. 193065). They suggested that this interaction is important for actin-filament assembly and focal adhesion stability. Zimmer et al. (1996) cloned human and mouse VASP from genomic cosmid libraries. They determined that the human and mouse VASP genes are 89% identical at the amino acid level and are both assembled of 13 exons and span a genomic DNA region of approximately 20 kb. They mapped human VASP to chromosome 19q13.2-q13.3 using fluorescence in situ hybridization. They noted that VASP is located about 92 kb distal to ERCC1 (OMIM Ref. No. 126380) and about 300 kb proximal to the myotonic dystrophy protein kinase gene (OMIM Ref. No. 160900).

[83333] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83334] Brindle, N. P. J.; Holt, M. R.; Davies, J. E.; Price, C. J.; Critchley, D. R. : The focal-adhesion vasodilator-stimulated phosphoprotein (VASP) binds to the proline-rich domain in vinculin. Biochem. J. 318: 753-757, 1996. ; and

[83335] Zimmer, M.; Fink, T.; Fischer, L.; Hauser, W.; Scherer, K.;

Lichter, P.; Walter, U. : Cloning of the VASP (vasodilator-stimulated phosphoprotein) genes in human and mouse: structure, seque.

[83336] Further studies establishing the function and utilities of VASP are found in John Hopkins OMIM database record ID 601703, and in sited publications numbered 2862-2864 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Wingless-type MMTV Integration Site Family, Member 1 (WNT1, Accession NM_005430) is another VGAM2463 host target gene. WNT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WNT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT1 BINDING SITE, designated SEQ ID:11897, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83337] Another function of VGAM2463 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 1 (WNT1, Accession NM_005430), a gene which may have a role in development of the central nervous system. Accordingly, utilities of VGAM2463 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with WNT1. The function of WNT1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM381.Wingless-type MMTV Integration Site Family, Member 5B (WNT5B, Accession NM_032642) is another VGAM2463 host target gene. WNT5B BINDING SITE1 and WNT5B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by WNT5B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WNT5B BINDING SITE1 and WNT5B BINDING SITE2, designated SEQ ID:26360 and SEQ ID:25058 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83338] Another function of VGAM2463 is therefore inhibition of Wingless-type MMTV Integration Site Family, Member 5B (WNT5B, Accession NM_032642), a gene which is the ligand for members of the frizzled family of seven transmembrane receptors and may be a signaling molecule . Accordingly, utilities of VGAM2463 include diagnosis,

prevention and treatment of diseases and clinical conditions associated with WNT5B. The function of WNT5B and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1928.A Kinase (PRKA) Anchor Protein 11 (AKAP11, Accession NM_016248) is another VGAM2463 host target gene. AKAP11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AKAP11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP11 BINDING SITE, designated SEQ ID:18375, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83339] Another function of VGAM2463 is therefore inhibition of A Kinase (PRKA) Anchor Protein 11 (AKAP11, Accession NM_016248). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP11. Angiomotin (AMOT, Accession NM_133265) is another VGAM2463 host target gene. AMOT BINDING SITE is HOST TARGET

binding site found in the 5` untranslated region of mRNA encoded by AMOT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AMOT BINDING SITE, designated SEQ ID:28419, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83340] Another function of VGAM2463 is therefore inhibition of Angiomotin (AMOT, Accession NM_133265). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AMOT. BA108L7.2 (Accession NM_030971) is another VGAM2463 host target gene. BA108L7.2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BA108L7.2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BA108L7.2 BINDING SITE, designated SEQ ID:25238, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83341] Another function of VGAM2463 is therefore inhibition of

BA108L7.2 (Accession NM_030971). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BA108L7.2. Bifunctional Apoptosis Regulator (BFAR, Accession XM_027311) is another VGAM2463 host target gene. BFAR BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BFAR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BFAR BINDING SITE, designated SEQ ID:30479, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83342] Another function of VGAM2463 is therefore inhibition of Bifunctional Apoptosis Regulator (BFAR, Accession XM_027311). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BFAR. Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769) is another VGAM2463 host target gene. C11orf11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C11orf11, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C11orf11 BINDING SITE, designated SEQ ID:44787, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83343] Another function of VGAM2463 is therefore inhibition of Chromosome 11 Open Reading Frame 11 (C11orf11, Accession XM_167769). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C11orf11. Chromosome 17 Open Reading Frame 31 (C17orf31, Accession NM_017575) is another VGAM2463 host target gene. C17orf31 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C17orf31, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C17orf31 BINDING SITE, designated SEQ ID:19004, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83344] Another function of VGAM2463 is therefore inhibition of

Chromosome 17 Open Reading Frame 31 (C17orf31, Accession NM_017575). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C17orf31. C1q and Tumor Necrosis Factor Related Protein 2 (C1QTNF2, Accession NM_031908) is another VGAM2463 host target gene. C1QTNF2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C1QTNF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C1QTNF2 BINDING SITE, designated SEQ ID:25651, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83345] Another function of VGAM2463 is therefore inhibition of C1q and Tumor Necrosis Factor Related Protein 2 (C1QTNF2, Accession NM_031908). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C1QTNF2. Chromosome 20 Open Reading Frame 142 (C20orf142, Accession XM_059257) is another VGAM2463 host target gene. C20orf142 BINDING SITE is HOST TAR-

GET binding site found in the 3` untranslated region of mRNA encoded by C20orf142, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf142 BINDING SITE, designated SEQ ID:36930, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83346] Another function of VGAM2463 is therefore inhibition of Chromosome 20 Open Reading Frame 142 (C20orf142, Accession XM_059257). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf142. Chromosome 22 Open Reading Frame 4 (C22orf4, Accession XM_027143) is another VGAM2463 host target gene. C22orf4 BINDING SITE1 and C22orf4 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by C22orf4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C22orf4 BINDING SITE1 and C22orf4 BINDING SITE2, designated SEQ ID:30422 and SEQ ID:30423 respectively,

to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83347] Another function of VGAM2463 is therefore inhibition of Chromosome 22 Open Reading Frame 4 (C22orf4, Accession XM_027143). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C22orf4. Calcium/calmodulin-dependent Protein Kinase Kinase 2, Beta (CAMKK2, Accession NM_006549) is another VGAM2463 host target gene. CAMKK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAMKK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAMKK2 BINDING SITE, designated SEQ ID:13311, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83348] Another function of VGAM2463 is therefore inhibition of Calcium/calmodulin-dependent Protein Kinase Kinase 2, Beta (CAMKK2, Accession NM_006549). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated

with CAMKK2. CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase) (CDIPT, Accession NM_006319) is another VGAM2463 host target gene. CDIPT BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDIPT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDIPT BINDING SITE, designated SEQ ID:13009, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83349] Another function of VGAM2463 is therefore inhibition of CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase) (CDIPT, Accession NM_006319). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDIPT. Cat Eye Syndrome Chromosome Region, Candidate 6 (CECR6, Accession NM_031890) is another VGAM2463 host target gene. CECR6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CECR6, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CECR6 BINDING SITE, designated SEQ ID:25637, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83350] Another function of VGAM2463 is therefore inhibition of Cat Eye Syndrome Chromosome Region, Candidate 6 (CECR6, Accession NM_031890). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CECR6. Choline Kinase (CHK, Accession NM_001277) is another VGAM2463 host target gene. CHK BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CHK, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CHK BINDING SITE, designated SEQ ID:6945, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83351] Another function of VGAM2463 is therefore inhibition of Choline Kinase (CHK, Accession NM_001277). Accord-

ingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CHK. Calsyntenin 3 (CLSTN3, Accession NM_014718) is another VGAM2463 host target gene. CLSTN3 BINDING SITE1 and CLSTN3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by CLSTN3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CLSTN3 BINDING SITE1 and CLSTN3 BINDING SITE2, designated SEQ ID:16274 and SEQ ID:16275 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83352] Another function of VGAM2463 is therefore inhibition of Calsyntenin 3 (CLSTN3, Accession NM_014718). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CLSTN3. Cyclin M3 (CNNM3, Accession NM_017623) is another VGAM2463 host target gene. CNNM3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNNM3, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNNM3 BINDING SITE, designated SEQ ID:19124, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83353] Another function of VGAM2463 is therefore inhibition of Cyclin M3 (CNNM3, Accession NM_017623). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNNM3. DCNP1 (Accession NM_130848) is another VGAM2463 host target gene. DCNP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DCNP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DCNP1 BINDING SITE, designated SEQ ID:28384, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83354] Another function of VGAM2463 is therefore inhibition of DCNP1 (Accession NM_130848). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with DCNP1. Diacylglycerol Kinase, Delta 130kDa (DGKD, Accession XM_002384) is another VGAM2463 host target gene. DGKD BINDING SITE1 and DGKD BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DGKD, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGKD BINDING SITE1 and DGKD BINDING SITE2, designated SEQ ID:29880 and SEQ ID:29882 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83355] Another function of VGAM2463 is therefore inhibition of Diacylglycerol Kinase, Delta 130kDa (DGKD, Accession XM_002384). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGKD. DKFZP434N178 (Accession XM_050278) is another VGAM2463 host target gene. DKFZP434N178 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434N178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434N178 BINDING SITE, designated SEQ ID:35596, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83356] Another function of VGAM2463 is therefore inhibition of DKFZP434N178 (Accession XM_050278). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434N178. DKFZp547I094 (Accession NM_032155) is another VGAM2463 host target gene. DKFZp547I094 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp547I094, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547I094 BINDING SITE, designated SEQ ID:25856, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83357] Another function of VGAM2463 is therefore inhibition of DKFZp547I094 (Accession NM_032155). Accordingly, utilities of VGAM2463 include diagnosis, prevention and

treatment of diseases and clinical conditions associated with DKFZp547I094. DKFZp547M072 (Accession XM_028067) is another VGAM2463 host target gene. DKFZp547M072 BINDING SITE1 and DKFZp547M072 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DKFZp547M072, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp547M072 BINDING SITE1 and DKFZp547M072 BINDING SITE2, designated SEQ ID:30617 and SEQ ID:30618 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83358] Another function of VGAM2463 is therefore inhibition of DKFZp547M072 (Accession XM_028067). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp547M072. DKFZP586M1120 (Accession NM_031294) is another VGAM2463 host target gene. DKFZP586M1120 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP586M1120, corresponding to a HOST TARGET bind-

ing site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP586M1120 BINDING SITE, designated SEQ ID:25321, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83359] Another function of VGAM2463 is therefore inhibition of DKFZP586M1120 (Accession NM_031294). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP586M1120. DKFZp762A227 (Accession NM_014096) is another VGAM2463 host target gene. DKFZp762A227 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZp762A227, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp762A227 BINDING SITE, designated SEQ ID:15319, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83360] Another function of VGAM2463 is therefore inhibition of DKFZp762A227 (Accession NM_014096). Accordingly,

utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762A227. EFS2 (Accession NM_005864) is another VGAM2463 host target gene. EFS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EFS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EFS2 BINDING SITE, designated SEQ ID:12477, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83361] Another function of VGAM2463 is therefore inhibition of EFS2 (Accession NM_005864). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EFS2. Ets2 Repressor Factor (ERF, Accession NM_006494) is another VGAM2463 host target gene. ERF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ERF, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ERF BINDING SITE,

designated SEQ ID:13235, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83362] Another function of VGAM2463 is therefore inhibition of Ets2 Repressor Factor (ERF, Accession NM_006494). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ERF. Fem-1 Homolog B (C. elegans) (FEM1B, Accession NM_015322) is another VGAM2463 host target gene. FEM1B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FEM1B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FEM1B BINDING SITE, designated SEQ ID:17641, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83363] Another function of VGAM2463 is therefore inhibition of Fem-1 Homolog B (C. elegans) (FEM1B, Accession NM_015322). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FEM1B. FHX (Accession

NM_018416) is another VGAM2463 host target gene. FHX BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FHX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FHX BINDING SITE, designated SEQ ID:20458, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83364] Another function of VGAM2463 is therefore inhibition of FHX (Accession NM_018416). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FHX. FLJ00024 (Accession XM_033361) is another VGAM2463 host target gene. FLJ00024 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ00024, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00024 BINDING SITE, designated SEQ ID:31890, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83365] Another function of VGAM2463 is therefore inhibition of FLJ00024 (Accession XM_033361). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00024. FLJ00058 (Accession XM_086123) is another VGAM2463 host target gene. FLJ00058 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ00058, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ00058 BINDING SITE, designated SEQ ID:38510, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83366] Another function of VGAM2463 is therefore inhibition of FLJ00058 (Accession XM_086123). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ00058. FLJ10276 (Accession NM_018045) is another VGAM2463 host target gene. FLJ10276 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10276, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10276 BINDING SITE, designated SEQ ID:19792, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83367] Another function of VGAM2463 is therefore inhibition of FLJ10276 (Accession NM_018045). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10276. FLJ10769 (Accession NM_018210) is another VGAM2463 host target gene. FLJ10769 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10769, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10769 BINDING SITE, designated SEQ ID:20113, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83368] Another function of VGAM2463 is therefore inhibition of FLJ10769 (Accession NM_018210). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ10769. FLJ11807 (Accession NM_024954) is another VGAM2463 host target gene. FLJ11807 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11807, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11807 BINDING SITE, designated SEQ ID:24512, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83369] Another function of VGAM2463 is therefore inhibition of FLJ11807 (Accession NM_024954). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11807. FLJ13114 (Accession NM_024541) is another VGAM2463 host target gene. FLJ13114 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13114, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13114 BINDING SITE, designated SEQ ID:23752, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM

RNA, also designated SEQ ID:5174.

[83370] Another function of VGAM2463 is therefore inhibition of FLJ13114 (Accession NM_024541). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13114. FLJ13154 (Accession NM_024598) is another VGAM2463 host target gene. FLJ13154 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13154, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13154 BINDING SITE, designated SEQ ID:23844, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83371] Another function of VGAM2463 is therefore inhibition of FLJ13154 (Accession NM_024598). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13154. FLJ13158 (Accession NM_024909) is another VGAM2463 host target gene. FLJ13158 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13158, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13158 BINDING SITE, designated SEQ ID:24410, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83372] Another function of VGAM2463 is therefore inhibition of FLJ13158 (Accession NM_024909). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13158. FLJ13189 (Accession NM_024882) is another VGAM2463 host target gene. FLJ13189 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ13189, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13189 BINDING SITE, designated SEQ ID:24332, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83373] Another function of VGAM2463 is therefore inhibition of FLJ13189 (Accession NM_024882). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ13189. FLJ13193 (Accession NM_032177) is another VGAM2463 host target gene. FLJ13193 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13193, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13193 BINDING SITE, designated SEQ ID:25892, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83374] Another function of VGAM2463 is therefore inhibition of FLJ13193 (Accession NM_032177). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13193. FLJ13612 (Accession NM_025202) is another VGAM2463 host target gene. FLJ13612 BINDING SITE1 and FLJ13612 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ13612, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13612 BINDING SITE1 and FLJ13612

BINDING SITE2, designated SEQ ID:24861 and SEQ ID:24862 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83375] Another function of VGAM2463 is therefore inhibition of FLJ13612 (Accession NM_025202). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13612. FLJ14154 (Accession NM_024845) is another VGAM2463 host target gene. FLJ14154 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14154, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14154 BINDING SITE, designated SEQ ID:24271, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83376] Another function of VGAM2463 is therefore inhibition of FLJ14154 (Accession NM_024845). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14154. FLJ14249 (Accession NM_106552) is another

VGAM2463 host target gene. FLJ14249 BINDING SITE1 and FLJ14249 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ14249, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14249 BINDING SITE1 and FLJ14249 BINDING SITE2, designated SEQ ID:28170 and SEQ ID:22800 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83377] Another function of VGAM2463 is therefore inhibition of FLJ14249 (Accession NM_106552). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14249. FLJ14442 (Accession NM_032785) is another VGAM2463 host target gene. FLJ14442 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14442, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14442 BINDING SITE, designated SEQ ID:26537, to the nucleotide

sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83378] Another function of VGAM2463 is therefore inhibition of FLJ14442 (Accession NM_032785). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14442. FLJ20378 (Accession NM_017795) is another VGAM2463 host target gene. FLJ20378 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20378, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20378 BINDING SITE, designated SEQ ID:19436, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83379] Another function of VGAM2463 is therefore inhibition of FLJ20378 (Accession NM_017795). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20378. FLJ20651 (Accession NM_017919) is another VGAM2463 host target gene. FLJ20651 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ20651, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20651 BINDING SITE, designated SEQ ID:19575, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83380] Another function of VGAM2463 is therefore inhibition of FLJ20651 (Accession NM_017919). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20651. FLJ20694 (Accession NM_017928) is another VGAM2463 host target gene. FLJ20694 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20694, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20694 BINDING SITE, designated SEQ ID:19608, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83381] Another function of VGAM2463 is therefore inhibition of FLJ20694 (Accession NM_017928). Accordingly, utilities of

VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20694. FLJ21596 (Accession NM_024823) is another VGAM2463 host target gene. FLJ21596 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21596, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21596 BINDING SITE, designated SEQ ID:24212, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83382] Another function of VGAM2463 is therefore inhibition of FLJ21596 (Accession NM_024823). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21596. FLJ22551 (Accession NM_024708) is another VGAM2463 host target gene. FLJ22551 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22551, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22551

BINDING SITE, designated SEQ ID:24027, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83383] Another function of VGAM2463 is therefore inhibition of FLJ22551 (Accession NM_024708). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22551. FLJ22679 (Accession NM_032227) is another VGAM2463 host target gene. FLJ22679 BINDING SITE1 and FLJ22679 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ22679, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22679 BINDING SITE1 and FLJ22679 BINDING SITE2, designated SEQ ID:25951 and SEQ ID:19264 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83384] Another function of VGAM2463 is therefore inhibition of FLJ22679 (Accession NM_032227). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ22679. FLJ23537 (Accession NM_024889) is another VGAM2463 host target gene. FLJ23537 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23537, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23537 BINDING SITE, designated SEQ ID:24364, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83385] Another function of VGAM2463 is therefore inhibition of FLJ23537 (Accession NM_024889). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23537. FLJ23563 (Accession XM_041701) is another VGAM2463 host target gene. FLJ23563 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23563, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23563 BINDING SITE, designated SEQ ID:33564, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM

RNA, also designated SEQ ID:5174.

[83386] Another function of VGAM2463 is therefore inhibition of FLJ23563 (Accession XM_041701). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23563. FLJ31952 (Accession NM_144682) is another VGAM2463 host target gene. FLJ31952 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ31952, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ31952 BINDING SITE, designated SEQ ID:29499, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83387] Another function of VGAM2463 is therefore inhibition of FLJ31952 (Accession NM_144682). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ31952. FLJ32389 (Accession NM_144617) is another VGAM2463 host target gene. FLJ32389 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ32389, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32389 BINDING SITE, designated SEQ ID:29434, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83388] Another function of VGAM2463 is therefore inhibition of FLJ32389 (Accession NM_144617). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32389. FLJ32884 (Accession NM_144702) is another VGAM2463 host target gene. FLJ32884 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ32884, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32884 BINDING SITE, designated SEQ ID:29527, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83389] Another function of VGAM2463 is therefore inhibition of FLJ32884 (Accession NM_144702). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ32884. Frequenin Homolog (Drosophila) (FREQ, Accession NM_014286) is another VGAM2463 host target gene. FREQ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FREQ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FREQ BINDING SITE, designated SEQ ID:15563, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83390] Another function of VGAM2463 is therefore inhibition of Frequenin Homolog (Drosophila) (FREQ, Accession NM_014286). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FREQ. GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568) is another VGAM2463 host target gene. GABARAPL3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GABARAPL3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of GABARAPL3 BINDING SITE, designated SEQ ID:26299, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83391] Another function of VGAM2463 is therefore inhibition of GABA(A) Receptors Associated Protein Like 3 (GABARAPL3, Accession NM_032568). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABARAPL3. Gamma-aminobutyric Acid (GABA) B Receptor, 1 (GABBR1, Accession NM_001470) is another VGAM2463 host target gene. GABBR1 BINDING SITE1 and GABBR1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GABBR1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GABBR1 BINDING SITE1 and GABBR1 BINDING SITE2, designated SEQ ID:7205 and SEQ ID:22422 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83392] Another function of VGAM2463 is therefore inhibition of

Gamma-aminobutyric Acid (GABA) B Receptor, 1 (GABBR1, Accession NM_001470). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GABBR1. G Protein Pathway Suppressor 2 (GPS2, Accession XM_102749) is another VGAM2463 host target gene. GPS2 BINDING SITE1 and GPS2 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by GPS2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GPS2 BINDING SITE1 and GPS2 BINDING SITE2, designated SEQ ID:42148 and SEQ ID:10826 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83393] Another function of VGAM2463 is therefore inhibition of G Protein Pathway Suppressor 2 (GPS2, Accession XM_102749). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GPS2. GS3955 (Accession NM_021643) is another VGAM2463 host target gene. GS3955 BINDING SITE is HOST TARGET binding site found

in the 5` untranslated region of mRNA encoded by GS3955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GS3955 BINDING SITE, designated SEQ ID:22302, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83394] Another function of VGAM2463 is therefore inhibition of GS3955 (Accession NM_021643). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GS3955. Histidyl-tRNA Synthetase 2 (HARS2, Accession NM_080820) is another VGAM2463 host target gene. HARS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HARS2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HARS2 BINDING SITE, designated SEQ ID:28079, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83395] Another function of VGAM2463 is therefore inhibition of Histidyl-tRNA Synthetase 2 (HARS2, Accession NM_080820). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HARS2. Hypocretin (orexin) Receptor 1 (HCRTR1, Accession NM_001525) is another VGAM2463 host target gene. HCRTR1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HCRTR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCRTR1 BINDING SITE, designated SEQ ID:7263, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83396] Another function of VGAM2463 is therefore inhibition of Hypocretin (orexin) Receptor 1 (HCRTR1, Accession NM_001525). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCRTR1. Hect Domain and RLD 3 (HERC3, Accession NM_014606) is another VGAM2463 host target gene. HERC3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region

of mRNA encoded by HERC3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HERC3 BINDING SITE, designated SEQ ID:15972, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83397] Another function of VGAM2463 is therefore inhibition of Hect Domain and RLD 3 (HERC3, Accession NM_014606). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HERC3. Hairy/enhancer-of-split Related with YRPW Motif-like (HEYL, Accession NM_014571) is another VGAM2463 host target gene. HEYL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HEYL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HEYL BINDING SITE, designated SEQ ID:15930, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83398] Another function of VGAM2463 is therefore inhibition of

Hairy/enhancer-of-split Related with YRPW Motif-like (HEYL, Accession NM_014571). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HEYL. HNT (Accession NM_016522) is another VGAM2463 host target gene. HNT BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HNT, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HNT BINDING SITE, designated SEQ ID:18594, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83399] Another function of VGAM2463 is therefore inhibition of HNT (Accession NM_016522). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HNT. HRIHFB2122 (Accession NM_007032) is another VGAM2463 host target gene. HRIHFB2122 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HRIHFB2122, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRI-HFB2122 BINDING SITE, designated SEQ ID:13900, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83400] Another function of VGAM2463 is therefore inhibition of HRIHFB2122 (Accession NM_007032). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRIHFB2122. Integrin, Alpha 10 (ITGA10, Accession XM_002097) is another VGAM2463 host target gene. ITGA10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGA10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA10 BINDING SITE, designated SEQ ID:29862, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83401] Another function of VGAM2463 is therefore inhibition of Integrin, Alpha 10 (ITGA10, Accession XM_002097). Accordingly, utilities of VGAM2463 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with ITGA10. KIAA0152 (Accession NM_014730) is another VGAM2463 host target gene. KIAA0152 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0152, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0152 BINDING SITE, designated SEQ ID:16336, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83402] Another function of VGAM2463 is therefore inhibition of KIAA0152 (Accession NM_014730). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0152. KIAA0237 (Accession NM_014747) is another VGAM2463 host target gene. KIAA0237 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0237, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0237 BINDING SITE, designated SEQ ID:16451, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83403] Another function of VGAM2463 is therefore inhibition of KIAA0237 (Accession NM_014747). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0237. KIAA0247 (Accession NM_014734) is another VGAM2463 host target gene. KIAA0247 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0247, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0247 BINDING SITE, designated SEQ ID:16377, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83404] Another function of VGAM2463 is therefore inhibition of KIAA0247 (Accession NM_014734). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0247. KIAA0256 (Accession XM_034905) is another VGAM2463 host target gene. KIAA0256 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0256, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0256 BINDING SITE, designated SEQ ID:32185, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83405] Another function of VGAM2463 is therefore inhibition of KIAA0256 (Accession XM_034905). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0256. KIAA0284 (Accession XM_032235) is another VGAM2463 host target gene. KIAA0284 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0284, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0284 BINDING SITE, designated SEQ ID:31619, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83406] Another function of VGAM2463 is therefore inhibition of

KIAA0284 (Accession XM_032235). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0284. KIAA0321 (Accession XM_031077) is another VGAM2463 host target gene. KIAA0321 BINDING SITE1 and KIAA0321 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0321, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0321 BINDING SITE1 and KIAA0321 BINDING SITE2, designated SEQ ID:31267 and SEQ ID:31268 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83407] Another function of VGAM2463 is therefore inhibition of KIAA0321 (Accession XM_031077). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0321. KIAA0450 (Accession NM_014638) is another VGAM2463 host target gene. KIAA0450 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0450, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0450 BINDING SITE, designated SEQ ID:16031, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83408] Another function of VGAM2463 is therefore inhibition of KIAA0450 (Accession NM_014638). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0450. KIAA0451 (Accession NM_014826) is another VGAM2463 host target gene. KIAA0451 BINDING SITE1 and KIAA0451 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA0451, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0451 BINDING SITE1 and KIAA0451 BINDING SITE2, designated SEQ ID:16805 and SEQ ID:16810 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83409] Another function of VGAM2463 is therefore inhibition of

KIAA0451 (Accession NM_014826). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0451. KIAA0720 (Accession XM_030970) is another VGAM2463 host target gene. KIAA0720 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0720, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0720 BINDING SITE, designated SEQ ID:31238, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83410] Another function of VGAM2463 is therefore inhibition of KIAA0720 (Accession XM_030970). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0720. KIAA0775 (Accession NM_014726) is another VGAM2463 host target gene. KIAA0775 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0775, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0775 BINDING SITE, designated SEQ ID:16322, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83411] Another function of VGAM2463 is therefore inhibition of KIAA0775 (Accession NM_014726). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0775. KIAA0794 (Accession XM_087353) is another VGAM2463 host target gene. KIAA0794 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0794, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0794 BINDING SITE, designated SEQ ID:39180, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83412] Another function of VGAM2463 is therefore inhibition of KIAA0794 (Accession XM_087353). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0794. KIAA0889 (Accession NM_015377) is another

VGAM2463 host target gene. KIAA0889 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0889, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0889 BINDING SITE, designated SEQ ID:17679, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83413] Another function of VGAM2463 is therefore inhibition of KIAA0889 (Accession NM_015377). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0889. KIAA0937 (Accession XM_166213) is another VGAM2463 host target gene. KIAA0937 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0937, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0937 BINDING SITE, designated SEQ ID:44017, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83414] Another function of VGAM2463 is therefore inhibition of KIAA0937 (Accession XM_166213). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0937. KIAA0939 (Accession XM_030524) is another VGAM2463 host target gene. KIAA0939 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0939, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0939 BINDING SITE, designated SEQ ID:31062, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83415] Another function of VGAM2463 is therefore inhibition of KIAA0939 (Accession XM_030524). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0939. KIAA1042 (Accession NM_014965) is another VGAM2463 host target gene. KIAA1042 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1042, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1042 BINDING SITE, designated SEQ ID:17351, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83416] Another function of VGAM2463 is therefore inhibition of KIAA1042 (Accession NM_014965). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1042. KIAA1076 (Accession XM_037523) is another VGAM2463 host target gene. KIAA1076 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1076, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1076 BINDING SITE, designated SEQ ID:32640, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83417] Another function of VGAM2463 is therefore inhibition of KIAA1076 (Accession XM_037523). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1076. KIAA1138 (Accession XM_030721) is another VGAM2463 host target gene. KIAA1138 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1138, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1138 BINDING SITE, designated SEQ ID:31127, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83418] Another function of VGAM2463 is therefore inhibition of KIAA1138 (Accession XM_030721). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1138. KIAA1172 (Accession XM_047889) is another VGAM2463 host target gene. KIAA1172 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1172, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1172 BINDING SITE, designated SEQ ID:35077, to the nucleotide sequence of VGAM2463 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5174.

[83419] Another function of VGAM2463 is therefore inhibition of KIAA1172 (Accession XM_047889). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1172. KIAA1185 (Accession XM_031399) is another VGAM2463 host target gene. KIAA1185 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1185, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1185 BINDING SITE, designated SEQ ID:31371, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83420] Another function of VGAM2463 is therefore inhibition of KIAA1185 (Accession XM_031399). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1185. KIAA1193 (Accession XM_041843) is another VGAM2463 host target gene. KIAA1193 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1193, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1193 BINDING SITE, designated SEQ ID:33582, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83421] Another function of VGAM2463 is therefore inhibition of KIAA1193 (Accession XM_041843). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1193. KIAA1434 (Accession XM_045585) is another VGAM2463 host target gene. KIAA1434 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1434, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1434 BINDING SITE, designated SEQ ID:34489, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83422] Another function of VGAM2463 is therefore inhibition of KIAA1434 (Accession XM_045585). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1434. KIAA1538 (Accession XM_049474) is another VGAM2463 host target gene. KIAA1538 BINDING SITE1 through KIAA1538 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1538, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1538 BINDING SITE1 through KIAA1538 BINDING SITE3, designated SEQ ID:35426, SEQ ID:35427 and SEQ ID:35428 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83423] Another function of VGAM2463 is therefore inhibition of KIAA1538 (Accession XM_049474). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1538. KIAA1656 (Accession XM_038022) is another VGAM2463 host target gene. KIAA1656 BINDING SITE1 and KIAA1656 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1656, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1656 BINDING SITE1 and KIAA1656 BINDING SITE2, designated SEQ ID:32730 and SEQ ID:32731 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83424] Another function of VGAM2463 is therefore inhibition of KIAA1656 (Accession XM_038022). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1656. KIAA1775 (Accession NM_033100) is another VGAM2463 host target gene. KIAA1775 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1775, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1775 BINDING SITE, designated SEQ ID:26944, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83425] Another function of VGAM2463 is therefore inhibition of KIAA1775 (Accession NM_033100). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1775. KIAA1831 (Accession XM_033366) is another VGAM2463 host target gene. KIAA1831 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1831, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1831 BINDING SITE, designated SEQ ID:31904, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83426] Another function of VGAM2463 is therefore inhibition of KIAA1831 (Accession XM_033366). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1831. KIAA1855 (Accession XM_166453) is another VGAM2463 host target gene. KIAA1855 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1855, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1855 BINDING SITE, designated SEQ ID:44361, to the

nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83427] Another function of VGAM2463 is therefore inhibition of KIAA1855 (Accession XM_166453). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1855. KIAA1862 (Accession XM_044212) is another VGAM2463 host target gene. KIAA1862 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1862, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1862 BINDING SITE, designated SEQ ID:34175, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83428] Another function of VGAM2463 is therefore inhibition of KIAA1862 (Accession XM_044212). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1862. KIAA1904 (Accession XM_056282) is another VGAM2463 host target gene. KIAA1904 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA1904, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1904 BINDING SITE, designated SEQ ID:36381, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83429] Another function of VGAM2463 is therefore inhibition of KIAA1904 (Accession XM_056282). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1904. KIAA1938 (Accession XM_166407) is another VGAM2463 host target gene. KIAA1938 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1938, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1938 BINDING SITE, designated SEQ ID:44280, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83430] Another function of VGAM2463 is therefore inhibition of KIAA1938 (Accession XM_166407). Accordingly, utilities

of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1938. KIAA1949 (Accession XM_175173) is another VGAM2463 host target gene. KIAA1949 BINDING SITE1 through KIAA1949 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1949, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1949 BINDING SITE1 through KIAA1949 BINDING SITE3, designated SEQ ID:46669, SEQ ID:46714 and SEQ ID:44210 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83431] Another function of VGAM2463 is therefore inhibition of KIAA1949 (Accession XM_175173). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1949. Leucine-rich Repeat LGI Family, Member 2 (LGI2, Accession NM_018176) is another VGAM2463 host target gene. LGI2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LGI2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LGI2 BINDING SITE, designated SEQ ID:20001, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83432] Another function of VGAM2463 is therefore inhibition of Leucine-rich Repeat LGI Family, Member 2 (LGI2, Accession NM_018176). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LGI2. LHPP (Accession NM_022126) is another VGAM2463 host target gene. LHPP BINDING SITE1 through LHPP BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LHPP, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LHPP BINDING SITE1 through LHPP BINDING SITE4, designated SEQ ID:22675, SEQ ID:22676, SEQ ID:22677 and SEQ ID:22679 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83433] Another function of VGAM2463 is therefore inhibition of LHPP (Accession NM_022126). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LHPP. MGC10812 (Accession NM_031425) is another VGAM2463 host target gene. MGC10812 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC10812, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10812 BINDING SITE, designated SEQ ID:25414, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83434] Another function of VGAM2463 is therefore inhibition of MGC10812 (Accession NM_031425). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10812. MGC10986 (Accession NM_030576) is another VGAM2463 host target gene. MGC10986 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC10986, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC10986 BINDING SITE, designated SEQ ID:24951, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83435] Another function of VGAM2463 is therefore inhibition of MGC10986 (Accession NM_030576). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC10986. MGC15854 (Accession NM_145029) is another VGAM2463 host target gene. MGC15854 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC15854, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC15854 BINDING SITE, designated SEQ ID:29643, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83436] Another function of VGAM2463 is therefore inhibition of MGC15854 (Accession NM_145029). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

MGC15854. MGC16824 (Accession NM_020314) is another VGAM2463 host target gene. MGC16824 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC16824, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16824 BINDING SITE, designated SEQ ID:21572, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83437] Another function of VGAM2463 is therefore inhibition of MGC16824 (Accession NM_020314). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC16824. MGC20255 (Accession NM_052848) is another VGAM2463 host target gene. MGC20255 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC20255, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC20255 BINDING SITE, designated SEQ ID:27429, to the nucleotide sequence of VGAM2463 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5174.

[83438] Another function of VGAM2463 is therefore inhibition of MGC20255 (Accession NM_052848). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC20255. MGC21621 (Accession NM_145015) is another VGAM2463 host target gene. MGC21621 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC21621, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC21621 BINDING SITE, designated SEQ ID:29621, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83439] Another function of VGAM2463 is therefore inhibition of MGC21621 (Accession NM_145015). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21621. MGC2574 (Accession NM_024098) is another VGAM2463 host target gene. MGC2574 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC2574, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2574 BINDING SITE, designated SEQ ID:23536, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83440] Another function of VGAM2463 is therefore inhibition of MGC2574 (Accession NM_024098). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2574. MGC2817 (Accession XM_046613) is another VGAM2463 host target gene. MGC2817 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC2817, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2817 BINDING SITE, designated SEQ ID:34763, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83441] Another function of VGAM2463 is therefore inhibition of MGC2817 (Accession XM_046613). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC2817. MGC4342 (Accession NM_024329) is another VGAM2463 host target gene. MGC4342 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4342, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4342 BINDING SITE, designated SEQ ID:23624, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83442] Another function of VGAM2463 is therefore inhibition of MGC4342 (Accession NM_024329). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4342. Neuroblastoma, Suppression of Tumorigenicity 1 (NBL1, Accession XM_001434) is another VGAM2463 host target gene. NBL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NBL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NBL1 BINDING SITE, designated

SEQ ID:29839, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83443] Another function of VGAM2463 is therefore inhibition of Neuroblastoma, Suppression of Tumorigenicity 1 (NBL1, Accession XM_001434). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NBL1. NFASC (Accession XM_046808) is another VGAM2463 host target gene. NFASC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NFASC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFASC BINDING SITE, designated SEQ ID:34831, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83444] Another function of VGAM2463 is therefore inhibition of NFASC (Accession XM_046808). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFASC. Nuclear Factor of Activated T-cells 5, Tonicity-responsive

(NFAT5, Accession NM_138714) is another VGAM2463 host target gene. NFAT5 BINDING SITE1 and NFAT5 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NFAT5, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFAT5 BINDING SITE1 and NFAT5 BINDING SITE2, designated SEQ ID:28954 and SEQ ID:28958 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83445] Another function of VGAM2463 is therefore inhibition of Nuclear Factor of Activated T-cells 5, Tonicity-responsive (NFAT5, Accession NM_138714). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFAT5. NTT73 (Accession NM_018057) is another VGAM2463 host target gene. NTT73 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NTT73, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NTT73 BINDING SITE, des-

ignated SEQ ID:19825, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83446] Another function of VGAM2463 is therefore inhibition of NTT73 (Accession NM_018057). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTT73. Nucleoredoxin (NXN, Accession NM_022463) is another VGAM2463 host target gene. NXN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NXN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NXN BINDING SITE, designated SEQ ID:22809, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83447] Another function of VGAM2463 is therefore inhibition of Nucleoredoxin (NXN, Accession NM_022463). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXN. Ornithine Decarboxylase Antizyme 3 (OAZ3, Accession NM_016178) is another VGAM2463 host target

gene. OAZ3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by OAZ3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OAZ3 BINDING SITE, designated SEQ ID:18280, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83448] Another function of VGAM2463 is therefore inhibition of Ornithine Decarboxylase Antizyme 3 (OAZ3, Accession NM_016178). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OAZ3. Prefoldin 1 (PFDN1, Accession NM_002622) is another VGAM2463 host target gene. PFDN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PFDN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PFDN1 BINDING SITE, designated SEQ ID:8483, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83449] Another function of VGAM2463 is therefore inhibition of Prefoldin 1 (PFDN1, Accession NM_002622). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PFDN1. PIF1 (Accession XM_027898) is another VGAM2463 host target gene. PIF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIF1 BINDING SITE, designated SEQ ID:30586, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83450] Another function of VGAM2463 is therefore inhibition of PIF1 (Accession XM_027898). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIF1. Phospholipase A2, Group III (PLA2G3, Accession NM_015715) is another VGAM2463 host target gene. PLA2G3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PLA2G3, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLA2G3 BINDING SITE, designated SEQ ID:17928, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83451] Another function of VGAM2463 is therefore inhibition of Phospholipase A2, Group III (PLA2G3, Accession NM_015715). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLA2G3. POLD3 (Accession XM_166243) is another VGAM2463 host target gene. POLD3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by POLD3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of POLD3 BINDING SITE, designated SEQ ID:44056, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83452] Another function of VGAM2463 is therefore inhibition of POLD3 (Accession XM_166243). Accordingly, utilities of

VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with POLD3. PP3501 (Accession NM_021731) is another VGAM2463 host target gene. PP3501 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PP3501, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP3501 BINDING SITE, designated SEQ ID:22332, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83453] Another function of VGAM2463 is therefore inhibition of PP3501 (Accession NM_021731). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP3501. PR Domain Containing 11 (PRDM11, Accession NM_020229) is another VGAM2463 host target gene. PRDM11 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRDM11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of PRDM11 BINDING SITE, designated SEQ ID:21501, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83454] Another function of VGAM2463 is therefore inhibition of PR Domain Containing 11 (PRDM11, Accession NM_020229). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDM11. PR Domain Containing 7 (PRDM7, Accession NM_052996) is another VGAM2463 host target gene. PRDM7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRDM7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRDM7 BINDING SITE, designated SEQ ID:27569, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83455] Another function of VGAM2463 is therefore inhibition of PR Domain Containing 7 (PRDM7, Accession NM_052996). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical condi-

tions associated with PRDM7. PRO0233 (Accession NM_014121) is another VGAM2463 host target gene. PRO0233 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO0233, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO0233 BINDING SITE, designated SEQ ID:15373, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83456] Another function of VGAM2463 is therefore inhibition of PRO0233 (Accession NM_014121). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO0233. PRO1048 (Accession NM_018497) is another VGAM2463 host target gene. PRO1048 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO1048, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO1048 BINDING SITE, designated SEQ ID:20557, to the nucleotide

sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83457] Another function of VGAM2463 is therefore inhibition of PRO1048 (Accession NM_018497). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO1048. Protein Tyrosine Phosphatase, Non-receptor Type 3 (PTPN3, Accession NM_002829) is another VGAM2463 host target gene. PTPN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTPN3 BINDING SITE, designated SEQ ID:8706, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83458] Another function of VGAM2463 is therefore inhibition of Protein Tyrosine Phosphatase, Non-receptor Type 3 (PTPN3, Accession NM_002829). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPN3. RAB40C, Member RAS Oncogene Family (RAB40C, Acces-

sion NM_021168) is another VGAM2463 host target gene. RAB40C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RAB40C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB40C BINDING SITE, designated SEQ ID:22147, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83459] Another function of VGAM2463 is therefore inhibition of RAB40C, Member RAS Oncogene Family (RAB40C, Accession NM_021168). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB40C. RAB6B, Member RAS Oncogene Family (RAB6B, Accession NM_016577) is another VGAM2463 host target gene. RAB6B BINDING SITE1 and RAB6B BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RAB6B, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAB6B BINDING SITE1 and RAB6B BINDING

SITE2, designated SEQ ID:18653 and SEQ ID:18654 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83460] Another function of VGAM2463 is therefore inhibition of RAB6B, Member RAS Oncogene Family (RAB6B, Accession NM_016577). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAB6B. RBPMS (Accession NM_006867) is another VGAM2463 host target gene. RBPMS BINDING SITE1 and RBPMS BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by RBPMS, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBPMS BINDING SITE1 and RBPMS BINDING SITE2, designated SEQ ID:13738 and SEQ ID:8824 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83461] Another function of VGAM2463 is therefore inhibition of RBPMS (Accession NM_006867). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with RBPMS. SAE1 (Accession NM_005500) is another VGAM2463 host target gene. SAE1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SAE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SAE1 BINDING SITE, designated SEQ ID:12004, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83462] Another function of VGAM2463 is therefore inhibition of SAE1 (Accession NM_005500). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SAE1. SARM (Accession NM_015077) is another VGAM2463 host target gene. SARM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SARM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SARM BINDING SITE, designated SEQ ID:17458, to the nucleotide sequence of VGAM2463 RNA,

herein designated VGAM RNA, also designated SEQ ID:5174.

[83463] Another function of VGAM2463 is therefore inhibition of SARM (Accession NM_015077). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SARM. SCAMP5 (Accession NM_138967) is another VGAM2463 host target gene. SCAMP5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCAMP5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAMP5 BINDING SITE, designated SEQ ID:29075, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83464] Another function of VGAM2463 is therefore inhibition of SCAMP5 (Accession NM_138967). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAMP5. SCYA22 (Accession XM_165651) is another VGAM2463 host target gene. SCYA22 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by SCYA22, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCYA22 BINDING SITE, designated SEQ ID:43715, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83465] Another function of VGAM2463 is therefore inhibition of SCYA22 (Accession XM_165651). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCYA22. Solute Carrier Family 38, Member 5 (SLC38A5, Accession NM_033518) is another VGAM2463 host target gene. SLC38A5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC38A5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC38A5 BINDING SITE, designated SEQ ID:27298, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83466] Another function of VGAM2463 is therefore inhibition of

Solute Carrier Family 38, Member 5 (SLC38A5, Accession NM_033518). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC38A5. Syntaphilin (SNPH, Accession NM_014723) is another VGAM2463 host target gene. SNPH BINDING SITE1 through SNPH BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SNPH, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SNPH BINDING SITE1 through SNPH BINDING SITE3, designated SEQ ID:16294, SEQ ID:16297 and SEQ ID:16298 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83467] Another function of VGAM2463 is therefore inhibition of Syntaphilin (SNPH, Accession NM_014723). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SNPH. SPBPBP (Accession NM_006692) is another VGAM2463 host target gene. SPBPBP BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by SPBPBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPBPBP BINDING SITE, designated SEQ ID:13510, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83468] Another function of VGAM2463 is therefore inhibition of SPBPBP (Accession NM_006692). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPBPBP. SPEC1 (Accession NM_020239) is another VGAM2463 host target gene. SPEC1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPEC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPEC1 BINDING SITE, designated SEQ ID:21516, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83469] Another function of VGAM2463 is therefore inhibition of SPEC1 (Accession NM_020239). Accordingly, utilities of

VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPEC1. Serine Protease Inhibitor, Kunitz Type 1 (SPINT1, Accession XM_031510) is another VGAM2463 host target gene. SPINT1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SPINT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SPINT1 BINDING SITE, designated SEQ ID:31392, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83470] Another function of VGAM2463 is therefore inhibition of Serine Protease Inhibitor, Kunitz Type 1 (SPINT1, Accession XM_031510). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SPINT1. SSH2 (Accession XM_030846) is another VGAM2463 host target gene. SSH2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SSH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Ta-

ble 2 illustrates the complementarity of the nucleotide sequences of SSH2 BINDING SITE, designated SEQ ID:31182, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83471] Another function of VGAM2463 is therefore inhibition of SSH2 (Accession XM_030846). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSH2. TCF-3 (Accession NM_031283) is another VGAM2463 host target gene. TCF-3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCF-3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF-3 BINDING SITE, designated SEQ ID:25306, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83472] Another function of VGAM2463 is therefore inhibition of TCF-3 (Accession NM_031283). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF-3. Translocation Protein 1 (TLOC1, Accession NM_003262) is

another VGAM2463 host target gene. TLOC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TLOC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TLOC1 BINDING SITE, designated SEQ ID:9273, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83473] Another function of VGAM2463 is therefore inhibition of Translocation Protein 1 (TLOC1, Accession NM_003262). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLOC1. Tankyrase 1 Binding Protein 1, 182kDa (TNKS1BP1, Accession NM_033396) is another VGAM2463 host target gene. TNKS1BP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TNKS1BP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNKS1BP1 BINDING SITE, designated SEQ ID:27224, to the nucleotide sequence of VGAM2463 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5174.

[83474] Another function of VGAM2463 is therefore inhibition of Tankyrase 1 Binding Protein 1, 182kDa (TNKS1BP1, Accession NM_033396). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNKS1BP1. Trinucleotide Repeat Containing 4 (TNRC4, Accession NM_007185) is another VGAM2463 host target gene. TNRC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TNRC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TNRC4 BINDING SITE, designated SEQ ID:14041, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83475] Another function of VGAM2463 is therefore inhibition of Trinucleotide Repeat Containing 4 (TNRC4, Accession NM_007185). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TNRC4. TOLLIP (Accession NM_019009) is another VGAM2463 host target gene.

TOLLIP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOLLIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOLLIP BINDING SITE, designated SEQ ID:21092, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83476] Another function of VGAM2463 is therefore inhibition of TOLLIP (Accession NM_019009). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOLLIP. Target of Myb1 (chicken) (TOM1, Accession NM_005488) is another VGAM2463 host target gene. TOM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOM1 BINDING SITE, designated SEQ ID:11986, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83477] Another function of VGAM2463 is therefore inhibition of Target of Myb1 (chicken) (TOM1, Accession NM_005488). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOM1. Torsin Family 2, Member A (TOR2A, Accession NM_130459) is another VGAM2463 host target gene. TOR2A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TOR2A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TOR2A BINDING SITE, designated SEQ ID:28221, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83478] Another function of VGAM2463 is therefore inhibition of Torsin Family 2, Member A (TOR2A, Accession NM_130459). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TOR2A. TSC22 (Accession NM_006022) is another VGAM2463 host target gene. TSC22 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TSC22,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TSC22 BINDING SITE, designated SEQ ID:12640, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83479] Another function of VGAM2463 is therefore inhibition of TSC22 (Accession NM_006022). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TSC22. Tweety Homolog 2 (Drosophila) (TTYH2, Accession NM_032646) is another VGAM2463 host target gene. TTYH2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TTYH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTYH2 BINDING SITE, designated SEQ ID:26378, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83480] Another function of VGAM2463 is therefore inhibition of

Tweety Homolog 2 (Drosophila) (TTYH2, Accession NM_032646). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTYH2. TUSP (Accession NM_020245) is another VGAM2463 host target gene. TUSP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TUSP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TUSP BINDING SITE, designated SEQ ID:21528, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83481] Another function of VGAM2463 is therefore inhibition of TUSP (Accession NM_020245). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TUSP. Vav 3 Oncogene (VAV3, Accession NM_006113) is another VGAM2463 host target gene. VAV3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VAV3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complemen-

tarity of the nucleotide sequences of VAV3 BINDING SITE, designated SEQ ID:12760, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83482] Another function of VGAM2463 is therefore inhibition of Vav 3 Oncogene (VAV3, Accession NM_006113). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VAV3. Zinc Finger Protein 95 Homolog (mouse) (ZFP95, Accession NM_014569) is another VGAM2463 host target gene. ZFP95 BINDING SITE1 and ZFP95 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ZFP95, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZFP95 BINDING SITE1 and ZFP95 BINDING SITE2, designated SEQ ID:15921 and SEQ ID:29711 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83483] Another function of VGAM2463 is therefore inhibition of Zinc Finger Protein 95 Homolog (mouse) (ZFP95, Accession NM_014569). Accordingly, utilities of VGAM2463 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with ZFP95. LOC115509 (Accession XM_056092) is another VGAM2463 host target gene. LOC115509 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115509, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115509 BINDING SITE, designated SEQ ID:36363, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83484] Another function of VGAM2463 is therefore inhibition of LOC115509 (Accession XM_056092). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115509. LOC123242 (Accession XM_063548) is another VGAM2463 host target gene. LOC123242 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC123242, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC123242 BINDING SITE, designated SEQ ID:37244, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83485] Another function of VGAM2463 is therefore inhibition of LOC123242 (Accession XM_063548). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC123242. LOC124753 (Accession XM_058837) is another VGAM2463 host target gene. LOC124753 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC124753, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124753 BINDING SITE, designated SEQ ID:36761, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83486] Another function of VGAM2463 is therefore inhibition of LOC124753 (Accession XM_058837). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124753. LOC126208 (Accession XM_058999) is another VGAM2463 host target gene. LOC126208 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC126208, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126208 BINDING SITE, designated SEQ ID:36815, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83487] Another function of VGAM2463 is therefore inhibition of LOC126208 (Accession XM_058999). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126208. LOC127703 (Accession XM_059172) is another VGAM2463 host target gene. LOC127703 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC127703, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127703 BINDING SITE, designated SEQ ID:36907, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83488] Another function of VGAM2463 is therefore inhibition of

LOC127703 (Accession XM_059172). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127703. LOC128077 (Accession XM_059208) is another VGAM2463 host target gene. LOC128077 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC128077, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC128077 BINDING SITE, designated SEQ ID:36918, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83489] Another function of VGAM2463 is therefore inhibition of LOC128077 (Accession XM_059208). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128077. LOC132671 (Accession NM_145263) is another VGAM2463 host target gene. LOC132671 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC132671, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC132671 BINDING SITE, designated SEQ ID:29777, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83490] Another function of VGAM2463 is therefore inhibition of LOC132671 (Accession NM_145263). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC132671. LOC136288 (Accession XM_059832) is another VGAM2463 host target gene. LOC136288 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC136288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC136288 BINDING SITE, designated SEQ ID:37099, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83491] Another function of VGAM2463 is therefore inhibition of LOC136288 (Accession XM_059832). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC136288. LOC145371 (Accession XM_085123) is an-

other VGAM2463 host target gene. LOC145371 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145371, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145371 BINDING SITE, designated SEQ ID:37846, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83492] Another function of VGAM2463 is therefore inhibition of LOC145371 (Accession XM_085123). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145371. LOC145988 (Accession XM_085290) is another VGAM2463 host target gene. LOC145988 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145988, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145988 BINDING SITE, designated SEQ ID:38042, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83493] Another function of VGAM2463 is therefore inhibition of LOC145988 (Accession XM_085290). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145988. LOC146237 (Accession XM_096954) is another VGAM2463 host target gene. LOC146237 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146237, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146237 BINDING SITE, designated SEQ ID:40666, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83494] Another function of VGAM2463 is therefore inhibition of LOC146237 (Accession XM_096954). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146237. LOC146488 (Accession XM_047748) is another VGAM2463 host target gene. LOC146488 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146488, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146488 BINDING SITE, designated SEQ ID:35046, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83495] Another function of VGAM2463 is therefore inhibition of LOC146488 (Accession XM_047748). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146488. LOC146780 (Accession XM_097086) is another VGAM2463 host target gene. LOC146780 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146780, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146780 BINDING SITE, designated SEQ ID:40741, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83496] Another function of VGAM2463 is therefore inhibition of LOC146780 (Accession XM_097086). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC146780. LOC146957 (Accession XM_085652) is another VGAM2463 host target gene. LOC146957 BINDING SITE1 and LOC146957 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC146957, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146957 BINDING SITE1 and LOC146957 BINDING SITE2, designated SEQ ID:38278 and SEQ ID:38279 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83497] Another function of VGAM2463 is therefore inhibition of LOC146957 (Accession XM_085652). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146957. LOC148946 (Accession XM_097557) is another VGAM2463 host target gene. LOC148946 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148946, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC148946 BINDING SITE, designated SEQ ID:40939, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83498] Another function of VGAM2463 is therefore inhibition of LOC148946 (Accession XM_097557). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148946. LOC149684 (Accession XM_097710) is another VGAM2463 host target gene. LOC149684 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149684, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149684 BINDING SITE, designated SEQ ID:41048, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83499] Another function of VGAM2463 is therefore inhibition of LOC149684 (Accession XM_097710). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149684. LOC149912 (Accession XM_097743) is another VGAM2463 host target gene. LOC149912 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149912, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149912 BINDING SITE, designated SEQ ID:41086, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83500] Another function of VGAM2463 is therefore inhibition of LOC149912 (Accession XM_097743). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149912. LOC151174 (Accession XM_098013) is another VGAM2463 host target gene. LOC151174 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151174, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151174 BINDING SITE, designated SEQ ID:41312, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83501] Another function of VGAM2463 is therefore inhibition of

LOC151174 (Accession XM_098013). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151174. LOC151201 (Accession XM_098021) is another VGAM2463 host target gene. LOC151201 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151201, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151201 BINDING SITE, designated SEQ ID:41328, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83502] Another function of VGAM2463 is therefore inhibition of LOC151201 (Accession XM_098021). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151201. LOC151473 (Accession XM_087215) is another VGAM2463 host target gene. LOC151473 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151473, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC151473 BINDING SITE, designated SEQ ID:39119, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83503] Another function of VGAM2463 is therefore inhibition of LOC151473 (Accession XM_087215). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151473. LOC151516 (Accession XM_087229) is another VGAM2463 host target gene. LOC151516 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151516, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151516 BINDING SITE, designated SEQ ID:39128, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83504] Another function of VGAM2463 is therefore inhibition of LOC151516 (Accession XM_087229). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151516. LOC151657 (Accession XM_098100) is an-

other VGAM2463 host target gene. LOC151657 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151657, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151657 BINDING SITE, designated SEQ ID:41382, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83505] Another function of VGAM2463 is therefore inhibition of LOC151657 (Accession XM_098100). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151657. LOC151904 (Accession XM_087334) is another VGAM2463 host target gene. LOC151904 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151904, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151904 BINDING SITE, designated SEQ ID:39173, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83506] Another function of VGAM2463 is therefore inhibition of LOC151904 (Accession XM_087334). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151904. LOC153688 (Accession XM_098416) is another VGAM2463 host target gene. LOC153688 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153688, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153688 BINDING SITE, designated SEQ ID:41659, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83507] Another function of VGAM2463 is therefore inhibition of LOC153688 (Accession XM_098416). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153688. LOC154877 (Accession XM_098626) is another VGAM2463 host target gene. LOC154877 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154877, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154877 BINDING SITE, designated SEQ ID:41743, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83508] Another function of VGAM2463 is therefore inhibition of LOC154877 (Accession XM_098626). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154877. LOC157349 (Accession XM_088298) is another VGAM2463 host target gene. LOC157349 BINDING SITE1 and LOC157349 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC157349, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157349 BINDING SITE1 and LOC157349 BINDING SITE2, designated SEQ ID:39593 and SEQ ID:39595 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83509] Another function of VGAM2463 is therefore inhibition of LOC157349 (Accession XM_088298). Accordingly, utilities

of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157349. LOC157918 (Accession XM_098842) is another VGAM2463 host target gene. LOC157918 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC157918, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157918 BINDING SITE, designated SEQ ID:41896, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83510] Another function of VGAM2463 is therefore inhibition of LOC157918 (Accession XM_098842). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157918. LOC157919 (Accession XM_088420) is another VGAM2463 host target gene. LOC157919 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157919, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC157919 BINDING SITE, designated SEQ ID:39683, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83511] Another function of VGAM2463 is therefore inhibition of LOC157919 (Accession XM_088420). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157919. LOC158187 (Accession XM_098892) is another VGAM2463 host target gene. LOC158187 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158187, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158187 BINDING SITE, designated SEQ ID:41923, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83512] Another function of VGAM2463 is therefore inhibition of LOC158187 (Accession XM_098892). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158187. LOC158235 (Accession XM_098897) is another VGAM2463 host target gene. LOC158235 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158235, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158235 BINDING SITE, designated SEQ ID:41924, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83513] Another function of VGAM2463 is therefore inhibition of LOC158235 (Accession XM_098897). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158235. LOC158288 (Accession XM_098912) is another VGAM2463 host target gene. LOC158288 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC158288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158288 BINDING SITE, designated SEQ ID:41929, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83514] Another function of VGAM2463 is therefore inhibition of

LOC158288 (Accession XM_098912). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158288. LOC165721 (Accession XM_093388) is another VGAM2463 host target gene. LOC165721 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC165721, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC165721 BINDING SITE, designated SEQ ID:40191, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83515] Another function of VGAM2463 is therefore inhibition of LOC165721 (Accession XM_093388). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC165721. LOC165741 (Accession XM_105272) is another VGAM2463 host target gene. LOC165741 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC165741, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC165741 BINDING SITE, designated SEQ ID:42191, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83516] Another function of VGAM2463 is therefore inhibition of LOC165741 (Accession XM_105272). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC165741. LOC196463 (Accession XM_113725) is another VGAM2463 host target gene. LOC196463 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196463, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196463 BINDING SITE, designated SEQ ID:42374, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83517] Another function of VGAM2463 is therefore inhibition of LOC196463 (Accession XM_113725). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196463. LOC196955 (Accession XM_085210) is an-

other VGAM2463 host target gene. LOC196955 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC196955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196955 BINDING SITE, designated SEQ ID:37936, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83518] Another function of VGAM2463 is therefore inhibition of LOC196955 (Accession XM_085210). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196955. LOC200010 (Accession XM_117174) is another VGAM2463 host target gene. LOC200010 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200010, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200010 BINDING SITE, designated SEQ ID:43278, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83519] Another function of VGAM2463 is therefore inhibition of LOC200010 (Accession XM_117174). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200010. LOC200269 (Accession XM_114175) is another VGAM2463 host target gene. LOC200269 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200269, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200269 BINDING SITE, designated SEQ ID:42760, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83520] Another function of VGAM2463 is therefore inhibition of LOC200269 (Accession XM_114175). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC200269. LOC201245 (Accession XM_113326) is another VGAM2463 host target gene. LOC201245 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201245, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201245 BINDING SITE, designated SEQ ID:42230, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83521] Another function of VGAM2463 is therefore inhibition of LOC201245 (Accession XM_113326). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201245. LOC201294 (Accession XM_113950) is another VGAM2463 host target gene. LOC201294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201294 BINDING SITE, designated SEQ ID:42567, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83522] Another function of VGAM2463 is therefore inhibition of LOC201294 (Accession XM_113950). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC201294. LOC201562 (Accession XM_114343) is another VGAM2463 host target gene. LOC201562 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC201562, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201562 BINDING SITE, designated SEQ ID:42883, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83523] Another function of VGAM2463 is therefore inhibition of LOC201562 (Accession XM_114343). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201562. LOC201702 (Accession XM_114365) is another VGAM2463 host target gene. LOC201702 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC201702, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201702 BINDING SITE, designated SEQ ID:42901, to the nucleotide sequence of VGAM2463 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5174.

[83524] Another function of VGAM2463 is therefore inhibition of LOC201702 (Accession XM_114365). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201702. LOC203248 (Accession XM_114659) is another VGAM2463 host target gene. LOC203248 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203248, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203248 BINDING SITE, designated SEQ ID:43020, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83525] Another function of VGAM2463 is therefore inhibition of LOC203248 (Accession XM_114659). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203248. LOC203504 (Accession XM_117550) is another VGAM2463 host target gene. LOC203504 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC203504, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC203504 BINDING SITE, designated SEQ ID:43571, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83526] Another function of VGAM2463 is therefore inhibition of LOC203504 (Accession XM_117550). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC203504. LOC219540 (Accession XM_168047) is another VGAM2463 host target gene. LOC219540 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219540, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219540 BINDING SITE, designated SEQ ID:44958, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83527] Another function of VGAM2463 is therefore inhibition of LOC219540 (Accession XM_168047). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC219540. LOC219654 (Accession XM_166095) is another VGAM2463 host target gene. LOC219654 BINDING SITE1 and LOC219654 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC219654, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219654 BINDING SITE1 and LOC219654 BINDING SITE2, designated SEQ ID:43875 and SEQ ID:43877 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83528] Another function of VGAM2463 is therefore inhibition of LOC219654 (Accession XM_166095). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219654. LOC219688 (Accession XM_167568) is another VGAM2463 host target gene. LOC219688 BINDING SITE1 and LOC219688 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC219688, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219688 BINDING SITE1 and LOC219688 BINDING SITE2, designated SEQ ID:44699 and SEQ ID:43984 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83529] Another function of VGAM2463 is therefore inhibition of LOC219688 (Accession XM_167568). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219688. LOC221042 (Accession XM_167669) is another VGAM2463 host target gene. LOC221042 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221042, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221042 BINDING SITE, designated SEQ ID:44756, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83530] Another function of VGAM2463 is therefore inhibition of LOC221042 (Accession XM_167669). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC221042. LOC221474 (Accession XM_166464) is another VGAM2463 host target gene. LOC221474 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221474, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221474 BINDING SITE, designated SEQ ID:44380, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83531] Another function of VGAM2463 is therefore inhibition of LOC221474 (Accession XM_166464). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221474. LOC221683 (Accession XM_168089) is another VGAM2463 host target gene. LOC221683 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221683, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221683 BINDING SITE, designated SEQ ID:45004, to

the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83532] Another function of VGAM2463 is therefore inhibition of LOC221683 (Accession XM_168089). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221683. LOC221922 (Accession XM_166555) is another VGAM2463 host target gene. LOC221922 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221922, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221922 BINDING SITE, designated SEQ ID:44534, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83533] Another function of VGAM2463 is therefore inhibition of LOC221922 (Accession XM_166555). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221922. LOC253216 (Accession XM_170765) is another VGAM2463 host target gene. LOC253216 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC253216, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253216 BINDING SITE, designated SEQ ID:45520, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83534] Another function of VGAM2463 is therefore inhibition of LOC253216 (Accession XM_170765). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253216. LOC253609 (Accession XM_172986) is another VGAM2463 host target gene. LOC253609 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253609, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253609 BINDING SITE, designated SEQ ID:46259, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83535] Another function of VGAM2463 is therefore inhibition of LOC253609 (Accession XM_172986). Accordingly, utilities

of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253609. LOC253715 (Accession XM_173053) is another VGAM2463 host target gene. LOC253715 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253715, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253715 BINDING SITE, designated SEQ ID:46311, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83536] Another function of VGAM2463 is therefore inhibition of LOC253715 (Accession XM_173053). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253715. LOC253805 (Accession XM_172854) is another VGAM2463 host target gene. LOC253805 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253805, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC253805 BINDING SITE, designated SEQ ID:46136, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83537] Another function of VGAM2463 is therefore inhibition of LOC253805 (Accession XM_172854). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253805. LOC254057 (Accession XM_173085) is another VGAM2463 host target gene. LOC254057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC254057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254057 BINDING SITE, designated SEQ ID:46348, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83538] Another function of VGAM2463 is therefore inhibition of LOC254057 (Accession XM_173085). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254057. LOC254532 (Accession XM_172961) is another VGAM2463 host target gene. LOC254532 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254532, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254532 BINDING SITE, designated SEQ ID:46210, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83539] Another function of VGAM2463 is therefore inhibition of LOC254532 (Accession XM_172961). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254532. LOC255040 (Accession XM_172837) is another VGAM2463 host target gene. LOC255040 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255040 BINDING SITE, designated SEQ ID:46109, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83540] Another function of VGAM2463 is therefore inhibition of

LOC255040 (Accession XM_172837). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255040. LOC255041 (Accession XM_172838) is another VGAM2463 host target gene. LOC255041 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC255041, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255041 BINDING SITE, designated SEQ ID:46112, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83541] Another function of VGAM2463 is therefore inhibition of LOC255041 (Accession XM_172838). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255041. LOC256267 (Accession XM_173007) is another VGAM2463 host target gene. LOC256267 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256267, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC256267 BINDING SITE, designated SEQ ID:46278, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83542] Another function of VGAM2463 is therefore inhibition of LOC256267 (Accession XM_173007). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256267. LOC256846 (Accession XM_170921) is another VGAM2463 host target gene. LOC256846 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256846, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256846 BINDING SITE, designated SEQ ID:45697, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83543] Another function of VGAM2463 is therefore inhibition of LOC256846 (Accession XM_170921). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256846. LOC257106 (Accession XM_170910) is an-

other VGAM2463 host target gene. LOC257106 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257106, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257106 BINDING SITE, designated SEQ ID:45677, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83544] Another function of VGAM2463 is therefore inhibition of LOC257106 (Accession XM_170910). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257106. LOC51236 (Accession NM_016458) is another VGAM2463 host target gene. LOC51236 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51236, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51236 BINDING SITE, designated SEQ ID:18572, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83545] Another function of VGAM2463 is therefore inhibition of LOC51236 (Accession NM_016458). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51236. LOC51337 (Accession NM_016647) is another VGAM2463 host target gene. LOC51337 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51337, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51337 BINDING SITE, designated SEQ ID:18763, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83546] Another function of VGAM2463 is therefore inhibition of LOC51337 (Accession NM_016647). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51337. LOC57105 (Accession NM_020377) is another VGAM2463 host target gene. LOC57105 BINDING SITE1 and LOC57105 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC57105, corresponding to HOST TARGET binding sites

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57105 BINDING SITE1 and LOC57105 BINDING SITE2, designated SEQ ID:21640 and SEQ ID:21642 respectively, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83547] Another function of VGAM2463 is therefore inhibition of LOC57105 (Accession NM_020377). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57105. LOC84548 (Accession XM_048904) is another VGAM2463 host target gene. LOC84548 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC84548, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC84548 BINDING SITE, designated SEQ ID:35299, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83548] Another function of VGAM2463 is therefore inhibition of LOC84548 (Accession XM_048904). Accordingly, utilities

of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC84548. LOC90072 (Accession XM_028702) is another VGAM2463 host target gene. LOC90072 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90072, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90072 BINDING SITE, designated SEQ ID:30729, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83549] Another function of VGAM2463 is therefore inhibition of LOC90072 (Accession XM_028702). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90072. LOC90288 (Accession XM_030669) is another VGAM2463 host target gene. LOC90288 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC90288 BINDING SITE, designated SEQ ID:31118, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83550] Another function of VGAM2463 is therefore inhibition of LOC90288 (Accession XM_030669). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90288. LOC90550 (Accession XM_054582) is another VGAM2463 host target gene. LOC90550 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90550, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90550 BINDING SITE, designated SEQ ID:36178, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83551] Another function of VGAM2463 is therefore inhibition of LOC90550 (Accession XM_054582). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90550. LOC90736 (Accession XM_033811) is another VGAM2463 host target gene. LOC90736 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90736, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90736 BINDING SITE, designated SEQ ID:31957, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83552] Another function of VGAM2463 is therefore inhibition of LOC90736 (Accession XM_033811). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90736. LOC90917 (Accession XM_034861) is another VGAM2463 host target gene. LOC90917 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90917, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90917 BINDING SITE, designated SEQ ID:32166, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83553] Another function of VGAM2463 is therefore inhibition of

LOC90917 (Accession XM_034861). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90917. LOC91397 (Accession XM_038219) is another VGAM2463 host target gene. LOC91397 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91397, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91397 BINDING SITE, designated SEQ ID:32780, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83554] Another function of VGAM2463 is therefore inhibition of LOC91397 (Accession XM_038219). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91397. LOC91960 (Accession XM_041872) is another VGAM2463 host target gene. LOC91960 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91960, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC91960 BINDING SITE, designated SEQ ID:33613, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83555] Another function of VGAM2463 is therefore inhibition of LOC91960 (Accession XM_041872). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91960. LOC92230 (Accession XM_043733) is another VGAM2463 host target gene. LOC92230 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92230, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92230 BINDING SITE, designated SEQ ID:34008, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83556] Another function of VGAM2463 is therefore inhibition of LOC92230 (Accession XM_043733). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92230. LOC92405 (Accession XM_044914) is another

VGAM2463 host target gene. LOC92405 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92405, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92405 BINDING SITE, designated SEQ ID:34304, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83557] Another function of VGAM2463 is therefore inhibition of LOC92405 (Accession XM_044914). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92405. LOC92466 (Accession XM_045251) is another VGAM2463 host target gene. LOC92466 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92466, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92466 BINDING SITE, designated SEQ ID:34397, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83558] Another function of VGAM2463 is therefore inhibition of LOC92466 (Accession XM_045251). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92466. LOC92710 (Accession XM_046811) is another VGAM2463 host target gene. LOC92710 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92710, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92710 BINDING SITE, designated SEQ ID:34835, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83559] Another function of VGAM2463 is therefore inhibition of LOC92710 (Accession XM_046811). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92710. LOC95702 (Accession XM_031446) is another VGAM2463 host target gene. LOC95702 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC95702, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC95702 BINDING SITE, designated SEQ ID:31383, to the nucleotide sequence of VGAM2463 RNA, herein designated VGAM RNA, also designated SEQ ID:5174.

[83560] Another function of VGAM2463 is therefore inhibition of LOC95702 (Accession XM_031446). Accordingly, utilities of VGAM2463 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC95702. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2464 (VGAM2464) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83561] VGAM2464 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2464 was detected is described hereinabove with reference to Figs. 1-8.

[83562] VGAM2464 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2464 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[83563] VGAM2464 gene encodes a VGAM2464 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2464 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2464 precursor RNA is designated SEQ ID:2450, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2450 is located at position 225307 relative to the genome of Mouse Cytomegalovirus 1.

[83564] VGAM2464 precursor RNA folds onto itself, forming VGAM2464 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83565] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2464 folded precursor RNA into VGAM2464

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2464 RNA is designated SEQ ID:5175, and is provided hereinbelow with reference to the sequence listing part.

[83566] VGAM2464 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2464 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2464 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83567] VGAM2464 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2464 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2464 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2464 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2464 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83568] The complementary binding of VGAM2464 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2464 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2464 host target RNA into VGAM2464 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[83569] It is appreciated that VGAM2464 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2464 host target genes. The mRNA of each one of this plurality of VGAM2464 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2464 RNA, herein designated VGAM RNA, and which when bound by VGAM2464 RNA causes inhibition of translation of respective one or more VGAM2464 host target proteins.

[83570] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2464 gene, herein designated VGAM GENE, on one or more VGAM2464 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83571] It is yet further appreciated that a function of VGAM2464 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2464 correlate with, and may be deduced from, the identity of the host target genes which VGAM2464 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83572] Nucleotide sequences of the VGAM2464 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2464 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2464 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2464 are further described hereinbelow with reference to Table 1.

[83573] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2464 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2464 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83574] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2464 gene, herein designated VGAM is inhibition of expression of VGAM2464 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2464 correlate with, and may be deduced from, the identity of the target genes which VGAM2464 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83575] B-cell CLL/lymphoma 7A (BCL7A, Accession NM_020993) is a VGAM2464 host target gene. BCL7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCL7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCL7A BINDING SITE, designated SEQ ID:21986, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, also designated SEQ ID:5175.

[83576] A function of VGAM2464 is therefore inhibition of B-cell CLL/lymphoma 7A (BCL7A, Accession NM_020993). Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCL7A. Hect Domain and RLD 2 (HERC2,

Accession NM_004667) is another VGAM2464 host target gene. HERC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HERC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HERC2 BINDING SITE, designated SEQ ID:11042, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, also designated SEQ ID:5175.

[83577] Another function of VGAM2464 is therefore inhibition of Hect Domain and RLD 2 (HERC2, Accession NM_004667), a gene which may be a guanine nucleotide exchange factor involved in intracellular protein transport. Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HERC2. The function of HERC2 has been established by previous studies. Prader-Willi syndrome (PWS; 176270) and Angelman syndrome (AS; 105830) result from deletions and loss of function of oppositely imprinted genes located within the proximal 2 Mb of the 15q11-q13 region. Low-copy repeat elements have been identified in the vicinity of the 3 deletion breakpoint hotspots using

molecular and cytologic methods. Using positional cloning from low-copy repeats flanking 15q11-q13, genomic sequence analysis, EST database searching, PCR, and long-range RT-PCR, Ji et al. (1999) obtained a cDNA encoding HERC2, which is identical to a partial cDNA, KIAA0393, identified by Nagase et al. (1997). Sequence analysis predicted that the 4,834-amino acid protein, which is 95% identical and 99% similar to the mouse protein, contains 3 RCC1-like domains (RLDs); a putative ZZ-type zinc finger motif with 6 conserved cysteines and 2 outlying histidine residues; a C-terminal HECT or E3 ubiquitin ligase (see OMIM Ref. No. UBE3A; 601623) domain; and several potential phosphorylation sites. The overall structure is similar to that of HERC1, although HERC1 has only 2 RLDs and no zinc finger motif. The C-terminal region of HERC2 resembles that of HERC3 (OMIM Ref. No. 605200). Northern blot analysis revealed ubiquitous expression of a 15.5-kb HERC2 transcript, with high levels in fetal tissues and adult skeletal muscle, heart, ovary, testis, and brain. Animal model experiments lend further support to the function of HERC2. The mouse Herc2 gene is located in the jdf2 (juvenile development and fertility-2) interval of chromosome 7C. Ji et al. (1999) identified splice junction

mutations in the Herc2 gene in chemically-induced jdf2 mutant alleles. The mutations led to exon skipping and premature termination, resulting in neuromuscular secretory vesicle defects, sperm acrosome defects, and juvenile lethality in jdf2 mice.

[83578] It is appreciated that the abovementioned animal model for HERC2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[83579] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83580] Ji, Y.; Walkowicz, M. J.; Buiting, K.; Johnson, D. K.; Tarvin, R. E.; Rinchik, E. M.; Horsthemke, B.; Stubbs, L.; Nicholls, R. D. : The ancestral gene for transcribed, low-copy repeats in the Prader-Willi/Angelman region encodes a large protein implicated in protein trafficking, which is deficient in mice with neuromuscular and spermiogenic abnormalities. Hum. Molec. Genet. 8: 533-542, 1999. ; and

[83581] Nagase, T.; Ishikawa, K.; Nakajima, D.; Ohira, M.; Seki, N.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. : Prediction of the coding sequences of unidentified human genes.

[83582] Further studies establishing the function and utilities of HERC2 are found in John Hopkins OMIM database record ID 605837, and in sited publications numbered 6435 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Integral Membrane Protein 2B (ITM2B, Accession NM_021999) is another VGAM2464 host target gene. ITM2B BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ITM2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITM2B BINDING SITE, designated SEQ ID:22538, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, also designated SEQ ID:5175.

[83583] Another function of VGAM2464 is therefore inhibition of Integral Membrane Protein 2B (ITM2B, Accession NM_021999), a gene which is a member of the type II integral membrane protein family. Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITM2B. The function of ITM2B and its association with various diseases and clinical conditions, has been established by

previous studies, as described hereinabove with reference to VGAM458.DKFZp586I021 (Accession NM_032271) is another VGAM2464 host target gene. DKFZp586I021 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DK-FZp586I021, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp586I021 BINDING SITE, designated SEQ ID:26017, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, also designated SEQ ID:5175.

[83584] Another function of VGAM2464 is therefore inhibition of DKFZp586I021 (Accession NM_032271). Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp586I021. KIAA1649 (Accession NM_032311) is another VGAM2464 host target gene. KIAA1649 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1649, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA1649 BINDING SITE, designated SEQ ID:26108, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, also designated SEQ ID:5175.

[83585] Another function of VGAM2464 is therefore inhibition of KIAA1649 (Accession NM_032311). Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1649. KIAA1856 (Accession XM_166549) is another VGAM2464 host target gene. KIAA1856 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1856, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1856 BINDING SITE, designated SEQ ID:44525, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, also designated SEQ ID:5175.

[83586] Another function of VGAM2464 is therefore inhibition of KIAA1856 (Accession XM_166549). Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1856. MCF.2 Cell Line Derived Transforming Sequence-like (MCF2L, Accession XM_027516) is another

VGAM2464 host target gene. MCF2L BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MCF2L, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MCF2L BINDING SITE, designated SEQ ID:30508, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, also designated SEQ ID:5175.

[83587] Another function of VGAM2464 is therefore inhibition of MCF.2 Cell Line Derived Transforming Sequence-like (MCF2L, Accession XM_027516). Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCF2L. MGC20235 (Accession NM_145041) is another VGAM2464 host target gene. MGC20235 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC20235, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC20235 BINDING SITE, designated SEQ ID:29668, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA,

also designated SEQ ID:5175.

[83588] Another function of VGAM2464 is therefore inhibition of MGC20235 (Accession NM_145041). Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC20235. WIT-1 (Accession NM_015855) is another VGAM2464 host target gene. WIT-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WIT-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WIT-1 BINDING SITE, designated SEQ ID:17990, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, also designated SEQ ID:5175.

[83589] Another function of VGAM2464 is therefore inhibition of WIT-1 (Accession NM_015855). Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WIT-1. LOC143888 (Accession XM_084669) is another VGAM2464 host target gene. LOC143888 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143888, corresponding

to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143888 BINDING SITE, designated SEQ ID:37670, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, also designated SEQ ID:5175.

[83590] Another function of VGAM2464 is therefore inhibition of LOC143888 (Accession XM_084669). Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143888. LOC147463 (Accession XM_085799) is another VGAM2464 host target gene. LOC147463 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147463, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147463 BINDING SITE, designated SEQ ID:38340, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, also designated SEQ ID:5175.

[83591] Another function of VGAM2464 is therefore inhibition of LOC147463 (Accession XM_085799). Accordingly, utilities of VGAM2464 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC147463. LOC91695 (Accession XM_040084) is another VGAM2464 host target gene. LOC91695 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91695, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91695 BINDING SITE, designated SEQ ID:33252, to the nucleotide sequence of VGAM2464 RNA, herein designated VGAM RNA, also designated SEQ ID:5175.

[83592] Another function of VGAM2464 is therefore inhibition of LOC91695 (Accession XM_040084). Accordingly, utilities of VGAM2464 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91695. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2465 (VGAM2465) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83593] VGAM2465 is a novel bioinformatically detected regula-

tory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2465 was detected is described hereinabove with reference to Figs. 1-8.

[83594] VGAM2465 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2465 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83595] VGAM2465 gene encodes a VGAM2465 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2465 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2465 precursor RNA is designated SEQ ID:2451, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2451 is located at position 161125 relative to the genome of Mouse Cytomegalovirus 1.

[83596] VGAM2465 precursor RNA folds onto itself, forming VGAM2465 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by

miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83597] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2465 folded precursor RNA into VGAM2465 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2465 RNA is designated SEQ ID:5176, and is provided hereinbelow with reference to the sequence listing part.

[83598] VGAM2465 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2465 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2465 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83599] VGAM2465 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2465 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2465 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2465 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2465 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83600] The complementary binding of VGAM2465 RNA, herein

designated VGAM RNA, to host target binding sites on VGAM2465 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2465 host target RNA into VGAM2465 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83601] It is appreciated that VGAM2465 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2465 host target genes. The mRNA of each one of this plurality of VGAM2465 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2465 RNA, herein designated VGAM RNA, and which when bound by VGAM2465 RNA causes inhibition of translation of respective one or more VGAM2465 host target proteins.

[83602] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2465 gene, herein designated VGAM GENE, on one or more VGAM2465 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other

known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83603] It is yet further appreciated that a function of VGAM2465 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2465 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2465 correlate with, and may be deduced from, the identity of the host target genes which VGAM2465 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83604] Nucleotide sequences of the VGAM2465 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the

`diced` VGAM2465 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2465 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2465 are further described hereinbelow with reference to Table 1.

[83605] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2465 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2465 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83606] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2465 gene, herein designated VGAM is inhibition of expression of VGAM2465 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2465 correlate with, and may be deduced from, the identity of the target genes which VGAM2465 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83607] Proteoglycan 1, Secretory Granule (PRG1, Accession NM_002727) is a VGAM2465 host target gene. PRG1 BINDING SITE is HOST TARGET binding site found in the

3` untranslated region of mRNA encoded by PRG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRG1 BINDING SITE, designated SEQ ID:8590, to the nucleotide sequence of VGAM2465 RNA, herein designated VGAM RNA, also designated SEQ ID:5176.

[83608] A function of VGAM2465 is therefore inhibition of Proteoglycan 1, Secretory Granule (PRG1, Accession NM_002727), a gene which protects cells from apoptosis induced by FAS or TNFA. Accordingly, utilities of VGAM2465 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRG1. The function of PRG1 has been established by previous studies. Transcription factors of the nuclear factor-kappa-B/rel (NF-kappa-B) family (OMIM Ref. No. 164011) may be important in cell survival by regulating unidentified, anti-apoptotic genes. Charles et al. (1993) cloned gly96, a mouse immediate-early gene inducible by serum growth factors. Schafer et al. (1996) cloned the rat homolog, PRG1, which was induced in response to the pituitary adenylate cyclase-activating polypeptide (PACAP; 102980). Kondratyev et al. (1996) cloned the human im-

mediate-early gene IEX1. The cDNA encodes 156-amino acid polypeptide containing a single predicted transmembrane domain. On Northern blots, they observed a 1.2-kb mRNA whose expression could be induced by ionizing radiation, 12-O-tetradecanoylphorbol-13-acetate (TPA), okadaic acid, and TNF-alpha (OMIM Ref. No. 191160); these agents are all activators of the protein kinase C (PKC; OMIM Ref. No. 176960) pathway. Pietzsch et al. (1997) cloned the same human gene, which they termed DIF2. The expression of the DIF2 mRNA is downregulated during differentiation of macrophages and upregulated by lipopolysaccharide (LPS) stimulation of monocytes. Northern blot analysis revealed that DIF2 is expressed most abundantly in monocytes, lymphocytes, and keratinocytes, and at a lesser level in several other human tissues and cell lines. Wu et al. (1998) described a gene that protects cells from apoptosis induced by FAS (OMIM Ref. No. 134637) or TNFA. The gene appeared to be the same as the immediate-early response gene IEX1 reported by Kondratyev et al. (1996), Charles et al. (1993), and Schafer et al. (1996), except that it had an in-frame insertion of 111 nucleotides at position 211 of the coding region of IEX1, and could encode a longer polypeptide with a 37-amino

acid insertion relative to IEX1. The longer IEX1 (referred to as IEX1L; the original IEX1 was referred to as IEX1S) was found to be generated from IEX1 in the absence of RNA splicing as it contained the entire intron sequence of IEX1. The transcription of IEX1L induced by TNF was decreased in cells with defective NF-kappa-B activation, rendering them sensitive to TNF-induced apoptosis, which was abolished by transfection with IEX1L. In support, overexpression of antisense IEX1L partially blocked TNF-induced expression of IEX1L and sensitized normal cells to killing. This study demonstrated a key role of IEX1L in cellular resistance to TNF-induced apoptosis. Pietzsch et al. (1998) cloned the genomic DNA of the DIF2 gene. They found that the gene consists of 2 exons and a single small intron. The 5-prime flanking region of the gene contains binding sites for transcription factors including NF-kappa-B, CEBP (OMIM Ref. No. 116897), and SP1 (OMIM Ref. No. 189906). Pietzsch et al. (1998) used fluorescence in situ hybridization to map the IER3 gene to human chromosome 6p21.3.

[83609] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83610] Pietzsch, A.; Buchler, C.; Schmitz, G. : Genomic organization, promoter cloning, and chromosomal localization of the Dif-2 gene. Biochem. Biophys. Res. Commun. 245: 651-657, 1998. ; and

[83611] Wu, M. X.; Ao, Z.; Prasad, K. V. S.; Wu, R.; Schlossman, S. F. : IEX-1L, an apoptosis inhibitor involved in NF-kappa-B-mediated cell survival. Science 281: 998-1001, 1998.

[83612] Further studies establishing the function and utilities of PRG1 are found in John Hopkins OMIM database record ID 602996, and in sited publications numbered 5412-5417 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.BSPECV (Accession NM_016642) is another VGAM2465 host target gene. BSPECV BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by BSPECV, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BSPECV BINDING SITE, designated SEQ ID:18747, to the nucleotide sequence of VGAM2465 RNA, herein designated VGAM RNA, also designated SEQ ID:5176.

[83613] Another function of VGAM2465 is therefore inhibition of BSPECV (Accession NM_016642). Accordingly, utilities of VGAM2465 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BSPECV. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2466 (VGAM2466) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83614] VGAM2466 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2466 was detected is described hereinabove with reference to Figs. 1-8.

[83615] VGAM2466 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2466 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83616] VGAM2466 gene encodes a VGAM2466 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes,

VGAM2466 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2466 precursor RNA is designated SEQ ID:2452, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2452 is located at position 94468 relative to the genome of Mouse Cytomegalovirus 1.

[83617] VGAM2466 precursor RNA folds onto itself, forming VGAM2466 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83618] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2466 folded precursor RNA into VGAM2466 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other

necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2466 RNA is designated SEQ ID:5177, and is provided hereinbelow with reference to the sequence listing part.

[83619] VGAM2466 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2466 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2466 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83620] VGAM2466 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2466 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2466 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the

number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2466 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2466 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83621] The complementary binding of VGAM2466 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2466 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2466 host target RNA into VGAM2466 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83622] It is appreciated that VGAM2466 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2466 host target genes. The mRNA of each one of this plurality of VGAM2466 host target genes

comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2466 RNA, herein designated VGAM RNA, and which when bound by VGAM2466 RNA causes inhibition of translation of respective one or more VGAM2466 host target proteins.

[83623] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2466 gene, herein designated VGAM GENE, on one or more VGAM2466 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83624] It is yet further appreciated that a function of VGAM2466 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2466 correlate with, and may be deduced from, the identity of the host target genes which VGAM2466 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83625] Nucleotide sequences of the VGAM2466 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2466 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2466 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2466 are further described hereinbelow with reference to Table 1.

[83626] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2466 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2466 RNA, herein designated VGAM RNA, are described hereinbelow

with reference to Table 2.

[83627] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2466 gene, herein designated VGAM is inhibition of expression of VGAM2466 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2466 correlate with, and may be deduced from, the identity of the target genes which VGAM2466 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83628] Rho GTPase Activating Protein 6 (ARHGAP6, Accession NM_001174) is a VGAM2466 host target gene. ARHGAP6 BINDING SITE1 and ARHGAP6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ARHGAP6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGAP6 BINDING SITE1 and ARHGAP6 BINDING SITE2, designated SEQ ID:6842 and SEQ ID:15084 respectively, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83629] A function of VGAM2466 is therefore inhibition of Rho GTPase Activating Protein 6 (ARHGAP6, Accession

NM_001174), a gene which activates the rho-type GTPases by converting them to an inactive GTP-bound state. Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP6. The function of ARHGAP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Dimethylarginine Dimethylaminohydrolase 2 (DDAH2, Accession NM_013974) is another VGAM2466 host target gene. DDAH2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DDAH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DDAH2 BINDING SITE, designated SEQ ID:15142, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83630] Another function of VGAM2466 is therefore inhibition of Dimethylarginine Dimethylaminohydrolase 2 (DDAH2, Accession NM_013974), a gene which regulates cellular methylarginine concentrations. Accordingly, utilities of

VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DDAH2. The function of DDAH2 has been established by previous studies. Dimethylarginine dimethylaminohydrolase (DDAH; EC 3.5.3.18) regulates cellular methylarginine concentrations, which in turn inhibit nitric oxide synthase (see OMIM Ref. No. 163728) activity. Leiper et al. (1999) isolated a cDNA encoding DDAHI (OMIM Ref. No. 604743) and, by screening a database of translated open reading frames with the deduced DDAHI peptide sequence, identified DDAHII. Both DDAHI and DDAHII cDNAs encode 285-amino acid proteins. The DDAHII amino acid sequence shares 98% identity with that of its mouse homolog and 62% identity with the sequence of DDAHI. Northern blot analysis detected a 2.0-kb DDAHII transcript expressed at highest levels in heart, kidney, and placenta. Leiper et al. (1999) expressed a histidine-tagged DDAHII clone in E. coli and assayed the cell lysate for DDAH activity. Recombinant DDAHII metabolized ADMA and L-NMMA, but not SDMA or L-arginine, demonstrating that DDAHII is a functional homolog of DDAHI. By RNA dot blot analysis, Tran et al. (2000) determined that DDAH2 expression predominates in more highly vascularized tis-

sues and in immune tissues, while DDAH1 expression predominates in tissues that also express the neuronal isoform of NOS (OMIM Ref. No. 163731). Genomic sequence analysis indicated that DDAH2 contains 8 exons with 3 transcription start sites that generate alternatively spliced transcripts.

[83631] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83632] Leiper, J. M,; Santa Maria, J.; Chubb, A.; MacAllister, R. J.; Charles, I. G.; Whitley, G. S.; Vallance, P. : Identification of two human dimethylarginine dimethylaminohydrolases with distinct tissue distributions and homology with microbial arginine deiminases. Biochem. J. 343: 209-214, 1999. ; and

[83633] Tran, C. T. L.; Fox, M. F.; Vallance, P.; Leiper, J. M. : Chromosomal localization, gene structure, and expression pattern of DDAH1: comparison with DDAH2 and implications for evolutio.

[83634] Further studies establishing the function and utilities of DDAH2 are found in John Hopkins OMIM database record ID 604744, and in sited publications numbered 6747-6748 listed in the bibliography section hereinbelow,

which are also hereby incorporated by reference.Diacylglycerol Kinase, Gamma 90kDa (DGKG, Accession NM_001346) is another VGAM2466 host target gene. DGKG BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DGKG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGKG BINDING SITE, designated SEQ ID:7026, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83635] Another function of VGAM2466 is therefore inhibition of Diacylglycerol Kinase, Gamma 90kDa (DGKG, Accession NM_001346), a gene which may convert diacylglycerol to phosphatidic acid. Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGKG. The function of DGKG and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM451.Homeo Box B3 (HOXB3, Accession NM_002146) is another VGAM2466 host target gene. HOXB3 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by HOXB3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOXB3 BINDING SITE, designated SEQ ID:7921, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83636] Another function of VGAM2466 is therefore inhibition of Homeo Box B3 (HOXB3, Accession NM_002146). Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOXB3. Oxytocin Receptor (OXTR, Accession NM_000916) is another VGAM2466 host target gene. OXTR BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by OXTR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OXTR BINDING SITE, designated SEQ ID:6619, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83637] Another function of VGAM2466 is therefore inhibition of Oxytocin Receptor (OXTR, Accession NM_000916), a gene

which induces inward ion currents. Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OXTR. The function of OXTR and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM636.ENDO180 (Accession NM_006039) is another VGAM2466 host target gene. ENDO180 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ENDO180, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ENDO180 BINDING SITE, designated SEQ ID:12675, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83638] Another function of VGAM2466 is therefore inhibition of ENDO180 (Accession NM_006039). Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ENDO180. FLJ14490 (Accession NM_032793) is another VGAM2466 host target gene. FLJ14490 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ14490, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14490 BINDING SITE, designated SEQ ID:26545, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83639] Another function of VGAM2466 is therefore inhibition of FLJ14490 (Accession NM_032793). Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14490. FLJ20435 (Accession NM_017821) is another VGAM2466 host target gene. FLJ20435 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20435, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20435 BINDING SITE, designated SEQ ID:19467, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83640] Another function of VGAM2466 is therefore inhibition of FLJ20435 (Accession NM_017821). Accordingly, utilities of

VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20435. FLJ22202 (Accession NM_024883) is another VGAM2466 host target gene. FLJ22202 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22202, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22202 BINDING SITE, designated SEQ ID:24336, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83641] Another function of VGAM2466 is therefore inhibition of FLJ22202 (Accession NM_024883). Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22202. KIAA0555 (Accession XM_011347) is another VGAM2466 host target gene. KIAA0555 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0555, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

KIAA0555 BINDING SITE, designated SEQ ID:30187, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83642] Another function of VGAM2466 is therefore inhibition of KIAA0555 (Accession XM_011347). Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0555. MGC4766 (Accession NM_031451) is another VGAM2466 host target gene. MGC4766 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC4766, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4766 BINDING SITE, designated SEQ ID:25465, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83643] Another function of VGAM2466 is therefore inhibition of MGC4766 (Accession NM_031451). Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4766. Nucleoredoxin (NXN, Accession NM_022463) is another VGAM2466 host target gene. NXN BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NXN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NXN BINDING SITE, designated SEQ ID:22805, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83644] Another function of VGAM2466 is therefore inhibition of Nucleoredoxin (NXN, Accession NM_022463). Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXN. LOC93349 (Accession NM_138402) is another VGAM2466 host target gene. LOC93349 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93349, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93349 BINDING SITE, designated SEQ ID:28768, to the nucleotide sequence of VGAM2466 RNA, herein designated VGAM RNA, also designated SEQ ID:5177.

[83645] Another function of VGAM2466 is therefore inhibition of

LOC93349 (Accession NM_138402). Accordingly, utilities of VGAM2466 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93349. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2467 (VGAM2467) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83646] VGAM2467 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2467 was detected is described hereinabove with reference to Figs. 1-8.

[83647] VGAM2467 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2467 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83648] VGAM2467 gene encodes a VGAM2467 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2467 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2467 precursor RNA is designated SEQ ID:2453, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2453 is located at position 175100 relative to the genome of Mouse Cytomegalovirus 1.

[83649] VGAM2467 precursor RNA folds onto itself, forming VGAM2467 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83650] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2467 folded precursor RNA into VGAM2467 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide se-

quence of VGAM2467 RNA is designated SEQ ID:5178, and is provided hereinbelow with reference to the sequence listing part.

[83651] VGAM2467 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2467 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2467 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83652] VGAM2467 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2467 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2467 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2467 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2467 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83653] The complementary binding of VGAM2467 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2467 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2467 host target RNA into VGAM2467 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83654] It is appreciated that VGAM2467 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2467 host target genes. The mRNA of each one of this plurality of VGAM2467 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2467 RNA, herein designated VGAM RNA, and which when bound by VGAM2467 RNA causes inhibition of translation of respective one or more VGAM2467 host target proteins.

[83655] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2467 gene, herein designated VGAM GENE, on one or more VGAM2467 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83656] It is yet further appreciated that a function of VGAM2467

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2467 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2467 correlate with, and may be deduced from, the identity of the host target genes which VGAM2467 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83657] Nucleotide sequences of the VGAM2467 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2467 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2467 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2467 are further described hereinbelow with reference to Table 1.

[83658] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2467 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2467 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83659] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2467 gene, herein designated VGAM is inhibition of expression of VGAM2467 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2467 correlate with, and may be deduced from, the identity of the target genes which VGAM2467 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83660] LOC154043 (Accession XM_087831) is a VGAM2467 host target gene. LOC154043 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC154043, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154043 BINDING SITE, designated SEQ ID:39458, to the nucleotide sequence of VGAM2467 RNA, herein designated VGAM RNA, also designated SEQ ID:5178.

[83661] A function of VGAM2467 is therefore inhibition of LOC154043 (Accession XM_087831). Accordingly, utilities of VGAM2467 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154043. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2468 (VGAM2468) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83662] VGAM2468 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2468 was detected is described hereinabove with reference to Figs. 1-8.

[83663] VGAM2468 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2468 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83664] VGAM2468 gene encodes a VGAM2468 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2468 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2468 precursor RNA is designated SEQ ID:2454, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2454 is located at position 64210 relative to the genome of Mouse Cytomegalovirus 1.

[83665] VGAM2468 precursor RNA folds onto itself, forming VGAM2468 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83666] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2468 folded precursor RNA into VGAM2468 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2468 RNA is designated SEQ ID:5179, and is provided hereinbelow with reference to the sequence listing part.

[83667] VGAM2468 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2468 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2468 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83668] VGAM2468 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2468 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2468 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2468 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2468 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83669] The complementary binding of VGAM2468 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2468 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2468 host target RNA into VGAM2468 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83670] It is appreciated that VGAM2468 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2468 host target genes. The mRNA of each one of this plurality of VGAM2468 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2468 RNA, herein designated VGAM RNA, and which when bound by VGAM2468 RNA causes inhibition of translation of respective one or more

VGAM2468 host target proteins.

[83671] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2468 gene, herein designated VGAM GENE, on one or more VGAM2468 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83672] It is yet further appreciated that a function of VGAM2468 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1.

Specific functions, and accordingly utilities, of VGAM2468 correlate with, and may be deduced from, the identity of the host target genes which VGAM2468 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83673] Nucleotide sequences of the VGAM2468 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2468 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2468 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2468 are further described hereinbelow with reference to Table 1.

[83674] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2468 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2468 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83675] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2468 gene, herein designated VGAM is inhibition of expression of VGAM2468 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2468 correlate with, and may be deduced from, the identity of the target genes which VGAM2468 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83676] Glycyl-tRNA Synthetase (GARS, Accession NM_002047) is a VGAM2468 host target gene. GARS BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GARS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GARS BINDING SITE, designated SEQ ID:7795, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83677] A function of VGAM2468 is therefore inhibition of Glycyl-tRNA Synthetase (GARS, Accession NM_002047), a gene which functions in protein biosynthesis. Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GARS. The function of GARS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM113.MAP/microtubule Affinity-regu-

lating Kinase 3 (MARK3, Accession NM_002376) is another VGAM2468 host target gene. MARK3 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MARK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MARK3 BINDING SITE, designated SEQ ID:8188, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83678] Another function of VGAM2468 is therefore inhibition of MAP/microtubule Affinity-regulating Kinase 3 (MARK3, Accession NM_002376), a gene which may be involved in cell cycle regulation. Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MARK3. The function of MARK3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM964.Ret Finger Protein 2 (RFP2, Accession NM_052811) is another VGAM2468 host target gene. RFP2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by RFP2, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RFP2 BINDING SITE, designated SEQ ID:27399, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83679] Another function of VGAM2468 is therefore inhibition of Ret Finger Protein 2 (RFP2, Accession NM_052811), a gene which may act as a tumor suppressor. Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RFP2. The function of RFP2 has been established by previous studies. B-cell chronic lymphocytic leukemia is often associated with the loss of a region on chromosome 13q14 between the retinoblastoma gene (RB1; 180200) and locus D13S25 (Liu et al., 1993; Liu et al., 1995), suggesting that a tumor suppressor gene may be located in this region. By constructing a cosmid contig corresponding to the minimally deleted region and screening a pre-B lymphocyte cDNA library, Kapanadze et al. (1998) isolated several clones, one of which contained an ORF encoding a deduced 407-amino acid protein, RFP2, which they called LEU5. RFP2 contains a zinc finger domain of the RING type

and shares significant homology with the RET finger protein (RFP; 602165) and the tumor suppressor gene BRCA1 (OMIM Ref. No. 113705). Kapanadze et al. (1998) mapped the RFP2 gene close to D13S272, bordering the minimally deleted region.

[83680] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83681] Kapanadze, B.; Kashuba, V.; Baranova, A.; Rasool, O.; van Everdink, W.; Liu, Y.; Syomova, A.; Corcoran, M.; Poltaraus, A.; Brodyansky, V.; Syomova, N.; Kazakov, A.; Ibbotson, R.; van den Berg, A.; Gizatullin, R.; Fedorova, L.; Sulimova, G.; Zelenin, A.; Deaven, L.; Lehrach, H.; Grander, D.; Buys, C.; Oscier, D.; Zabarovsky, E. R.; Einhorn, S.; Yankovsky, N. : A cosmid and cDNA fine physical map of a human chromosome 13q14 region frequently lost in B-cell chronic lymphocytic leukemia and identification of a new putative tumor suppressor gene, Leu5. FEBS Lett. 426: 266-270, 1998. ; and

[83682] Liu, Y.; Hermanson, M.; Grander, D.; Merup, M.; Wu, X.; Heyman, M.; Rasool, O.; Juliusson, G.; Gahrton, G.; Detlofsson, R. : 13q deletions in lymphoid malignancies. Blood 86: 1911-1915.

[83683] Further studies establishing the function and utilities of RFP2 are found in John Hopkins OMIM database record ID 605661, and in sited publications numbered 6409-6411 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.DKFZP434H204 (Accession XM_039153) is another VGAM2468 host target gene. DKFZP434H204 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP434H204, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434H204 BINDING SITE, designated SEQ ID:33016, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83684] Another function of VGAM2468 is therefore inhibition of DKFZP434H204 (Accession XM_039153). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434H204. F-box Only Protein 26 (FBXO26, Accession NM_024907) is another VGAM2468 host target gene. FBXO26 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

FBXO26, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBXO26 BINDING SITE, designated SEQ ID:24405, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83685] Another function of VGAM2468 is therefore inhibition of F-box Only Protein 26 (FBXO26, Accession NM_024907). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBXO26. FLJ12089 (Accession NM_024552) is another VGAM2468 host target gene. FLJ12089 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12089, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12089 BINDING SITE, designated SEQ ID:23771, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83686] Another function of VGAM2468 is therefore inhibition of

FLJ12089 (Accession NM_024552). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12089. FLJ32919 (Accession NM_144588) is another VGAM2468 host target gene. FLJ32919 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ32919, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ32919 BINDING SITE, designated SEQ ID:29408, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83687] Another function of VGAM2468 is therefore inhibition of FLJ32919 (Accession NM_144588). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ32919. KIAA0963 (Accession NM_014963) is another VGAM2468 host target gene. KIAA0963 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0963, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0963 BINDING SITE, designated SEQ ID:17343, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83688] Another function of VGAM2468 is therefore inhibition of KIAA0963 (Accession NM_014963). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0963. UDP-N-acteylglucosamine Pyrophosphorylase 1 (UAP1, Accession NM_003115) is another VGAM2468 host target gene. UAP1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by UAP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of UAP1 BINDING SITE, designated SEQ ID:9087, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83689] Another function of VGAM2468 is therefore inhibition of UDP-N-acteylglucosamine Pyrophosphorylase 1 (UAP1, Accession NM_003115). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with UAP1. XPO5 (Accession XM_166042) is another VGAM2468 host target gene. XPO5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by XPO5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XPO5 BINDING SITE, designated SEQ ID:43840, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83690] Another function of VGAM2468 is therefore inhibition of XPO5 (Accession XM_166042). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XPO5. LOC128402 (Accession XM_066002) is another VGAM2468 host target gene. LOC128402 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC128402, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC128402 BINDING SITE, designated SEQ ID:37317, to

the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83691] Another function of VGAM2468 is therefore inhibition of LOC128402 (Accession XM_066002). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128402. LOC146243 (Accession XM_096956) is another VGAM2468 host target gene. LOC146243 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC146243, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146243 BINDING SITE, designated SEQ ID:40676, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83692] Another function of VGAM2468 is therefore inhibition of LOC146243 (Accession XM_096956). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146243. LOC153811 (Accession XM_087779) is another VGAM2468 host target gene. LOC153811 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC153811, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153811 BINDING SITE, designated SEQ ID:39414, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83693] Another function of VGAM2468 is therefore inhibition of LOC153811 (Accession XM_087779). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153811. LOC157226 (Accession XM_033876) is another VGAM2468 host target gene. LOC157226 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157226, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157226 BINDING SITE, designated SEQ ID:31975, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83694] Another function of VGAM2468 is therefore inhibition of LOC157226 (Accession XM_033876). Accordingly, utilities

of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157226. LOC222166 (Accession XM_168425) is another VGAM2468 host target gene. LOC222166 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222166, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222166 BINDING SITE, designated SEQ ID:45153, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83695] Another function of VGAM2468 is therefore inhibition of LOC222166 (Accession XM_168425). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222166. LOC93017 (Accession XM_048772) is another VGAM2468 host target gene. LOC93017 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93017, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC93017 BINDING SITE, designated SEQ ID:35254, to the nucleotide sequence of VGAM2468 RNA, herein designated VGAM RNA, also designated SEQ ID:5179.

[83696] Another function of VGAM2468 is therefore inhibition of LOC93017 (Accession XM_048772). Accordingly, utilities of VGAM2468 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93017. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2469 (VGAM2469) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83697] VGAM2469 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2469 was detected is described hereinabove with reference to Figs. 1-8.

[83698] VGAM2469 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2469 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83699] VGAM2469 gene encodes a VGAM2469 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2469 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2469 precursor RNA is designated SEQ ID:2455, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2455 is located at position 226054 relative to the genome of Mouse Cytomegalovirus 1.

[83700] VGAM2469 precursor RNA folds onto itself, forming VGAM2469 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83701] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2469 folded precursor RNA into VGAM2469 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2469 RNA is designated SEQ ID:5180, and is provided hereinbelow with reference to the sequence listing part.

[83702] VGAM2469 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2469 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2469 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83703] VGAM2469 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2469 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2469 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2469 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2469 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83704] The complementary binding of VGAM2469 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2469 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2469 host target RNA into VGAM2469 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83705] It is appreciated that VGAM2469 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2469 host target genes. The mRNA of each one of this plurality of VGAM2469 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2469 RNA, herein designated VGAM RNA, and which when bound by VGAM2469 RNA causes inhibition of translation of respective one or more VGAM2469 host target proteins.

[83706] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2469 gene, herein designated VGAM GENE, on one or more VGAM2469 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83707] It is yet further appreciated that a function of VGAM2469 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2469 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2469 correlate with, and may be deduced from, the identity of the host target genes which VGAM2469 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83708] Nucleotide sequences of the VGAM2469 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2469 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2469 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2469 are further described hereinbelow with reference to Table 1.

[83709] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2469 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2469 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83710] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2469 gene, herein designated VGAM is inhibition of expression of VGAM2469 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2469 correlate with, and may be deduced from, the identity of the target genes which VGAM2469 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83711] Diaphorase (NADH) (cytochrome b-5 reductase) (DIA1, Accession NM_007326) is a VGAM2469 host target gene. DIA1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DIA1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DIA1 BINDING SITE, designated SEQ ID:14245, to the nucleotide sequence of VGAM2469 RNA, herein designated VGAM RNA, also designated SEQ ID:5180.

[83712] A function of VGAM2469 is therefore inhibition of Di-

aphorase (NADH) (cytochrome b-5 reductase) (DIA1, Accession NM_007326). Accordingly, utilities of VGAM2469 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DIA1. Deleted In Lung and Esophageal Cancer 1 (DLEC1, Accession NM_007338) is another VGAM2469 host target gene. DLEC1 BINDING SITE1 and DLEC1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DLEC1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLEC1 BINDING SITE1 and DLEC1 BINDING SITE2, designated SEQ ID:14268 and SEQ ID:14262 respectively, to the nucleotide sequence of VGAM2469 RNA, herein designated VGAM RNA, also designated SEQ ID:5180.

[83713] Another function of VGAM2469 is therefore inhibition of Deleted In Lung and Esophageal Cancer 1 (DLEC1, Accession NM_007338). Accordingly, utilities of VGAM2469 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DLEC1. Neurotensin Receptor 1 (high affinity) (NTSR1, Accession NM_002531) is another VGAM2469 host target gene. NTSR1 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NTSR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NTSR1 BINDING SITE, designated SEQ ID:8365, to the nucleotide sequence of VGAM2469 RNA, herein designated VGAM RNA, also designated SEQ ID:5180.

[83714] Another function of VGAM2469 is therefore inhibition of Neurotensin Receptor 1 (high affinity) (NTSR1, Accession NM_002531), a gene which is associated with g proteins that activate a phosphatidylinositol- calcium second messenger system. Accordingly, utilities of VGAM2469 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NTSR1. The function of NTSR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM200.Golgi Autoantigen, Golgin Subfamily A, 1 (GOLGA1, Accession NM_002077) is another VGAM2469 host target gene. GOLGA1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GOLGA1, corresponding to a HOST TARGET

binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GOLGA1 BINDING SITE, designated SEQ ID:7858, to the nucleotide sequence of VGAM2469 RNA, herein designated VGAM RNA, also designated SEQ ID:5180.

[83715] Another function of VGAM2469 is therefore inhibition of Golgi Autoantigen, Golgin Subfamily A, 1 (GOLGA1, Accession NM_002077). Accordingly, utilities of VGAM2469 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLGA1. LOC149566 (Accession XM_097670) is another VGAM2469 host target gene. LOC149566 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149566, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149566 BINDING SITE, designated SEQ ID:41014, to the nucleotide sequence of VGAM2469 RNA, herein designated VGAM RNA, also designated SEQ ID:5180.

[83716] Another function of VGAM2469 is therefore inhibition of LOC149566 (Accession XM_097670). Accordingly, utilities

of VGAM2469 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149566. LOC150967 (Accession XM_087060) is another VGAM2469 host target gene. LOC150967 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150967, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150967 BINDING SITE, designated SEQ ID:39033, to the nucleotide sequence of VGAM2469 RNA, herein designated VGAM RNA, also designated SEQ ID:5180.

[83717] Another function of VGAM2469 is therefore inhibition of LOC150967 (Accession XM_087060). Accordingly, utilities of VGAM2469 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150967. LOC151124 (Accession XM_098006) is another VGAM2469 host target gene. LOC151124 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151124, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC151124 BINDING SITE, designated SEQ ID:41300, to the nucleotide sequence of VGAM2469 RNA, herein designated VGAM RNA, also designated SEQ ID:5180.

[83718] Another function of VGAM2469 is therefore inhibition of LOC151124 (Accession XM_098006). Accordingly, utilities of VGAM2469 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151124. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2470 (VGAM2470) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83719] VGAM2470 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2470 was detected is described hereinabove with reference to Figs. 1-8.

[83720] VGAM2470 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2470 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83721] VGAM2470 gene encodes a VGAM2470 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2470 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2470 precursor RNA is designated SEQ ID:2456, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2456 is located at position 195573 relative to the genome of Mouse Cytomegalovirus 1.

[83722] VGAM2470 precursor RNA folds onto itself, forming VGAM2470 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83723] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2470 folded precursor RNA into VGAM2470 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2470 RNA is designated SEQ ID:5181, and is provided hereinbelow with reference to the sequence listing part.

[83724] VGAM2470 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2470 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2470 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83725] VGAM2470 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2470 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2470 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2470 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2470 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83726] The complementary binding of VGAM2470 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2470 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2470 host target RNA into VGAM2470 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83727] It is appreciated that VGAM2470 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2470 host target genes. The mRNA of each one of this plurality of VGAM2470 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2470 RNA, herein designated VGAM RNA, and which when bound by VGAM2470 RNA causes inhibition of translation of respective one or more VGAM2470 host target proteins.

[83728] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2470 gene, herein designated VGAM GENE, on one or more VGAM2470 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83729] It is yet further appreciated that a function of VGAM2470 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2470 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2470 correlate with, and may be deduced from, the identity of the host target genes which VGAM2470 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83730] Nucleotide sequences of the VGAM2470 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2470 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2470 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2470 are further described hereinbelow with reference to Table 1.

[83731] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2470 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2470 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83732] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2470 gene, herein designated VGAM is inhibition of expression of VGAM2470 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2470 correlate with, and may be deduced from, the identity of the target genes which VGAM2470 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83733] Epithelial Membrane Protein 1 (EMP1, Accession NM_001423) is a VGAM2470 host target gene. EMP1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EMP1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EMP1 BINDING SITE, designated SEQ ID:7130, to the nucleotide sequence of VGAM2470 RNA, herein designated VGAM RNA, also designated SEQ ID:5181.

[83734] A function of VGAM2470 is therefore inhibition of Epithe-

lial Membrane Protein 1 (EMP1, Accession NM_001423), a gene which plays a role in squamous cell differentiation; member of the PMP22/EMP/MP20 family of membrane glycoproteins. Accordingly, utilities of VGAM2470 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMP1. The function of EMP1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM107.Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2471 (VGAM2471) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83735] VGAM2471 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2471 was detected is described hereinabove with reference to Figs. 1-8.

[83736] VGAM2471 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2471 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[83737] VGAM2471 gene encodes a VGAM2471 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2471 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2471 precursor RNA is designated SEQ ID:2457, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2457 is located at position 2006 relative to the genome of Mouse Cytomegalovirus 1.

[83738] VGAM2471 precursor RNA folds onto itself, forming VGAM2471 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83739] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2471 folded precursor RNA into VGAM2471 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2471 RNA is designated SEQ ID:5182, and is provided hereinbelow with reference to the sequence listing part.

[83740] VGAM2471 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2471 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2471 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83741] VGAM2471 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2471 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2471 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2471 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2471 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83742] The complementary binding of VGAM2471 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2471 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2471 host target RNA into VGAM2471 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83743] It is appreciated that VGAM2471 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2471 host target genes. The mRNA of each one of this plurality of VGAM2471 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2471 RNA, herein designated VGAM RNA, and which when bound by VGAM2471 RNA causes inhibition of translation of respective one or more VGAM2471 host target proteins.

[83744] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2471 gene, herein designated VGAM GENE, on one or more VGAM2471 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83745] It is yet further appreciated that a function of VGAM2471 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2471 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2471 correlate with, and may be deduced from, the identity of the host target genes which VGAM2471 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83746] Nucleotide sequences of the VGAM2471 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2471 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2471 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2471 are further described hereinbelow with reference to Table 1.

[83747] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2471 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2471 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83748] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2471 gene, herein designated VGAM is inhibition of expression of VGAM2471 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2471 correlate with, and may be deduced from, the identity of the target genes which VGAM2471 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83749] Neuro-oncological Ventral Antigen 1 (NOVA1, Accession NM_002515) is a VGAM2471 host target gene. NOVA1 BINDING SITE1 and NOVA1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by NOVA1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NOVA1 BINDING SITE1 and NOVA1 BINDING SITE2, designated SEQ ID:8349 and SEQ ID:13218 respectively, to the nucleotide sequence of

VGAM2471 RNA, herein designated VGAM RNA, also designated SEQ ID:5182.

[83750] A function of VGAM2471 is therefore inhibition of Neuro-oncological Ventral Antigen 1 (NOVA1, Accession NM_002515), a gene which may regulate rna splicing or metabolism in a specific subset of developing neurons. Accordingly, utilities of VGAM2471 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOVA1. The function of NOVA1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM521.KIAA0446 (Accession XM_044155) is another VGAM2471 host target gene. KIAA0446 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0446, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0446 BINDING SITE, designated SEQ ID:34144, to the nucleotide sequence of VGAM2471 RNA, herein designated VGAM RNA, also designated SEQ ID:5182.

[83751] Another function of VGAM2471 is therefore inhibition of

KIAA0446 (Accession XM_044155). Accordingly, utilities of VGAM2471 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0446. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2472 (VGAM2472) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83752] VGAM2472 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2472 was detected is described hereinabove with reference to Figs. 1-8.

[83753] VGAM2472 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2472 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83754] VGAM2472 gene encodes a VGAM2472 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2472 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2472 precursor RNA is designated SEQ ID:2458, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2458 is located at position 116628 relative to the genome of Mouse Cytomegalovirus 1.

[83755] VGAM2472 precursor RNA folds onto itself, forming VGAM2472 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83756] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2472 folded precursor RNA into VGAM2472 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide se-

quence of VGAM2472 RNA is designated SEQ ID:5183, and is provided hereinbelow with reference to the sequence listing part.

[83757] VGAM2472 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2472 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2472 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83758] VGAM2472 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2472 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2472 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2472 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2472 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83759] The complementary binding of VGAM2472 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2472 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2472 host target RNA into VGAM2472 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83760] It is appreciated that VGAM2472 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2472 host target genes. The mRNA of each one of this plurality of VGAM2472 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2472 RNA, herein designated VGAM RNA, and which when bound by VGAM2472 RNA causes inhibition of translation of respective one or more VGAM2472 host target proteins.

[83761] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2472 gene, herein designated VGAM GENE, on one or more VGAM2472 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83762] It is yet further appreciated that a function of VGAM2472

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2472 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2472 correlate with, and may be deduced from, the identity of the host target genes which VGAM2472 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83763] Nucleotide sequences of the VGAM2472 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2472 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2472 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2472 are further described hereinbelow with reference to Table 1.

[83764] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2472 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2472 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83765] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2472 gene, herein designated VGAM is inhibition of expression of VGAM2472 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2472 correlate with, and may be deduced from, the identity of the target genes which VGAM2472 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83766] Integrin, Alpha 11 (ITGA11, Accession NM_012211) is a VGAM2472 host target gene. ITGA11 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ITGA11, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA11 BINDING SITE, designated SEQ ID:14515, to the nucleotide sequence of VGAM2472 RNA, herein designated VGAM RNA, also designated SEQ ID:5183.

[83767] A function of VGAM2472 is therefore inhibition of Integrin, Alpha 11 (ITGA11, Accession NM_012211), a gene which acts as a collagen I receptor. Accordingly, utilities of VGAM2472 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

ITGA11. The function of ITGA11 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Surfactant, Pulmonary-associated Protein A2 (SFTPA2, Accession NM_006926) is another VGAM2472 host target gene. SFTPA2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SFTPA2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SFTPA2 BINDING SITE, designated SEQ ID:13809, to the nucleotide sequence of VGAM2472 RNA, herein designated VGAM RNA, also designated SEQ ID:5183.

[83768] Another function of VGAM2472 is therefore inhibition of Surfactant, Pulmonary-associated Protein A2 (SFTPA2, Accession NM_006926), a gene which plays a role in innate host defense in the lung. Accordingly, utilities of VGAM2472 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SFTPA2. The function of SFTPA2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with

reference to VGAM148.Serine/arginine Repetitive Matrix 1 (SRRM1, Accession NM_005839) is another VGAM2472 host target gene. SRRM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SRRM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SRRM1 BINDING SITE, designated SEQ ID:12450, to the nucleotide sequence of VGAM2472 RNA, herein designated VGAM RNA, also designated SEQ ID:5183.

[83769] Another function of VGAM2472 is therefore inhibition of Serine/arginine Repetitive Matrix 1 (SRRM1, Accession NM_005839). Accordingly, utilities of VGAM2472 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SRRM1. GREB1 (Accession XM_051545) is another VGAM2472 host target gene. GREB1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GREB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GREB1 BINDING SITE, designated SEQ

ID:35853, to the nucleotide sequence of VGAM2472 RNA, herein designated VGAM RNA, also designated SEQ ID:5183.

[83770] Another function of VGAM2472 is therefore inhibition of GREB1 (Accession XM_051545). Accordingly, utilities of VGAM2472 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GREB1. KIAA0537 (Accession NM_014840) is another VGAM2472 host target gene. KIAA0537 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0537, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0537 BINDING SITE, designated SEQ ID:16868, to the nucleotide sequence of VGAM2472 RNA, herein designated VGAM RNA, also designated SEQ ID:5183.

[83771] Another function of VGAM2472 is therefore inhibition of KIAA0537 (Accession NM_014840). Accordingly, utilities of VGAM2472 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0537. MGC4504 (Accession NM_024111) is another VGAM2472 host target gene. MGC4504 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4504, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4504 BINDING SITE, designated SEQ ID:23558, to the nucleotide sequence of VGAM2472 RNA, herein designated VGAM RNA, also designated SEQ ID:5183.

[83772] Another function of VGAM2472 is therefore inhibition of MGC4504 (Accession NM_024111). Accordingly, utilities of VGAM2472 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4504. Purinergic Receptor P2X, Ligand-gated Ion Channel, 5 (P2RX5, Accession NM_002561) is another VGAM2472 host target gene. P2RX5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by P2RX5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P2RX5 BINDING SITE, designated SEQ ID:8410, to the nucleotide sequence of VGAM2472 RNA, herein designated VGAM RNA, also designated SEQ ID:5183.

[83773] Another function of VGAM2472 is therefore inhibition of Purinergic Receptor P2X, Ligand-gated Ion Channel, 5 (P2RX5, Accession NM_002561). Accordingly, utilities of VGAM2472 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RX5. LOC148918 (Accession XM_086361) is another VGAM2472 host target gene. LOC148918 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC148918, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148918 BINDING SITE, designated SEQ ID:38615, to the nucleotide sequence of VGAM2472 RNA, herein designated VGAM RNA, also designated SEQ ID:5183.

[83774] Another function of VGAM2472 is therefore inhibition of LOC148918 (Accession XM_086361). Accordingly, utilities of VGAM2472 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148918. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2473 (VGAM2473) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83775] VGAM2473 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2473 was detected is described hereinabove with reference to Figs. 1-8.

[83776] VGAM2473 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2473 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83777] VGAM2473 gene encodes a VGAM2473 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2473 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2473 precursor RNA is designated SEQ ID:2459, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2459 is located at position 101492 relative to the genome of Mouse Cytomegalovirus 1.

[83778] VGAM2473 precursor RNA folds onto itself, forming

VGAM2473 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83779] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2473 folded precursor RNA into VGAM2473 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2473 RNA is designated SEQ ID:5184, and is provided hereinbelow with reference to the sequence listing part.

[83780] VGAM2473 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2473 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2473 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83781] VGAM2473 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2473 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2473 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2473 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2473 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83782] The complementary binding of VGAM2473 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2473 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2473 host target RNA into VGAM2473 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83783] It is appreciated that VGAM2473 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2473 host target genes. The mRNA of each one of this plurality of VGAM2473 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2473 RNA, herein designated VGAM RNA, and which when bound by VGAM2473 RNA causes inhibition of translation of respective one or more VGAM2473 host target proteins.

[83784] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2473 gene, herein designated VGAM GENE, on one or more VGAM2473 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83785] It is yet further appreciated that a function of VGAM2473 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2473 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2473 correlate with, and may be deduced from, the identity of the host target genes which VGAM2473 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[83786] Nucleotide sequences of the VGAM2473 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2473 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2473 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2473 are further described hereinbelow with reference to Table 1.

[83787] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2473 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2473 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83788] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2473 gene, herein designated VGAM is inhibition of expression of VGAM2473 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2473 correlate with, and may be deduced from, the identity of the target genes which VGAM2473 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[83789] Cyclin-dependent Kinase Inhibitor 1C (p57, Kip2) (CDKN1C, Accession NM_000076) is a VGAM2473 host target gene. CDKN1C BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CDKN1C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDKN1C BINDING SITE, designated SEQ ID:5521, to the nucleotide sequence of VGAM2473 RNA, herein designated VGAM RNA, also designated SEQ ID:5184.

[83790] A function of VGAM2473 is therefore inhibition of Cyclin-dependent Kinase Inhibitor 1C (p57, Kip2) (CDKN1C, Accession NM_000076). Accordingly, utilities of VGAM2473 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDKN1C. Dystrobrevin, Alpha (DTNA, Accession NM_001391) is another VGAM2473 host target gene. DTNA BINDING SITE1 through DTNA BINDING SITE4 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by DTNA, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Ta-

ble 2 illustrates the complementarity of the nucleotide sequences of DTNA BINDING SITE1 through DTNA BINDING SITE4, designated SEQ ID:7083, SEQ ID:26840, SEQ ID:26845 and SEQ ID:26850 respectively, to the nucleotide sequence of VGAM2473 RNA, herein designated VGAM RNA, also designated SEQ ID:5184.

[83791] Another function of VGAM2473 is therefore inhibition of Dystrobrevin, Alpha (DTNA, Accession NM_001391), a gene which may be involved in the formation and stability of synapses. Accordingly, utilities of VGAM2473 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DTNA. The function of DTNA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1021.Nucleolar Protein 4 (NOL4, Accession NM_003787) is another VGAM2473 host target gene. NOL4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NOL4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NOL4 BINDING SITE, designated SEQ ID:9875,

to the nucleotide sequence of VGAM2473 RNA, herein designated VGAM RNA, also designated SEQ ID:5184.

[83792] Another function of VGAM2473 is therefore inhibition of Nucleolar Protein 4 (NOL4, Accession NM_003787). Accordingly, utilities of VGAM2473 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NOL4. SC65 (Accession NM_006455) is another VGAM2473 host target gene. SC65 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SC65, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SC65 BINDING SITE, designated SEQ ID:13173, to the nucleotide sequence of VGAM2473 RNA, herein designated VGAM RNA, also designated SEQ ID:5184.

[83793] Another function of VGAM2473 is therefore inhibition of SC65 (Accession NM_006455). Accordingly, utilities of VGAM2473 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SC65. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger

2474 (VGAM2474) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83794] VGAM2474 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2474 was detected is described hereinabove with reference to Figs. 1-8.

[83795] VGAM2474 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2474 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83796] VGAM2474 gene encodes a VGAM2474 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2474 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2474 precursor RNA is designated SEQ ID:2460, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2460 is located at position 82294 relative to the genome of Mouse Cytomegalovirus 1.

[83797] VGAM2474 precursor RNA folds onto itself, forming

VGAM2474 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83798] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2474 folded precursor RNA into VGAM2474 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2474 RNA is designated SEQ ID:5185, and is provided hereinbelow with reference to the sequence listing part.

[83799] VGAM2474 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2474 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2474 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83800] VGAM2474 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2474 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2474 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2474 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2474 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83801] The complementary binding of VGAM2474 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2474 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2474 host target RNA into VGAM2474 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83802] It is appreciated that VGAM2474 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2474 host target genes. The mRNA of each one of this plurality of VGAM2474 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2474 RNA, herein designated VGAM RNA, and which when bound by VGAM2474 RNA causes inhibition of translation of respective one or more VGAM2474 host target proteins.

[83803] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2474 gene, herein designated VGAM GENE, on one or more VGAM2474 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83804] It is yet further appreciated that a function of VGAM2474 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2474 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2474 correlate with, and may be deduced from, the identity of the host target genes which VGAM2474 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[83805] Nucleotide sequences of the VGAM2474 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2474 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2474 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2474 are further described hereinbelow with reference to Table 1.

[83806] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2474 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2474 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83807] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2474 gene, herein designated VGAM is inhibition of expression of VGAM2474 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2474 correlate with, and may be deduced from, the identity of the target genes which VGAM2474 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[83808] KIAA0475 (Accession NM_014864) is a VGAM2474 host target gene. KIAA0475 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0475, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0475 BINDING SITE, designated SEQ ID:16945, to the nucleotide sequence of VGAM2474 RNA, herein designated VGAM RNA, also designated SEQ ID:5185.

[83809] A function of VGAM2474 is therefore inhibition of KIAA0475 (Accession NM_014864). Accordingly, utilities of VGAM2474 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0475. LOC257482 (Accession XM_168544) is another VGAM2474 host target gene. LOC257482 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257482, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257482 BINDING SITE, designated SEQ ID:45234, to

the nucleotide sequence of VGAM2474 RNA, herein designated VGAM RNA, also designated SEQ ID:5185.

[83810] Another function of VGAM2474 is therefore inhibition of LOC257482 (Accession XM_168544). Accordingly, utilities of VGAM2474 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC257482. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2475 (VGAM2475) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83811] VGAM2475 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2475 was detected is described hereinabove with reference to Figs. 1-8.

[83812] VGAM2475 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2475 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83813] VGAM2475 gene encodes a VGAM2475 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2475 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2475 precursor RNA is designated SEQ ID:2461, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2461 is located at position 190173 relative to the genome of Mouse Cytomegalovirus 1.

[83814] VGAM2475 precursor RNA folds onto itself, forming VGAM2475 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83815] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2475 folded precursor RNA into VGAM2475 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2475 RNA is designated SEQ ID:5186, and is provided hereinbelow with reference to the sequence listing part.

[83816] VGAM2475 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2475 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2475 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83817] VGAM2475 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2475 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2475 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2475 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2475 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83818] The complementary binding of VGAM2475 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2475 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2475 host target RNA into VGAM2475 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83819] It is appreciated that VGAM2475 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2475 host target genes. The mRNA of each one of this plurality of VGAM2475 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2475 RNA, herein designated VGAM RNA, and which when bound by VGAM2475 RNA causes inhibition of translation of respective one or more VGAM2475 host target proteins.

[83820] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2475 gene, herein designated VGAM GENE, on one or more VGAM2475 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83821] It is yet further appreciated that a function of VGAM2475 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2475 correlate with, and may be deduced from, the identity of the host target genes which VGAM2475 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83822] Nucleotide sequences of the VGAM2475 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2475 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2475 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2475 are further described hereinbelow with reference to Table 1.

[83823] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2475 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2475 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83824] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2475 gene, herein designated VGAM is inhibition of expression of VGAM2475 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2475 correlate with, and may be deduced from, the identity of the target genes which VGAM2475 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83825] Adenylate Kinase 1 (AK1, Accession NM_000476) is a VGAM2475 host target gene. AK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by AK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AK1 BINDING SITE, designated SEQ ID:6084, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83826] A function of VGAM2475 is therefore inhibition of Adenylate Kinase 1 (AK1, Accession NM_000476). Accordingly,

utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AK1. Cyclin-dependent Kinase 5, Regulatory Subunit 2 (p39) (CDK5R2, Accession NM_003936) is another VGAM2475 host target gene. CDK5R2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDK5R2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDK5R2 BINDING SITE, designated SEQ ID:10040, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83827] Another function of VGAM2475 is therefore inhibition of Cyclin-dependent Kinase 5, Regulatory Subunit 2 (p39) (CDK5R2, Accession NM_003936), a gene which acts as a regulatory subunit for the cyclin-dependent CDK5. Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDK5R2. The function of CDK5R2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM403.Early Growth Re-

sponse 2 (Krox-20 homolog, Drosophila) (EGR2, Accession NM_000399) is another VGAM2475 host target gene. EGR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EGR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EGR2 BINDING SITE, designated SEQ ID:5969, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83828] Another function of VGAM2475 is therefore inhibition of Early Growth Response 2 (Krox-20 homolog, Drosophila) (EGR2, Accession NM_000399), a gene which binds to two specific dna sites located in the promoter region of hox-1.4. Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EGR2. The function of EGR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM234.Fragile X Mental Retardation, Autosomal Homolog 2 (FXR2, Accession NM_004860) is another VGAM2475 host target gene. FXR2 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by FXR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FXR2 BINDING SITE, designated SEQ ID:11269, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83829] Another function of VGAM2475 is therefore inhibition of Fragile X Mental Retardation, Autosomal Homolog 2 (FXR2, Accession NM_004860), a gene which is a rna-binding protein. interacts with fmr1 and fxr1. Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FXR2. The function of FXR2 has been established by previous studies. Fragile X mental retardation is directly associated with the FMR1 gene at Xq27.3 (OMIM Ref. No. 309550). FMR1 is an RNA-binding protein, and mutations in the gene are believed to result in the absence or reduced expression of the protein or a functionally impaired mutant protein. FMR1 protein and the fragile X-related proteins 1 and 2 (FXR1; 600819 and FXR2) form a family with functional similarities, such as RNA binding, polyribosomal association, and nucleocytoplasmic shuttling.

Animal model experiments lend further support to the function of FXR2. Bontekoe et al. (2002) generated an Fxr2 knockout mouse model. No pathologic differences between knockout and wildtype mice were found in brain or testis; however, their behaviors were distinctive. Fxr2 knockout mice were hyperactive (i.e., traveled a greater distance, spent more time moving, and moved faster) in the open-field test, were impaired on the rotarod test, had reduced levels of prepulse inhibition, displayed less contextual conditioned fear, were impaired at locating the hidden platform in the Morris water task, and were less sensitive to a heat stimulus. The authors implicated a role for Fxr2 in central nervous system function.

[83830] It is appreciated that the abovementioned animal model for FXR2 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[83831] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83832] Bontekoe, C. J. M.; McIlwain, K. L.; Nieuwenhuizen, I. M.; Yuva-Paylor, L. A.; Nellis, A.; Willemsen, R.; Fang, Z.; Kirkpatrick, L.; Bakker, C. E.; McAninch, R.; Cheng, N. C.; Mer-

riweather, M.; Hoogeveen, A. T.; Nelson, D.; Paylor, R.; Oostra, B. A. : Knockout mouse model for Fxr2: a model for mental retardation. Hum. Molec. Genet. 11: 487-498, 2002. ; and

[83833] Tamanini, F.; Bontekoe, C.; Bakker, C. E.; van Unen, L.; Anar, B.; Willemsen, R.; Yoshida, M.; Galjaard, H.; Oostra, B. A.; Hoogeveen, A. T. : Different targets for the fragile X-relate.

[83834] Further studies establishing the function and utilities of FXR2 are found in John Hopkins OMIM database record ID 605339, and in sited publications numbered 2308, 7527-752 and 2309-2310 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Integrin, Alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3, Accession NM_002204) is another VGAM2475 host target gene. ITGA3 BINDING SITE1 and ITGA3 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ITGA3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ITGA3 BINDING SITE1 and ITGA3 BINDING SITE2, designated SEQ ID:7967 and SEQ ID:12010 respec-

tively, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83835] Another function of VGAM2475 is therefore inhibition of Integrin, Alpha 3 (antigen CD49C, alpha 3 subunit of VLA-3 receptor) (ITGA3, Accession NM_002204), a gene which is a receptor for fibronectin, laminin, collagen, epiligrin and thrombospondin. Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ITGA3. The function of ITGA3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1020.Nyctalopin (NYX, Accession NM_022567) is another VGAM2475 host target gene. NYX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NYX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NYX BINDING SITE, designated SEQ ID:22886, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83836] Another function of VGAM2475 is therefore inhibition of Nyctalopin (NYX, Accession NM_022567), a gene which functions as the von willebrand factor receptor and mediates von willebrand factor-dependent platelet adhesion to blood vessels. the adhesion of platelets to injured vascular surfaces in the arterial circulation is a critical initiating event in hemostasis (by similarity). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NYX. The function of NYX and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM206.Protein Kinase C and Casein Kinase Substrate In Neurons 1 (PACSIN1, Accession XM_166424) is another VGAM2475 host target gene. PACSIN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PACSIN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PACSIN1 BINDING SITE, designated SEQ ID:44311, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83837] Another function of VGAM2475 is therefore inhibition of Protein Kinase C and Casein Kinase Substrate In Neurons 1 (PACSIN1, Accession XM_166424). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PACSIN1. p21(CDKN1A)-activated Kinase 4 (PAK4, Accession NM_005884) is another VGAM2475 host target gene. PAK4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PAK4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAK4 BINDING SITE, designated SEQ ID:12506, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83838] Another function of VGAM2475 is therefore inhibition of p21(CDKN1A)-activated Kinase 4 (PAK4, Accession NM_005884). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAK4. Protein Phosphatase 2, Regulatory Subunit B (B56), Alpha Isoform (PPP2R5A, Accession NM_006243) is another VGAM2475 host target gene. PPP2R5A BINDING SITE is HOST TARGET binding site

found in the 3` untranslated region of mRNA encoded by PPP2R5A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PPP2R5A BINDING SITE, designated SEQ ID:12911, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83839] Another function of VGAM2475 is therefore inhibition of Protein Phosphatase 2, Regulatory Subunit B (B56), Alpha Isoform (PPP2R5A, Accession NM_006243), a gene which is a regulatory subunit of protein phosphatase 2A. Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PPP2R5A. The function of PPP2R5A and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM675.Protein Kinase, CAMP-dependent, Catalytic, Alpha (PRKACA, Accession NM_002730) is another VGAM2475 host target gene. PRKACA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRKACA, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRKACA BINDING SITE, designated SEQ ID:8596, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83840] Another function of VGAM2475 is therefore inhibition of Protein Kinase, CAMP-dependent, Catalytic, Alpha (PRKACA, Accession NM_002730), a gene which phosphorylates target proteins on serine or threonine residues. Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKACA. The function of PRKACA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM175.Runt-related Transcription Factor 3 (RUNX3, Accession NM_004350) is another VGAM2475 host target gene. RUNX3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RUNX3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of RUNX3 BINDING SITE, designated SEQ ID:10547, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83841] Another function of VGAM2475 is therefore inhibition of Runt-related Transcription Factor 3 (RUNX3, Accession NM_004350), a gene which binds to the core site, 5'-pygpyggt-3', of a number of enhancers and promoters. Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RUNX3. The function of RUNX3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1151.Secreted and Transmembrane 1 (SECTM1, Accession NM_003004) is another VGAM2475 host target gene. SECTM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SECTM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SECTM1 BINDING SITE, designated SEQ ID:8909, to the nucleotide sequence of VGAM2475 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5186.

[83842] Another function of VGAM2475 is therefore inhibition of Secreted and Transmembrane 1 (SECTM1, Accession NM_003004). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SECTM1. SH3-domain GRB2-like 1 (SH3GL1, Accession NM_003025) is another VGAM2475 host target gene. SH3GL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SH3GL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SH3GL1 BINDING SITE, designated SEQ ID:8963, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83843] Another function of VGAM2475 is therefore inhibition of SH3-domain GRB2-like 1 (SH3GL1, Accession NM_003025). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SH3GL1. SORCS1 (Accession NM_052918) is another VGAM2475 host target gene. SORCS1 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by SORCS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SORCS1 BINDING SITE, designated SEQ ID:27482, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83844] Another function of VGAM2475 is therefore inhibition of SORCS1 (Accession NM_052918). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SORCS1. SRY (sex determining region Y)-box 4 (SOX4, Accession NM_003107) is another VGAM2475 host target gene. SOX4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SOX4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX4 BINDING SITE, designated SEQ ID:9071, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83845] Another function of VGAM2475 is therefore inhibition of

SRY (sex determining region Y)-box 4 (SOX4, Accession NM_003107), a gene which binds with high affinity to the t-cell enhancer motif 5'-aacaaag-3' motif. Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX4. The function of SOX4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM409.T-cell Acute Lymphocytic Leukemia 1 (TAL1, Accession NM_003189) is another VGAM2475 host target gene. TAL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TAL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TAL1 BINDING SITE, designated SEQ ID:9168, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83846] Another function of VGAM2475 is therefore inhibition of T-cell Acute Lymphocytic Leukemia 1 (TAL1, Accession NM_003189), a gene which may help control cell growth and differentiation. Accordingly, utilities of VGAM2475 in-

clude diagnosis, prevention and treatment of diseases and clinical conditions associated with TAL1. The function of TAL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM172.20D7-FC4 (Accession XM_027578) is another VGAM2475 host target gene. 20D7-FC4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by 20D7-FC4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of 20D7-FC4 BINDING SITE, designated SEQ ID:30536, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83847] Another function of VGAM2475 is therefore inhibition of 20D7-FC4 (Accession XM_027578). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with 20D7-FC4. Chromosome 5 Open Reading Frame 5 (C5orf5, Accession NM_016603) is another VGAM2475 host target gene. C5orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by C5orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C5orf5 BINDING SITE, designated SEQ ID:18695, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83848] Another function of VGAM2475 is therefore inhibition of Chromosome 5 Open Reading Frame 5 (C5orf5, Accession NM_016603). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C5orf5. dJ309H15.1 (Accession NM_138574) is another VGAM2475 host target gene. dJ309H15.1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by dJ309H15.1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of dJ309H15.1 BINDING SITE, designated SEQ ID:28886, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83849] Another function of VGAM2475 is therefore inhibition of

dJ309H15.1 (Accession NM_138574). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with dJ309H15.1. DKFZP566K1924 (Accession XM_057469) is another VGAM2475 host target gene. DKFZP566K1924 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP566K1924, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566K1924 BINDING SITE, designated SEQ ID:36518, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83850] Another function of VGAM2475 is therefore inhibition of DKFZP566K1924 (Accession XM_057469). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566K1924. FLJ11767 (Accession NM_024593) is another VGAM2475 host target gene. FLJ11767 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11767, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11767 BINDING SITE, designated SEQ ID:23829, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83851] Another function of VGAM2475 is therefore inhibition of FLJ11767 (Accession NM_024593). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11767. FLJ14596 (Accession NM_032809) is another VGAM2475 host target gene. FLJ14596 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14596, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14596 BINDING SITE, designated SEQ ID:26570, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83852] Another function of VGAM2475 is therefore inhibition of FLJ14596 (Accession NM_032809). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ14596. FLJ20375 (Accession NM_017794) is another VGAM2475 host target gene. FLJ20375 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20375, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20375 BINDING SITE, designated SEQ ID:19431, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83853] Another function of VGAM2475 is therefore inhibition of FLJ20375 (Accession NM_017794). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20375. KIAA0450 (Accession NM_014638) is another VGAM2475 host target gene. KIAA0450 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA0450, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0450 BINDING SITE, designated SEQ ID:16026, to the nucleotide sequence of VGAM2475 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5186.

[83854] Another function of VGAM2475 is therefore inhibition of KIAA0450 (Accession NM_014638). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0450. KIAA1030 (Accession XM_167789) is another VGAM2475 host target gene. KIAA1030 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1030, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1030 BINDING SITE, designated SEQ ID:44817, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83855] Another function of VGAM2475 is therefore inhibition of KIAA1030 (Accession XM_167789). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1030. KIAA1045 (Accession XM_048592) is another VGAM2475 host target gene. KIAA1045 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1045, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1045 BINDING SITE, designated SEQ ID:35191, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83856] Another function of VGAM2475 is therefore inhibition of KIAA1045 (Accession XM_048592). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1045. KIAA1536 (Accession NM_020898) is another VGAM2475 host target gene. KIAA1536 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1536, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1536 BINDING SITE, designated SEQ ID:21922, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83857] Another function of VGAM2475 is therefore inhibition of KIAA1536 (Accession NM_020898). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1536. KIAA1538 (Accession XM_049474) is another VGAM2475 host target gene. KIAA1538 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1538, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1538 BINDING SITE, designated SEQ ID:35419, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83858] Another function of VGAM2475 is therefore inhibition of KIAA1538 (Accession XM_049474). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1538. KIAA1600 (Accession XM_049351) is another VGAM2475 host target gene. KIAA1600 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1600, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1600 BINDING SITE, designated SEQ ID:35389, to the

nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83859] Another function of VGAM2475 is therefore inhibition of KIAA1600 (Accession XM_049351). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1600. KIAA1643 (Accession XM_035371) is another VGAM2475 host target gene. KIAA1643 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1643, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1643 BINDING SITE, designated SEQ ID:32239, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83860] Another function of VGAM2475 is therefore inhibition of KIAA1643 (Accession XM_035371). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1643. MOST2 (Accession NM_020250) is another VGAM2475 host target gene. MOST2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated

region of mRNA encoded by MOST2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MOST2 BINDING SITE, designated SEQ ID:21553, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83861] Another function of VGAM2475 is therefore inhibition of MOST2 (Accession NM_020250). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MOST2. Phytanoyl-CoA Hydroxylase Interacting Protein (PHYHIP, Accession NM_014759) is another VGAM2475 host target gene. PHYHIP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PHYHIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PHYHIP BINDING SITE, designated SEQ ID:16508, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83862] Another function of VGAM2475 is therefore inhibition of

Phytanoyl-CoA Hydroxylase Interacting Protein (PHYHIP, Accession NM_014759). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PHYHIP. PR Domain Containing 8 (PRDM8, Accession NM_020226) is another VGAM2475 host target gene. PRDM8 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRDM8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRDM8 BINDING SITE, designated SEQ ID:21491, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83863] Another function of VGAM2475 is therefore inhibition of PR Domain Containing 8 (PRDM8, Accession NM_020226). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDM8. SBB103 (Accession NM_005785) is another VGAM2475 host target gene. SBB103 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SBB103, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SBB103 BINDING SITE, designated SEQ ID:12364, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83864] Another function of VGAM2475 is therefore inhibition of SBB103 (Accession NM_005785). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SBB103. Stathmin-like 3 (STMN3, Accession NM_015894) is another VGAM2475 host target gene. STMN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by STMN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of STMN3 BINDING SITE, designated SEQ ID:18036, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83865] Another function of VGAM2475 is therefore inhibition of Stathmin-like 3 (STMN3, Accession NM_015894). Accordingly, utilities of VGAM2475 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with STMN3. Tigger Transposable Element Derived 1 (TIGD1, Accession XM_114293) is another VGAM2475 host target gene. TIGD1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TIGD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIGD1 BINDING SITE, designated SEQ ID:42846, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83866] Another function of VGAM2475 is therefore inhibition of Tigger Transposable Element Derived 1 (TIGD1, Accession XM_114293). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIGD1. LOC143677 (Accession XM_096471) is another VGAM2475 host target gene. LOC143677 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143677, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of LOC143677 BINDING SITE, designated SEQ ID:40373, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83867] Another function of VGAM2475 is therefore inhibition of LOC143677 (Accession XM_096471). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143677. LOC154222 (Accession XM_098497) is another VGAM2475 host target gene. LOC154222 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC154222, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC154222 BINDING SITE, designated SEQ ID:41690, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83868] Another function of VGAM2475 is therefore inhibition of LOC154222 (Accession XM_098497). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC154222. LOC159090 (Accession XM_088749) is an-

other VGAM2475 host target gene. LOC159090 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC159090, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159090 BINDING SITE, designated SEQ ID:39938, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83869] Another function of VGAM2475 is therefore inhibition of LOC159090 (Accession XM_088749). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159090. LOC221100 (Accession XM_167753) is another VGAM2475 host target gene. LOC221100 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221100, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221100 BINDING SITE, designated SEQ ID:44776, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83870] Another function of VGAM2475 is therefore inhibition of LOC221100 (Accession XM_167753). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221100. LOC221935 (Accession XM_166537) is another VGAM2475 host target gene. LOC221935 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221935, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221935 BINDING SITE, designated SEQ ID:44498, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83871] Another function of VGAM2475 is therefore inhibition of LOC221935 (Accession XM_166537). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221935. LOC256942 (Accession XM_170544) is another VGAM2475 host target gene. LOC256942 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC256942, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256942 BINDING SITE, designated SEQ ID:45363, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83872] Another function of VGAM2475 is therefore inhibition of LOC256942 (Accession XM_170544). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256942. LOC91397 (Accession XM_038219) is another VGAM2475 host target gene. LOC91397 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91397, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91397 BINDING SITE, designated SEQ ID:32779, to the nucleotide sequence of VGAM2475 RNA, herein designated VGAM RNA, also designated SEQ ID:5186.

[83873] Another function of VGAM2475 is therefore inhibition of LOC91397 (Accession XM_038219). Accordingly, utilities of VGAM2475 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC91397. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2476 (VGAM2476) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83874] VGAM2476 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2476 was detected is described hereinabove with reference to Figs. 1-8.

[83875] VGAM2476 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2476 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83876] VGAM2476 gene encodes a VGAM2476 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2476 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2476 precursor RNA is designated SEQ ID:2462, and is provided hereinbelow with ref-

erence to the sequence listing part. Nucleotide sequence SEQ ID:2462 is located at position 136488 relative to the genome of Mouse Cytomegalovirus 1.

[83877] VGAM2476 precursor RNA folds onto itself, forming VGAM2476 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83878] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2476 folded precursor RNA into VGAM2476 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2476 RNA is designated SEQ ID:5187, and is provided hereinbelow with reference to the sequence listing part.

[83879] VGAM2476 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2476 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2476 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83880] VGAM2476 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2476 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2476 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2476 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in

untranslated regions of a VGAM2476 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83881] The complementary binding of VGAM2476 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2476 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2476 host target RNA into VGAM2476 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83882] It is appreciated that VGAM2476 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2476 host target genes. The mRNA of each one of this plurality of VGAM2476 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2476 RNA, herein designated VGAM RNA, and which when bound by VGAM2476 RNA causes

inhibition of translation of respective one or more VGAM2476 host target proteins.

[83883] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2476 gene, herein designated VGAM GENE, on one or more VGAM2476 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83884] It is yet further appreciated that a function of VGAM2476 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2476 include diagnosis, prevention and

treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2476 correlate with, and may be deduced from, the identity of the host target genes which VGAM2476 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83885] Nucleotide sequences of the VGAM2476 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2476 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2476 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2476 are further described hereinbelow with reference to Table 1.

[83886] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2476 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2476 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83887] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2476 gene, herein designated VGAM is inhibition of expression of VGAM2476 target genes. It is

appreciated that specific functions, and accordingly utilities, of VGAM2476 correlate with, and may be deduced from, the identity of the target genes which VGAM2476 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83888] Paired-like Homeodomain Transcription Factor 2 (PITX2, Accession NM_000325) is a VGAM2476 host target gene. PITX2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PITX2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PITX2 BINDING SITE, designated SEQ ID:5867, to the nucleotide sequence of VGAM2476 RNA, herein designated VGAM RNA, also designated SEQ ID:5187.

[83889] A function of VGAM2476 is therefore inhibition of Paired-like Homeodomain Transcription Factor 2 (PITX2, Accession NM_000325). Accordingly, utilities of VGAM2476 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PITX2. Fer-1-like 4 (C. elegans) (FER1L4, Accession NM_025206) is another VGAM2476 host target gene. FER1L4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FER1L4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FER1L4 BINDING SITE, designated SEQ ID:24874, to the nucleotide sequence of VGAM2476 RNA, herein designated VGAM RNA, also designated SEQ ID:5187.

[83890] Another function of VGAM2476 is therefore inhibition of Fer-1-like 4 (C. elegans) (FER1L4, Accession NM_025206). Accordingly, utilities of VGAM2476 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FER1L4. KIAA0876 (Accession XM_035625) is another VGAM2476 host target gene. KIAA0876 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0876, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0876 BINDING SITE, designated SEQ ID:32297, to the nucleotide sequence of VGAM2476 RNA, herein designated VGAM RNA, also designated SEQ ID:5187.

[83891] Another function of VGAM2476 is therefore inhibition of

KIAA0876 (Accession XM_035625). Accordingly, utilities of VGAM2476 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0876. KIAA1608 (Accession NM_024820) is another VGAM2476 host target gene. KIAA1608 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1608, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1608 BINDING SITE, designated SEQ ID:24210, to the nucleotide sequence of VGAM2476 RNA, herein designated VGAM RNA, also designated SEQ ID:5187.

[83892] Another function of VGAM2476 is therefore inhibition of KIAA1608 (Accession NM_024820). Accordingly, utilities of VGAM2476 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1608. LOC151124 (Accession XM_098006) is another VGAM2476 host target gene. LOC151124 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151124, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC151124 BINDING SITE, designated SEQ ID:41302, to the nucleotide sequence of VGAM2476 RNA, herein designated VGAM RNA, also designated SEQ ID:5187.

[83893] Another function of VGAM2476 is therefore inhibition of LOC151124 (Accession XM_098006). Accordingly, utilities of VGAM2476 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151124. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2477 (VGAM2477) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83894] VGAM2477 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2477 was detected is described hereinabove with reference to Figs. 1-8.

[83895] VGAM2477 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2477 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[83896] VGAM2477 gene encodes a VGAM2477 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2477 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2477 precursor RNA is designated SEQ ID:2463, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2463 is located at position 205607 relative to the genome of Mouse Cytomegalovirus 1.

[83897] VGAM2477 precursor RNA folds onto itself, forming VGAM2477 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83898] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2477 folded precursor RNA into VGAM2477 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide sequence of VGAM2477 RNA is designated SEQ ID:5188, and is provided hereinbelow with reference to the sequence listing part.

[83899] VGAM2477 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2477 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2477 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83900] VGAM2477 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2477 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2477 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2477 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2477 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83901] The complementary binding of VGAM2477 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2477 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2477 host target RNA into VGAM2477 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83902] It is appreciated that VGAM2477 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2477 host target genes. The mRNA of each one of this plurality of VGAM2477 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2477 RNA, herein designated VGAM RNA, and which when bound by VGAM2477 RNA causes inhibition of translation of respective one or more VGAM2477 host target proteins.

[83903] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2477 gene, herein designated VGAM GENE, on one or more VGAM2477 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83904] It is yet further appreciated that a function of VGAM2477 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2477 correlate with, and may be deduced from, the identity of the host target genes which VGAM2477 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[83905] Nucleotide sequences of the VGAM2477 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2477 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2477 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2477 are further described hereinbelow with reference to Table 1.

[83906] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2477 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2477 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83907] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2477 gene, herein designated VGAM is inhibition of expression of VGAM2477 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2477 correlate with, and may be deduced from, the identity of the target genes which VGAM2477 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83908] Inositol Polyphosphate Phosphatase-like 1 (INPPL1, Accession NM_001567) is a VGAM2477 host target gene. INPPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by INPPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of INPPL1 BINDING SITE, designated SEQ ID:7296, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ

ID:5188.

[83909] A function of VGAM2477 is therefore inhibition of Inositol Polyphosphate Phosphatase-like 1 (INPPL1, Accession NM_001567), a gene which hydrolyzes Ins(1,3,4,5)P4 and PtdIns(3,4,5)P3; contains an SH2-domain. Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INPPL1. The function of INPPL1 has been established by previous studies. Habib et al. (1998) raised antibodies against SHIP2 to examine the effects of growth factors and insulin (OMIM Ref. No. 176730) on the metabolism of this protein. Immunoblot analysis revealed that SHIP2 was widely expressed in fibroblast and nonhematopoietic tumor cell lines, unlike the SHIP protein (OMIM Ref. No. 601582), which was found only in cell lines of hematopoietic origin. The SHIP2 antiserum precipitated a protein of approximately 145 kD, along with an activity which hydrolyzed phosphatidylinositol 3,4,5-triphosphate to phosphatidylinositol 3,4-bisphosphate. Tyrosine phosphorylation of SHIP2 occurred in response to treatment of cells with EGF, platelet-derived growth factor (PDGF; OMIM Ref. No. 190040), nerve growth factor (NGF; 162030), insulin-like growth factor-1 (IGF1; 147440), or

insulin. EGF and PDGF induced transient tyrosine phosphorylation of SHIP2, while treatment of cells with NGF, IGF1, or insulin resulted in prolonged tyrosine phosphorylation of SHIP2. Habib et al. (1998) concluded that their data suggests that SHIP2 may play a significant role in regulation of phosphatidylinositol 3-prime-kinase signaling by growth factors and insulin. By PCR using primers from the INPPL1 cDNA sequence, Hejna et al. (1995) screened an NIGMS human/rodent somatic cell hybrid mapping panel and assigned the INPPL1 gene to chromosome 11. They narrowed the localization to 11q23 using a chromosome 11-specific deletion panel Animal model experiments lend further support to the function of INPPL1. Clement et al. (2001) generated mice lacking the Ship2 gene. Loss of Ship2 led to increased sensitivity to insulin, which was characterized by severe neonatal hypoglycemia, deregulated expression of the genes involved in gluconeogenesis, and perinatal death. Adult mice that were heterozygous for the Ship2 mutation had increased glucose tolerance and insulin sensitivity associated with an increased recruitment of the GLUT4 glucose transporter (OMIM Ref. No. 138190) and increased glycogen synthesis in skeletal muscles. Clement et al. (2001) suggested that

the results show that SHIP2 is a potent negative regulator of insulin signaling and insulin sensitivity in vivo.

[83910] It is appreciated that the abovementioned animal model for INPPL1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[83911] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83912] Habib, T.; Hejna, J. A.; Moses, R. E.; Decker, S. J. : Growth factors and insulin stimulate tyrosine phosphorylation of the 51C/SHIP2 protein. J. Biol. Chem. 273: 18605-18609, 1998. ; and

[83913] Clement, S.; Krause, U.; Desmedt, F.; Tanti, J.-F.; Behrends, J.; Pesesse, X.; Sasaki, T.; Penninger, J.; Doherty, M.; Malaisse, W.; Dumont, J. E.; Le Marchand-Brustel, Y.; Erneux, C.; H.

[83914] Further studies establishing the function and utilities of INPPL1 are found in John Hopkins OMIM database record ID 600829, and in sited publications numbered 7783-7787 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Jerky Homolog-like (mouse) (JRKL, Accession NM_003772) is an-

other VGAM2477 host target gene. JRKL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by JRKL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of JRKL BINDING SITE, designated SEQ ID:9856, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83915] Another function of VGAM2477 is therefore inhibition of Jerky Homolog-like (mouse) (JRKL, Accession NM_003772), a gene which is a Jerky-related protein and similar to centromere binding protein-B and other nuclear regulators. Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with JRKL. The function of JRKL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1546.Neurexin 2 (NRXN2, Accession NM_015080) is another VGAM2477 host target gene. NRXN2 BINDING SITE1 through NRXN2 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA en-

coded by NRXN2, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NRXN2 BINDING SITE1 through NRXN2 BINDING SITE3, designated SEQ ID:17470, SEQ ID:28986 and SEQ ID:28991 respectively, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83916] Another function of VGAM2477 is therefore inhibition of Neurexin 2 (NRXN2, Accession NM_015080), a gene which may be involved in cell recognition, cell adhesion, and may mediate intracellular signaling. Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRXN2. The function of NRXN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM178.UC28 (Accession NM_021635) is another VGAM2477 host target gene. UC28 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by UC28, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of UC28 BINDING SITE, designated SEQ ID:22280, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83917] Another function of VGAM2477 is therefore inhibition of UC28 (Accession NM_021635). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with UC28. Chromosome 9 Open Reading Frame 5 (C9orf5, Accession NM_032012) is another VGAM2477 host target gene. C9orf5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C9orf5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C9orf5 BINDING SITE, designated SEQ ID:25716, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83918] Another function of VGAM2477 is therefore inhibition of Chromosome 9 Open Reading Frame 5 (C9orf5, Accession NM_032012). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with C9orf5. FLJ12542 (Accession NM_024899) is another VGAM2477 host target gene. FLJ12542 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12542, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12542 BINDING SITE, designated SEQ ID:24383, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83919] Another function of VGAM2477 is therefore inhibition of FLJ12542 (Accession NM_024899). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12542. Golgi Phosphoprotein 2 (GOLPH2, Accession NM_016548) is another VGAM2477 host target gene. GOLPH2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GOLPH2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GOLPH2 BINDING SITE, designated SEQ

ID:18625, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83920] Another function of VGAM2477 is therefore inhibition of Golgi Phosphoprotein 2 (GOLPH2, Accession NM_016548). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GOLPH2. HTEX4 (Accession XM_175165) is another VGAM2477 host target gene. HTEX4 BINDING SITE1 through HTEX4 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by HTEX4, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HTEX4 BINDING SITE1 through HTEX4 BINDING SITE3, designated SEQ ID:46653, SEQ ID:46722 and SEQ ID:44217 respectively, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83921] Another function of VGAM2477 is therefore inhibition of HTEX4 (Accession XM_175165). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HTEX4.

KIAA0557 (Accession XM_085507) is another VGAM2477 host target gene. KIAA0557 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0557, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0557 BINDING SITE, designated SEQ ID:38209, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83922] Another function of VGAM2477 is therefore inhibition of KIAA0557 (Accession XM_085507). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0557. KIAA0783 (Accession NM_014660) is another VGAM2477 host target gene. KIAA0783 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0783, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0783 BINDING SITE, designated SEQ ID:16105, to the nucleotide sequence of VGAM2477 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5188.

[83923] Another function of VGAM2477 is therefore inhibition of KIAA0783 (Accession NM_014660). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0783. KIAA1143 (Accession XM_044014) is another VGAM2477 host target gene. KIAA1143 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1143, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1143 BINDING SITE, designated SEQ ID:34076, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83924] Another function of VGAM2477 is therefore inhibition of KIAA1143 (Accession XM_044014). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1143. KIAA1432 (Accession XM_039698) is another VGAM2477 host target gene. KIAA1432 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1432, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1432 BINDING SITE, designated SEQ ID:33152, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83925] Another function of VGAM2477 is therefore inhibition of KIAA1432 (Accession XM_039698). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1432. Protocadherin 20 (PCDH20, Accession NM_022843) is another VGAM2477 host target gene. PCDH20 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDH20, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH20 BINDING SITE, designated SEQ ID:23137, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83926] Another function of VGAM2477 is therefore inhibition of Protocadherin 20 (PCDH20, Accession NM_022843). Ac-

cordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH20. PRO2533 (Accession NM_018629) is another VGAM2477 host target gene. PRO2533 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRO2533, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRO2533 BINDING SITE, designated SEQ ID:20704, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83927] Another function of VGAM2477 is therefore inhibition of PRO2533 (Accession NM_018629). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRO2533. LOC118851 (Accession XM_061180) is another VGAM2477 host target gene. LOC118851 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC118851, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of LOC118851 BINDING SITE, designated SEQ ID:37203, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83928] Another function of VGAM2477 is therefore inhibition of LOC118851 (Accession XM_061180). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC118851. LOC127943 (Accession XM_059195) is another VGAM2477 host target gene. LOC127943 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC127943, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC127943 BINDING SITE, designated SEQ ID:36914, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83929] Another function of VGAM2477 is therefore inhibition of LOC127943 (Accession XM_059195). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC127943. LOC143154 (Accession XM_084441) is an-

other VGAM2477 host target gene. LOC143154 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC143154, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC143154 BINDING SITE, designated SEQ ID:37590, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83930] Another function of VGAM2477 is therefore inhibition of LOC143154 (Accession XM_084441). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC143154. LOC169966 (Accession XM_093010) is another VGAM2477 host target gene. LOC169966 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC169966, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC169966 BINDING SITE, designated SEQ ID:40167, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83931] Another function of VGAM2477 is therefore inhibition of LOC169966 (Accession XM_093010). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC169966. LOC219294 (Accession XM_167566) is another VGAM2477 host target gene. LOC219294 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219294, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219294 BINDING SITE, designated SEQ ID:44690, to the nucleotide sequence of VGAM2477 RNA, herein designated VGAM RNA, also designated SEQ ID:5188.

[83932] Another function of VGAM2477 is therefore inhibition of LOC219294 (Accession XM_167566). Accordingly, utilities of VGAM2477 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219294. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2478 (VGAM2478) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[83933] VGAM2478 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2478 was detected is described hereinabove with reference to Figs. 1-8.

[83934] VGAM2478 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2478 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83935] VGAM2478 gene encodes a VGAM2478 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2478 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2478 precursor RNA is designated SEQ ID:2464, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2464 is located at position 55947 relative to the genome of Mouse Cytomegalovirus 1.

[83936] VGAM2478 precursor RNA folds onto itself, forming VGAM2478 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83937] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2478 folded precursor RNA into VGAM2478 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2478 RNA is designated SEQ ID:5189, and is provided hereinbelow with reference to the sequence listing part.

[83938] VGAM2478 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2478 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2478 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83939] VGAM2478 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2478 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2478 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2478 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2478 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83940] The complementary binding of VGAM2478 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2478 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2478 host target RNA into VGAM2478 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83941] It is appreciated that VGAM2478 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2478 host target genes. The mRNA of each one of this plurality of VGAM2478 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2478 RNA, herein designated VGAM RNA, and which when bound by VGAM2478 RNA causes inhibition of translation of respective one or more VGAM2478 host target proteins.

[83942] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2478 gene, herein designated VGAM GENE, on one or more VGAM2478 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83943] It is yet further appreciated that a function of VGAM2478 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2478 correlate with, and may be deduced from, the identity of the host target genes which VGAM2478 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[83944] Nucleotide sequences of the VGAM2478 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2478 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2478 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2478 are further described hereinbelow with reference to Table 1.

[83945] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2478 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2478 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83946] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2478 gene, herein designated VGAM is inhibition of expression of VGAM2478 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2478 correlate with, and may be deduced from, the identity of the target genes which VGAM2478 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83947] Ras Homolog Gene Family, Member H (ARHH, Accession NM_004310) is a VGAM2478 host target gene. ARHH BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARHH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHH BINDING SITE, designated SEQ ID:10516, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83948] A function of VGAM2478 is therefore inhibition of Ras Homolog Gene Family, Member H (ARHH, Accession NM_004310), a gene which is a member of the Ras superfamily of small GTPases. Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHH. The function of ARHH has been established by previous studies. Non-Hodgkin lymphoma (NHL; OMIM Ref. No. 605027) is associated with several translocations between the LAZ3 (OMIM Ref. No. 109565) oncogene at 3q27 and other unrelated genes. Dallery et al. (1995) stated that translocations involving band 3q27 and the immunoglobulin (Ig) genes are the third most common specific abnor-

mality associated with NHL. LAZ3 rearrangements also occur in several NHLs without the involvement of Ig genes, as in the translocation t(3;4)(q27;p11) observed in the B-cell line VAL. Dallery et al. (1995) demonstrated that the consequence of this translocation is the expression of a chimeric transcript of LAZ3 and a new gene, which they termed TTF for 'translocation three four,' encoding a small G-like protein. Analysis of a full-length TTF cDNA revealed that the gene encodes a 191-amino acid polypeptide with similarity to members of the Ras superfamily (see OMIM Ref. No. 139150). The highest degree of identity was found with the Rho-like CDC42 protein (OMIM Ref. No. 116952). Dallery et al. (1995) reported that the sequence contains residues normally associated with binding and hydrolysis of guanosine triphosphate. Northern blot analysis showed that TTF is expressed in hemopoietic cell lines only. Dallery-Prudhomme et al. (1997) examined the genomic organization of the RhoH/TTF gene and demonstrated that it is encoded on 2 exons spanning 35 kb of the genome. The entire coding region resides on the second exon. Dallery-Prudhomme et al. (1997) used fluorescence in situ hybridization to map the gene to chromosome 4p13. See also ARHA (OMIM Ref. No.

165390). In addition to immunoglobulin V genes, the 5-prime sequences of BCL6 (OMIM Ref. No. 109565) and FAS (TNFRSF6; 134637) are mutated in normal germinal center B lymphocytes. Genomic instability promotes tumorigenesis through defective chromosome segregation and DNA mismatch repair inactivation. By screening 18 loci for mutations, Pasqualucci et al. (2001) identified changes in the germline sequences of PIM1 (OMIM Ref. No. 164960), MYC (OMIM Ref. No. 190080), ARHH, and/or PAX5 (OMIM Ref. No. 167414), in addition to BCL6, in a majority of diffuse large-cell lymphomas (DLCLs; OMIM Ref. No. 601889). No mutations in PIM1, MYC, ARHH, and PAX5 were detected in germinal-center lymphocytes, naive B cells, or B-cell malignancies other than DLCLs. ARHH mutations, which were observed in 46% of DLCLs, resided within noncoding sequences, suggesting an effect on regulation of ARHH expression. FISH analysis indicated that hypermutation in these genes is not due to chromosomal translocation, as seen in Burkitt lymphoma (OMIM Ref. No. 113970). Chromosomal translocation, however, may be an outcome of hypermutation. Specific features of the hypermutation process, including the predominance of single nucleotide substitutions with occasional dele-

tions or duplications, a preference for transitions over transversions, and a specific motif targeting RGYW, were recognizable in each of the hypermutated loci. Pasqualucci et al. (2001) proposed that aberrant hypermutation of regulatory and coding sequences of genes that do not represent physiologic targets may provide the basis for DLCL pathogenesis and explain its phenotypic and clinical heterogeneity. This hypermutation malfunction is unlikely to be due to defective DNA mismatch repair and does not appear to involve activation-induced deaminase (AICDA; 605257)

[83949] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[83950] Dallery, E.; Galiegue-Zouitina, S.; Collyn-d'Hooghe, M.; Quief, S.; Denis, C.; Hildebrand, M.-P.; Lantoine, D.; Deweindt, C.; Tilly, H.; Bastard, C.; Kerckaert, J.-P. : TTF, a gene encoding a novel small G protein, fuses to the lymphoma-associated LAZ3 gene by t(3;4) chromosomal translocation. Oncogene 10: 2171-2178, 1995. ; and

[83951] Pasqualucci, L.; Neumeister, P.; Goossens, T.; Nanjangud, G.; Chaganti, R. S. K.; Kuppers, R.; Dalla-Favera, R. : Hypermutation of multiple proto-oncogenes in B-cell diffuse

large-cell.

[83952] Further studies establishing the function and utilities of ARHH are found in John Hopkins OMIM database record ID 602037, and in sited publications numbered 951-95 and 11110 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Myxovirus (influenza virus) Resistance 1, Interferon-inducible Protein P78 (mouse) (MX1, Accession NM_002462) is another VGAM2478 host target gene. MX1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MX1 BINDING SITE, designated SEQ ID:8293, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83953] Another function of VGAM2478 is therefore inhibition of Myxovirus (influenza virus) Resistance 1, Interferon-inducible Protein P78 (mouse) (MX1, Accession NM_002462), a gene which is responsible for a specific antiviral state against influenza virus infection. Accordingly, utilities of VGAM2478 include diagnosis, prevention

and treatment of diseases and clinical conditions associated with MX1. The function of MX1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM973.V-myb Myeloblastosis Viral Oncogene Homolog (avian)-like 1 (MYBL1, Accession XM_034274) is another VGAM2478 host target gene. MYBL1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MYBL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYBL1 BINDING SITE, designated SEQ ID:32043, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83954] Another function of VGAM2478 is therefore inhibition of V-myb Myeloblastosis Viral Oncogene Homolog (avian)-like 1 (MYBL1, Accession XM_034274), a gene which could have a role in the proliferation and/or differentiation of neurogenic, spermatogenic and b-lymphoid cells. Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical con-

ditions associated with MYBL1. The function of MYBL1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM184.Synaptogyrin 3 (SYNGR3, Accession NM_004209) is another VGAM2478 host target gene. SYNGR3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SYNGR3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SYNGR3 BINDING SITE, designated SEQ ID:10408, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83955] Another function of VGAM2478 is therefore inhibition of Synaptogyrin 3 (SYNGR3, Accession NM_004209). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SYNGR3. Cyclin M2 (CNNM2, Accession NM_017649) is another VGAM2478 host target gene. CNNM2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

CNNM2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNNM2 BINDING SITE, designated SEQ ID:19154, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83956] Another function of VGAM2478 is therefore inhibition of Cyclin M2 (CNNM2, Accession NM_017649). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNNM2. FLJ10759 (Accession NM_018207) is another VGAM2478 host target gene. FLJ10759 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10759, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10759 BINDING SITE, designated SEQ ID:20102, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83957] Another function of VGAM2478 is therefore inhibition of FLJ10759 (Accession NM_018207). Accordingly, utilities of

VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10759. FLJ20507 (Accession XM_012558) is another VGAM2478 host target gene. FLJ20507 BINDING SITE1 and FLJ20507 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by FLJ20507, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20507 BINDING SITE1 and FLJ20507 BINDING SITE2, designated SEQ ID:30219 and SEQ ID:19511 respectively, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83958] Another function of VGAM2478 is therefore inhibition of FLJ20507 (Accession XM_012558). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20507. KIAA1656 (Accession XM_038022) is another VGAM2478 host target gene. KIAA1656 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1656, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1656 BINDING SITE, designated SEQ ID:32734, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83959] Another function of VGAM2478 is therefore inhibition of KIAA1656 (Accession XM_038022). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1656. KIAA1912 (Accession XM_055636) is another VGAM2478 host target gene. KIAA1912 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1912, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1912 BINDING SITE, designated SEQ ID:36312, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83960] Another function of VGAM2478 is therefore inhibition of KIAA1912 (Accession XM_055636). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA1912. KIAA1940 (Accession XM_086981) is another VGAM2478 host target gene. KIAA1940 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1940, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1940 BINDING SITE, designated SEQ ID:39006, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83961] Another function of VGAM2478 is therefore inhibition of KIAA1940 (Accession XM_086981). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1940. MGC4309 (Accession NM_024115) is another VGAM2478 host target gene. MGC4309 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC4309, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC4309 BINDING SITE, designated SEQ ID:23568, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM

RNA, also designated SEQ ID:5189.

[83962] Another function of VGAM2478 is therefore inhibition of MGC4309 (Accession NM_024115). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4309. MAP Kinase-interacting Serine/threonine Kinase 1 (MKNK1, Accession NM_003684) is another VGAM2478 host target gene. MKNK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MKNK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MKNK1 BINDING SITE, designated SEQ ID:9793, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83963] Another function of VGAM2478 is therefore inhibition of MAP Kinase-interacting Serine/threonine Kinase 1 (MKNK1, Accession NM_003684). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MKNK1. poly(A) Binding Protein, Cytoplasmic 5 (PABPC5, Accession NM_080832) is another VGAM2478 host target

gene. PABPC5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PABPC5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PABPC5 BINDING SITE, designated SEQ ID:28097, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83964] Another function of VGAM2478 is therefore inhibition of poly(A) Binding Protein, Cytoplasmic 5 (PABPC5, Accession NM_080832). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PABPC5. Phosphatidylinositol-4-phosphate 5-kinase, Type II, Beta (PIP5K2B, Accession NM_003559) is another VGAM2478 host target gene. PIP5K2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIP5K2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIP5K2B BINDING SITE, designated SEQ ID:9612, to the nucleotide sequence of VGAM2478 RNA,

herein designated VGAM RNA, also designated SEQ ID:5189.

[83965] Another function of VGAM2478 is therefore inhibition of Phosphatidylinositol-4-phosphate 5-kinase, Type II, Beta (PIP5K2B, Accession NM_003559). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIP5K2B. SCYD1 (Accession XM_165650) is another VGAM2478 host target gene. SCYD1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCYD1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCYD1 BINDING SITE, designated SEQ ID:43710, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83966] Another function of VGAM2478 is therefore inhibition of SCYD1 (Accession XM_165650). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCYD1. SEC14-like 1 (S. cerevisiae) (SEC14L1, Accession NM_003003) is another VGAM2478 host target gene.

SEC14L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC14L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC14L1 BINDING SITE, designated SEQ ID:8904, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83967] Another function of VGAM2478 is therefore inhibition of SEC14-like 1 (S. cerevisiae) (SEC14L1, Accession NM_003003). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC14L1. SMURF2 (Accession NM_022739) is another VGAM2478 host target gene. SMURF2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SMURF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMURF2 BINDING SITE, designated SEQ ID:22946, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ

ID:5189.

[83968] Another function of VGAM2478 is therefore inhibition of SMURF2 (Accession NM_022739). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMURF2. LOC115704 (Accession XM_056533) is another VGAM2478 host target gene. LOC115704 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC115704, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC115704 BINDING SITE, designated SEQ ID:36402, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83969] Another function of VGAM2478 is therefore inhibition of LOC115704 (Accession XM_056533). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC115704. LOC124602 (Accession XM_058829) is another VGAM2478 host target gene. LOC124602 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC124602, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124602 BINDING SITE, designated SEQ ID:36760, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83970] Another function of VGAM2478 is therefore inhibition of LOC124602 (Accession XM_058829). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124602. LOC147299 (Accession XM_085763) is another VGAM2478 host target gene. LOC147299 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC147299, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147299 BINDING SITE, designated SEQ ID:38332, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83971] Another function of VGAM2478 is therefore inhibition of LOC147299 (Accession XM_085763). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC147299. LOC149194 (Accession XM_086458) is another VGAM2478 host target gene. LOC149194 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149194, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149194 BINDING SITE, designated SEQ ID:38671, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83972] Another function of VGAM2478 is therefore inhibition of LOC149194 (Accession XM_086458). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149194. LOC151521 (Accession XM_098076) is another VGAM2478 host target gene. LOC151521 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151521, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151521 BINDING SITE, designated SEQ ID:41367, to

the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83973] Another function of VGAM2478 is therefore inhibition of LOC151521 (Accession XM_098076). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151521. LOC157349 (Accession XM_088298) is another VGAM2478 host target gene. LOC157349 BINDING SITE1 through LOC157349 BINDING SITE3 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by LOC157349, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC157349 BINDING SITE1 through LOC157349 BINDING SITE3, designated SEQ ID:39590, SEQ ID:39591 and SEQ ID:39592 respectively, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83974] Another function of VGAM2478 is therefore inhibition of LOC157349 (Accession XM_088298). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157349. LOC220110 (Accession XM_167882) is an-

other VGAM2478 host target gene. LOC220110 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC220110, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC220110 BINDING SITE, designated SEQ ID:44894, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83975] Another function of VGAM2478 is therefore inhibition of LOC220110 (Accession XM_167882). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC220110. LOC222031 (Accession XM_168371) is another VGAM2478 host target gene. LOC222031 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC222031, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222031 BINDING SITE, designated SEQ ID:45133, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83976] Another function of VGAM2478 is therefore inhibition of LOC222031 (Accession XM_168371). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC222031. LOC92578 (Accession XM_045900) is another VGAM2478 host target gene. LOC92578 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92578, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92578 BINDING SITE, designated SEQ ID:34607, to the nucleotide sequence of VGAM2478 RNA, herein designated VGAM RNA, also designated SEQ ID:5189.

[83977] Another function of VGAM2478 is therefore inhibition of LOC92578 (Accession XM_045900). Accordingly, utilities of VGAM2478 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92578. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2479 (VGAM2479) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[83978] VGAM2479 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2479 was detected is described hereinabove with reference to Figs. 1-8.

[83979] VGAM2479 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2479 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[83980] VGAM2479 gene encodes a VGAM2479 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2479 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2479 precursor RNA is designated SEQ ID:2465, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2465 is located at position 167759 relative to the genome of Mouse Cytomegalovirus 1.

[83981] VGAM2479 precursor RNA folds onto itself, forming VGAM2479 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[83982] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2479 folded precursor RNA into VGAM2479 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 42%) nucleotide sequence of VGAM2479 RNA is designated SEQ ID:5190, and is provided hereinbelow with reference to the sequence listing part.

[83983] VGAM2479 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2479 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2479 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[83984] VGAM2479 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2479 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2479 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2479 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2479 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[83985] The complementary binding of VGAM2479 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2479 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2479 host target RNA into VGAM2479 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[83986] It is appreciated that VGAM2479 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2479 host target genes. The mRNA of each one of this plurality of VGAM2479 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2479 RNA, herein designated VGAM RNA, and which when bound by VGAM2479 RNA causes inhibition of translation of respective one or more VGAM2479 host target proteins.

[83987] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2479 gene, herein designated VGAM GENE, on one or more VGAM2479 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[83988] It is yet further appreciated that a function of VGAM2479 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2479 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2479 correlate with, and may be deduced from, the identity of the host target genes which VGAM2479 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[83989] Nucleotide sequences of the VGAM2479 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2479 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2479 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2479 are further described hereinbelow with reference to Table 1.

[83990] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2479 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2479 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[83991] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2479 gene, herein designated VGAM is inhibition of expression of VGAM2479 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2479 correlate with, and may be deduced from, the identity of the target genes which VGAM2479 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[83992] Vasoactive Intestinal Peptide Receptor 1 (VIPR1, Accession NM_004624) is a VGAM2479 host target gene. VIPR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VIPR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VIPR1 BINDING SITE, designated SEQ ID:10994, to the nucleotide sequence of VGAM2479 RNA, herein designated VGAM RNA, also designated SEQ ID:5190.

[83993] A function of VGAM2479 is therefore inhibition of Vasoactive Intestinal Peptide Receptor 1 (VIPR1, Accession NM_004624), a gene which binds vip and is mediated by g proteins which activate adenylyl cyclase. Accordingly, utilities of VGAM2479 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VIPR1. The function of VIPR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM548.DKFZp762E1511 (Accession XM_003460) is another VGAM2479 host target gene. DKFZp762E1511 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

DKFZp762E1511, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZp762E1511 BINDING SITE, designated SEQ ID:29931, to the nucleotide sequence of VGAM2479 RNA, herein designated VGAM RNA, also designated SEQ ID:5190.

[83994] Another function of VGAM2479 is therefore inhibition of DKFZp762E1511 (Accession XM_003460). Accordingly, utilities of VGAM2479 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZp762E1511. LOC123242 (Accession XM_063548) is another VGAM2479 host target gene. LOC123242 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC123242, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC123242 BINDING SITE, designated SEQ ID:37245, to the nucleotide sequence of VGAM2479 RNA, herein designated VGAM RNA, also designated SEQ ID:5190.

[83995] Another function of VGAM2479 is therefore inhibition of

LOC123242 (Accession XM_063548). Accordingly, utilities of VGAM2479 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC123242. LOC139248 (Accession XM_066582) is another VGAM2479 host target gene. LOC139248 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC139248, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC139248 BINDING SITE, designated SEQ ID:37337, to the nucleotide sequence of VGAM2479 RNA, herein designated VGAM RNA, also designated SEQ ID:5190.

[83996] Another function of VGAM2479 is therefore inhibition of LOC139248 (Accession XM_066582). Accordingly, utilities of VGAM2479 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC139248. LOC196955 (Accession XM_085210) is another VGAM2479 host target gene. LOC196955 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC196955, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC196955 BINDING SITE, designated SEQ ID:37937, to the nucleotide sequence of VGAM2479 RNA, herein designated VGAM RNA, also designated SEQ ID:5190.

[83997] Another function of VGAM2479 is therefore inhibition of LOC196955 (Accession XM_085210). Accordingly, utilities of VGAM2479 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196955. LOC253216 (Accession XM_170765) is another VGAM2479 host target gene. LOC253216 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253216, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253216 BINDING SITE, designated SEQ ID:45516, to the nucleotide sequence of VGAM2479 RNA, herein designated VGAM RNA, also designated SEQ ID:5190.

[83998] Another function of VGAM2479 is therefore inhibition of LOC253216 (Accession XM_170765). Accordingly, utilities of VGAM2479 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253216. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2480 (VGAM2480) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[83999] VGAM2480 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2480 was detected is described hereinabove with reference to Figs. 1-8.

[84000] VGAM2480 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2480 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84001] VGAM2480 gene encodes a VGAM2480 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2480 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2480 precursor RNA is designated SEQ ID:2466, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2466 is located at position 131305 relative to the genome of Mouse Cytomegalovirus 1.

[84002] VGAM2480 precursor RNA folds onto itself, forming VGAM2480 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84003] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2480 folded precursor RNA into VGAM2480 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2480 RNA is designated SEQ ID:5191, and is provided hereinbelow with reference to the sequence listing part.

[84004] VGAM2480 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2480 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2480 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84005] VGAM2480 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2480 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2480 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2480 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2480 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84006] The complementary binding of VGAM2480 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2480 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2480 host target RNA into VGAM2480 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84007] It is appreciated that VGAM2480 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2480 host target genes. The mRNA of each one of this plurality of VGAM2480 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2480 RNA, herein designated VGAM RNA, and which when bound by VGAM2480 RNA causes inhibition of translation of respective one or more

VGAM2480 host target proteins.

[84008] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2480 gene, herein designated VGAM GENE, on one or more VGAM2480 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84009] It is yet further appreciated that a function of VGAM2480 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2480 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1.

Specific functions, and accordingly utilities, of VGAM2480 correlate with, and may be deduced from, the identity of the host target genes which VGAM2480 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84010] Nucleotide sequences of the VGAM2480 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2480 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2480 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2480 are further described hereinbelow with reference to Table 1.

[84011] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2480 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2480 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84012] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2480 gene, herein designated VGAM is inhibition of expression of VGAM2480 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2480 correlate with, and may be deduced from, the identity of the target genes which VGAM2480 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84013] LOC155376 (Accession XM_088240) is a VGAM2480 host target gene. LOC155376 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC155376, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155376 BINDING SITE, designated SEQ ID:39563, to the nucleotide sequence of VGAM2480 RNA, herein designated VGAM RNA, also designated SEQ ID:5191.

[84014] A function of VGAM2480 is therefore inhibition of LOC155376 (Accession XM_088240). Accordingly, utilities of VGAM2480 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155376. LOC219513 (Accession XM_169166) is another VGAM2480 host target gene. LOC219513 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219513, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219513 BINDING SITE, designated SEQ ID:45289, to the nucleotide sequence of VGAM2480 RNA, herein designated VGAM RNA, also designated SEQ ID:5191.

[84015] Another function of VGAM2480 is therefore inhibition of LOC219513 (Accession XM_169166). Accordingly, utilities of VGAM2480 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219513. LOC222233 (Accession XM_168560) is another VGAM2480 host target gene. LOC222233 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC222233, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC222233 BINDING SITE, designated SEQ ID:45241, to the nucleotide sequence of VGAM2480 RNA, herein designated VGAM RNA, also designated SEQ ID:5191.

[84016] Another function of VGAM2480 is therefore inhibition of LOC222233 (Accession XM_168560). Accordingly, utilities of VGAM2480 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC222233. LOC253532 (Accession XM_171152) is another VGAM2480 host target gene. LOC253532 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253532, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253532 BINDING SITE, designated SEQ ID:45949, to the nucleotide sequence of VGAM2480 RNA, herein designated VGAM RNA, also designated SEQ ID:5191.

[84017] Another function of VGAM2480 is therefore inhibition of LOC253532 (Accession XM_171152). Accordingly, utilities of VGAM2480 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253532. LOC254875 (Accession XM_171170) is another VGAM2480 host target gene. LOC254875 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254875, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC254875 BINDING SITE, designated SEQ ID:45953, to the nucleotide sequence of VGAM2480 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5191.

[84018] Another function of VGAM2480 is therefore inhibition of LOC254875 (Accession XM_171170). Accordingly, utilities of VGAM2480 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254875. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2481 (VGAM2481) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84019] VGAM2481 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2481 was detected is described hereinabove with reference to Figs. 1-8.

[84020] VGAM2481 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2481 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84021] VGAM2481 gene encodes a VGAM2481 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other

miRNA genes, and unlike most ordinary genes, VGAM2481 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2481 precursor RNA is designated SEQ ID:2467, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2467 is located at position 96988 relative to the genome of Mouse Cytomegalovirus 1.

[84022] VGAM2481 precursor RNA folds onto itself, forming VGAM2481 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84023] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2481 folded precursor RNA into VGAM2481 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex

comprising an enzyme called Dicer together with other necessary proteins. A probable (over 68%) nucleotide sequence of VGAM2481 RNA is designated SEQ ID:5192, and is provided hereinbelow with reference to the sequence listing part.

[84024] VGAM2481 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2481 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2481 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84025] VGAM2481 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2481 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2481 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and

BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2481 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2481 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84026] The complementary binding of VGAM2481 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2481 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2481 host target RNA into VGAM2481 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84027] It is appreciated that VGAM2481 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2481 host target genes. The mRNA of

each one of this plurality of VGAM2481 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2481 RNA, herein designated VGAM RNA, and which when bound by VGAM2481 RNA causes inhibition of translation of respective one or more VGAM2481 host target proteins.

[84028] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2481 gene, herein designated VGAM GENE, on one or more VGAM2481 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science

294,779 (2001)).

[84029] It is yet further appreciated that a function of VGAM2481 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2481 correlate with, and may be deduced from, the identity of the host target genes which VGAM2481 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84030] Nucleotide sequences of the VGAM2481 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2481 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2481 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2481 are further described hereinbelow with reference to Table 1.

[84031] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2481 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2481 RNA,

herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84032] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2481 gene, herein designated VGAM is inhibition of expression of VGAM2481 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2481 correlate with, and may be deduced from, the identity of the target genes which VGAM2481 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84033] EH-domain Containing 2 (EHD2, Accession NM_014601) is a VGAM2481 host target gene. EHD2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EHD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EHD2 BINDING SITE, designated SEQ ID:15961, to the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, also designated SEQ ID:5192.

[84034] A function of VGAM2481 is therefore inhibition of EH-domain Containing 2 (EHD2, Accession NM_014601). Accordingly, utilities of VGAM2481 include diagnosis, pre-

vention and treatment of diseases and clinical conditions associated with EHD2. NORE1 (Accession NM_031437) is another VGAM2481 host target gene. NORE1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NORE1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NORE1 BINDING SITE, designated SEQ ID:25442, to the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, also designated SEQ ID:5192.

[84035] Another function of VGAM2481 is therefore inhibition of NORE1 (Accession NM_031437), a gene which may modulate intracellular signal transduction pathways. Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NORE1. The function of NORE1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM276.Nuclear Receptor Subfamily 5, Group A, Member 2 (NR5A2, Accession NM_003822) is another VGAM2481 host target gene. NR5A2 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by NR5A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NR5A2 BINDING SITE, designated SEQ ID:9913, to the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, also designated SEQ ID:5192.

[84036] Another function of VGAM2481 is therefore inhibition of Nuclear Receptor Subfamily 5, Group A, Member 2 (NR5A2, Accession NM_003822), a gene which is a member of nuclear receptor superfamily of trancriptional activators and activates the hepatitis B virus (HBV) promoter. Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NR5A2. The function of NR5A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM375.DKFZP566H073 (Accession NM_015528) is another VGAM2481 host target gene. DKFZP566H073 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP566H073,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP566H073 BINDING SITE, designated SEQ ID:17796, to the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, also designated SEQ ID:5192.

[84037] Another function of VGAM2481 is therefore inhibition of DKFZP566H073 (Accession NM_015528). Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP566H073. FLJ20514 (Accession NM_017856) is another VGAM2481 host target gene. FLJ20514 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ20514, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20514 BINDING SITE, designated SEQ ID:19533, to the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, also designated SEQ ID:5192.

[84038] Another function of VGAM2481 is therefore inhibition of FLJ20514 (Accession NM_017856). Accordingly, utilities of

VGAM2481 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20514. KIAA1879 (Accession XM_056635) is another VGAM2481 host target gene. KIAA1879 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1879, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1879 BINDING SITE, designated SEQ ID:36413, to the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, also designated SEQ ID:5192.

[84039] Another function of VGAM2481 is therefore inhibition of KIAA1879 (Accession XM_056635). Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1879. Protein Tyrosine Phosphatase, Non-receptor Type Substrate 1 (PTPNS1, Accession NM_080792) is another VGAM2481 host target gene. PTPNS1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTPNS1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of PTPNS1 BINDING SITE, designated SEQ ID:28053, to the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, also designated SEQ ID:5192.

[84040] Another function of VGAM2481 is therefore inhibition of Protein Tyrosine Phosphatase, Non-receptor Type Substrate 1 (PTPNS1, Accession NM_080792). Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTPNS1. LOC124930 (Accession XM_058867) is another VGAM2481 host target gene. LOC124930 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC124930, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124930 BINDING SITE, designated SEQ ID:36768, to the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, also designated SEQ ID:5192.

[84041] Another function of VGAM2481 is therefore inhibition of LOC124930 (Accession XM_058867). Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC124930. LOC147160 (Accession XM_097202) is another VGAM2481 host target gene. LOC147160 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147160, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147160 BINDING SITE, designated SEQ ID:40808, to the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, also designated SEQ ID:5192.

[84042] Another function of VGAM2481 is therefore inhibition of LOC147160 (Accession XM_097202). Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147160. LOC147669 (Accession XM_097262) is another VGAM2481 host target gene. LOC147669 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147669, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147669 BINDING SITE, designated SEQ ID:40854, to the nucleotide sequence of VGAM2481 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5192.

[84043] Another function of VGAM2481 is therefore inhibition of LOC147669 (Accession XM_097262). Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147669. LOC163682 (Accession XM_099402) is another VGAM2481 host target gene. LOC163682 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC163682, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC163682 BINDING SITE, designated SEQ ID:42094, to the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, also designated SEQ ID:5192.

[84044] Another function of VGAM2481 is therefore inhibition of LOC163682 (Accession XM_099402). Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC163682. LOC90342 (Accession XM_031009) is another VGAM2481 host target gene. LOC90342 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90342, corre-

sponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90342 BINDING SITE, designated SEQ ID:31250, to the nucleotide sequence of VGAM2481 RNA, herein designated VGAM RNA, also designated SEQ ID:5192.

[84045] Another function of VGAM2481 is therefore inhibition of LOC90342 (Accession XM_031009). Accordingly, utilities of VGAM2481 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90342. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2482 (VGAM2482) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84046] VGAM2482 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2482 was detected is described hereinabove with reference to Figs. 1-8.

[84047] VGAM2482 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus

1. VGAM2482 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84048] VGAM2482 gene encodes a VGAM2482 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2482 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2482 precursor RNA is designated SEQ ID:2468, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2468 is located at position 182861 relative to the genome of Mouse Cytomegalovirus 1.

[84049] VGAM2482 precursor RNA folds onto itself, forming VGAM2482 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84050] An enzyme complex designated DICER COMPLEX, `dices`

the VGAM2482 folded precursor RNA into VGAM2482 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2482 RNA is designated SEQ ID:5193, and is provided hereinbelow with reference to the sequence listing part.

[84051] VGAM2482 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2482 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2482 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84052] VGAM2482 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2482 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nu-

cleotide sequence of VGAM2482 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2482 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2482 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84053] The complementary binding of VGAM2482 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2482 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2482 host target RNA into VGAM2482 host target protein,

herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84054] It is appreciated that VGAM2482 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2482 host target genes. The mRNA of each one of this plurality of VGAM2482 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2482 RNA, herein designated VGAM RNA, and which when bound by VGAM2482 RNA causes inhibition of translation of respective one or more VGAM2482 host target proteins.

[84055] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2482 gene, herein designated VGAM GENE, on one or more VGAM2482 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are

also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84056] It is yet further appreciated that a function of VGAM2482 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2482 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2482 correlate with, and may be deduced from, the identity of the host target genes which VGAM2482 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84057] Nucleotide sequences of the VGAM2482 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2482 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2482 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2482 are further described hereinbelow with reference to Table 1.

[84058] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2482 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2482 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84059] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2482 gene, herein designated VGAM is inhibition of expression of VGAM2482 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2482 correlate with, and may be deduced from, the identity of the target genes which VGAM2482 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84060] DiGeorge Syndrome Critical Region Gene 2 (DGCR2, Accession NM_005137) is a VGAM2482 host target gene. DGCR2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DGCR2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGCR2 BINDING SITE, designated SEQ

ID:11614, to the nucleotide sequence of VGAM2482 RNA, herein designated VGAM RNA, also designated SEQ ID:5193.

[84061] A function of VGAM2482 is therefore inhibition of DiGeorge Syndrome Critical Region Gene 2 (DGCR2, Accession NM_005137), a gene which could intervene in cell-cell or cell-matrix interactions. Accordingly, utilities of VGAM2482 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGCR2. The function of DGCR2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1485.Arginyl Aminopeptidase (aminopeptidase B)-like 1 (RNPEPL1, Accession NM_018226) is another VGAM2482 host target gene. RNPEPL1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNPEPL1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNPEPL1 BINDING SITE, designated SEQ ID:20161, to the nucleotide sequence of VGAM2482 RNA, herein designated VGAM RNA, also designated SEQ ID:5193.

[84062] Another function of VGAM2482 is therefore inhibition of Arginyl Aminopeptidase (aminopeptidase B)-like 1 (RNPEPL1, Accession NM_018226). Accordingly, utilities of VGAM2482 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNPEPL1. Cyclin M1 (CNNM1, Accession NM_020348) is another VGAM2482 host target gene. CNNM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CNNM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CNNM1 BINDING SITE, designated SEQ ID:21608, to the nucleotide sequence of VGAM2482 RNA, herein designated VGAM RNA, also designated SEQ ID:5193.

[84063] Another function of VGAM2482 is therefore inhibition of Cyclin M1 (CNNM1, Accession NM_020348). Accordingly, utilities of VGAM2482 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CNNM1. DKFZP564D166 (Accession NM_030658) is another VGAM2482 host target gene. DKFZP564D166 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DK-

FZP564D166, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564D166 BINDING SITE, designated SEQ ID:24991, to the nucleotide sequence of VGAM2482 RNA, herein designated VGAM RNA, also designated SEQ ID:5193.

[84064] Another function of VGAM2482 is therefore inhibition of DKFZP564D166 (Accession NM_030658). Accordingly, utilities of VGAM2482 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564D166. FLJ12057 (Accession NM_024768) is another VGAM2482 host target gene. FLJ12057 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ12057, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12057 BINDING SITE, designated SEQ ID:24125, to the nucleotide sequence of VGAM2482 RNA, herein designated VGAM RNA, also designated SEQ ID:5193.

[84065] Another function of VGAM2482 is therefore inhibition of FLJ12057 (Accession NM_024768). Accordingly, utilities of

VGAM2482 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12057. SS-56 (Accession XM_006063) is another VGAM2482 host target gene. SS-56 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SS-56, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SS-56 BINDING SITE, designated SEQ ID:29989, to the nucleotide sequence of VGAM2482 RNA, herein designated VGAM RNA, also designated SEQ ID:5193.

[84066] Another function of VGAM2482 is therefore inhibition of SS-56 (Accession XM_006063). Accordingly, utilities of VGAM2482 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SS-56. LOC147515 (Accession XM_097243) is another VGAM2482 host target gene. LOC147515 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147515, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC147515 BINDING SITE, designated SEQ ID:40842, to the nucleotide sequence of VGAM2482 RNA, herein designated VGAM RNA, also designated SEQ ID:5193.

[84067] Another function of VGAM2482 is therefore inhibition of LOC147515 (Accession XM_097243). Accordingly, utilities of VGAM2482 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC147515. LOC92841 (Accession XM_047583) is another VGAM2482 host target gene. LOC92841 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC92841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92841 BINDING SITE, designated SEQ ID:35003, to the nucleotide sequence of VGAM2482 RNA, herein designated VGAM RNA, also designated SEQ ID:5193.

[84068] Another function of VGAM2482 is therefore inhibition of LOC92841 (Accession XM_047583). Accordingly, utilities of VGAM2482 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92841. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2483 (VGAM2483) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84069] VGAM2483 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2483 was detected is described hereinabove with reference to Figs. 1-8.

[84070] VGAM2483 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2483 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84071] VGAM2483 gene encodes a VGAM2483 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2483 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2483 precursor RNA is designated SEQ ID:2469, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2469 is located at position 166603 relative to the

genome of Mouse Cytomegalovirus 1.

[84072] VGAM2483 precursor RNA folds onto itself, forming VGAM2483 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84073] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2483 folded precursor RNA into VGAM2483 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 52%) nucleotide sequence of VGAM2483 RNA is designated SEQ ID:5194, and is provided hereinbelow with reference to the sequence listing part.

[84074] VGAM2483 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2483 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2483 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84075] VGAM2483 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2483 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2483 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2483 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2483 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84076] The complementary binding of VGAM2483 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2483 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2483 host target RNA into VGAM2483 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84077] It is appreciated that VGAM2483 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2483 host target genes. The mRNA of each one of this plurality of VGAM2483 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2483 RNA, herein designated VGAM RNA, and which when bound by VGAM2483 RNA causes inhibition of translation of respective one or more VGAM2483 host target proteins.

[84078] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2483 gene, herein designated VGAM GENE, on one or more VGAM2483 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84079] It is yet further appreciated that a function of VGAM2483 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2483

correlate with, and may be deduced from, the identity of the host target genes which VGAM2483 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84080] Nucleotide sequences of the VGAM2483 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2483 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2483 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2483 are further described hereinbelow with reference to Table 1.

[84081] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2483 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2483 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84082] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2483 gene, herein designated VGAM is inhibition of expression of VGAM2483 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2483 correlate with, and may be deduced

from, the identity of the target genes which VGAM2483 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84083] BTG Family, Member 2 (BTG2, Accession NM_006763) is a VGAM2483 host target gene. BTG2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BTG2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BTG2 BINDING SITE, designated SEQ ID:13628, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84084] A function of VGAM2483 is therefore inhibition of BTG Family, Member 2 (BTG2, Accession NM_006763). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BTG2. CDP-diacylglycerol Synthase (phosphatidate cytidylyltransferase) 2 (CDS2, Accession NM_003818) is another VGAM2483 host target gene. CDS2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDS2, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDS2 BINDING SITE, designated SEQ ID:9911, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84085] Another function of VGAM2483 is therefore inhibition of CDP-diacylglycerol Synthase (phosphatidate cytidylyltransferase) 2 (CDS2, Accession NM_003818), a gene which is a key regulator of the amount of PIP2 available for signaling. Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDS2. The function of CDS2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM900.Fibulin 1 (FBLN1, Accession NM_006485) is another VGAM2483 host target gene. FBLN1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FBLN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FBLN1 BINDING SITE, designated SEQ ID:13212, to the nucleotide sequence of

VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84086] Another function of VGAM2483 is therefore inhibition of Fibulin 1 (FBLN1, Accession NM_006485), a gene which secreted glycoprotein; has EGF-like repeats, similar to anaphylatoxins C3a, C4a, and C5a. Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FBLN1. The function of FBLN1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1770.Glycyl-tRNA Synthetase (GARS, Accession NM_002047) is another VGAM2483 host target gene. GARS BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GARS, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GARS BINDING SITE, designated SEQ ID:7797, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84087] Another function of VGAM2483 is therefore inhibition of Glycyl-tRNA Synthetase (GARS, Accession NM_002047), a

gene which functions in protein biosynthesis. Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GARS. The function of GARS and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM113.Glyoxalase I (GLO1, Accession NM_006708) is another VGAM2483 host target gene. GLO1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GLO1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GLO1 BINDING SITE, designated SEQ ID:13532, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84088] Another function of VGAM2483 is therefore inhibition of Glyoxalase I (GLO1, Accession NM_006708), a gene which converts methylglyoxal and glutathione to S-lactoylglutathione. Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GLO1. The function of GLO1 and its association with various diseases and clinical

conditions, has been established by previous studies, as described hereinabove with reference to VGAM786.Matrilin 1, Cartilage Matrix Protein (MATN1, Accession NM_002379) is another VGAM2483 host target gene. MATN1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MATN1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MATN1 BINDING SITE, designated SEQ ID:8195, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84089] Another function of VGAM2483 is therefore inhibition of Matrilin 1, Cartilage Matrix Protein (MATN1, Accession NM_002379), a gene which a major component of the extracellular matrix of nonarticular cartilage. Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MATN1. The function of MATN1 has been established by previous studies. Cartilage matrix protein is a major component of the extracellular matrix of nonarticular cartilage. Jenkins et al. (1990) used a partial chicken CMP

cDNA probe to isolate 3 overlapping human genomic clones. From one of these clones, a probe containing 2 human CMP exons was isolated and used to map the gene to 1p35 by a combination of Southern blot analysis of somatic cell hybrids and in situ chromosomal hybridization. The genomic probe was also used to screen a human retina cDNA library. The protein sequence predicted by the cDNA clones has 496 amino acids, including a 22-residue signal peptide. The structure of the CMP gene (also symbolized CRTM) and polypeptide were strikingly similar in the chicken and in the human. The human gene spans 12 kb and has 8 exons and 7 introns. By linkage studies, Loughlin et al. (1994) demonstrated that the CRTM gene segregated independently of several heritable chondrodysplasias: hypochondroplasia, achondroplasia, autosomal dominant SED tarda, and multiple epiphyseal dysplasia. CMP was alternatively named matrilin-1 by Deak et al. (1997) when they discovered matrilin-2 (OMIM Ref. No. 602108). Wagener et al. (1997) found that matrilin-1 is a trimer of identical ellipsoid subunits assembled via their C-terminal extension domains in a coiled-coil alpha-helix. The matrilins, including matrilin-2 and matrilin-3 (OMIM Ref. No. 602109), represent a subfamily

of extracellular matrix proteins containing the von Willebrand factor type A (vWFA)-like domain. (The vWFA-like domain was first described in von Willebrand factor (OMIM Ref. No. 193400) where it plays a key role in promoting platelet adhesion to the subendothelin. Several vWFA-like domains have been implicated in interactions with collagen.) In some patients with rheumatoid arthritis (RA; 180300) and relapsing polychondritis (RP), an immune response against cartilage collagen II can be detected. However, study of responses against noncollagenous components of cartilage are limited. If an autoimmune response to cartilage proteins is involved in RA and RP, the different patterns of the affected tissues can best be explained if the respective targets are proteins with specific tissue distributions. Whereas RA preferentially affects diarthrodial joints, RP is characterized by inflammatory attacks on cartilage in different organs, and, preferentially, in the perichondrial layer of cartilage. The inflammatory infiltrates consist of neutrophils, lymphocytes, macrophages, and plasma cells. In early lesions, eosinophils can be observed close to the affected cartilage. A classic appearance of the patient with RP is 'saddle nose,' caused by erosive inflammation of the nasal septum. Another typical symptom is

an inflamed external ear (89% of cases), which in some instances leads to ossified ear cartilages (OMIM Ref. No. 165670). Occasionally, joints are affected as a seronegative nonerosive arthritis. The most serious complication of RP is the involvement of the laryngotracheal cartilage, sometimes leading to lethal breathing difficulties. Early signs of airway involvement are cough, dysphonia, and tenderness over the thyroid cartilage. Remarkably, RP is associated with the same HLA haplotype (DR4) as RA, which carries with it approximately the same relative risk (Zeuner et al., 1997; Lang et al., 1993). To investigate whether the tissue distribution of relapsing polychondritis may be explained by a specific immune response, Hansson et al. (1999) immunized rats with matrilin-1, which is expressed predominantly in tracheal cartilage. After 2 to 3 weeks, some rats developed severe inspiratory stridor. They had swollen noses and/or epistaxis, but showed neither joint nor outer ear affection. The inflammatory lesions involved chronic active erosions of cartilage. Female rats were more susceptible than males. The disease susceptibility was controlled by MHC genes, some haplotypes being high responders and others resistant, and by non-MHC genes as well, as indicated by strain differences (the

LEW strain was susceptible, and the DA strain resistant). All strains mounted a pronounced IgG response to matrilin-1. The findings suggested that different cartilage proteins are involved in pathogenic models of RP and RA.

[84090] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84091] Jenkins, R. N.; Osborne-Lawrence, S. L.; Sinclair, A. K.; Eddy, R. L., Jr.; Byers, M. G.; Shows, T. B.; Duby, A. D. : Structure and chromosomal location of the human gene encoding cartilage matrix protein. J. Biol. Chem. 265: 19624-19631, 1990. ; and

[84092] Deak, F.; Piecha, D.; Bachrati, C.; Paulsson, M.; Kiss, I. : Primary structure and expression of matrilin-2, the closest relative of cartilage matrix protein within the von Willebrand fa.

[84093] Further studies establishing the function and utilities of MATN1 are found in John Hopkins OMIM database record ID 115437, and in sited publications numbered 12587-12591, 1258 and 12592-12594 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Proteoglycan 1, Secretory Granule (PRG1, Accession NM_002727) is another VGAM2483 host

target gene. PRG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PRG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PRG1 BINDING SITE, designated SEQ ID:8591, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84094] Another function of VGAM2483 is therefore inhibition of Proteoglycan 1, Secretory Granule (PRG1, Accession NM_002727), a gene which protects cells from apoptosis induced by FAS or TNFA. Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRG1. The function of PRG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2465.Pituitary Tumor-transforming 1 Interacting Protein (PTTG1IP, Accession NM_004339) is another VGAM2483 host target gene. PTTG1IP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PTTG1IP, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PTTG1IP BINDING SITE, designated SEQ ID:10536, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84095] Another function of VGAM2483 is therefore inhibition of Pituitary Tumor-transforming 1 Interacting Protein (PTTG1IP, Accession NM_004339), a gene which facilitates the translocation of PTTG to the nucleus. Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PTTG1IP. The function of PTTG1IP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM131.WTAP (Accession NM_004906) is another VGAM2483 host target gene. WTAP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by WTAP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of WTAP BINDING SITE, designated SEQ ID:11345, to the nu-

cleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84096] Another function of VGAM2483 is therefore inhibition of WTAP (Accession NM_004906), a gene which plays a role in both transcriptional and posttranscriptional regulation of certain cellular genes. Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with WTAP. The function of WTAP and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM874.Cystatin F (leukocystatin) (CST7, Accession NM_003650) is another VGAM2483 host target gene. CST7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CST7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CST7 BINDING SITE, designated SEQ ID:9726, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84097] Another function of VGAM2483 is therefore inhibition of Cystatin F (leukocystatin) (CST7, Accession NM_003650).

Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CST7. Cytochrome P450, Subfamily IIS, Polypeptide 1 (CYP2S1, Accession NM_030622) is another VGAM2483 host target gene. CYP2S1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP2S1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP2S1 BINDING SITE, designated SEQ ID:24965, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84098] Another function of VGAM2483 is therefore inhibition of Cytochrome P450, Subfamily IIS, Polypeptide 1 (CYP2S1, Accession NM_030622). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP2S1. DKFZP564I0422 (Accession NM_031435) is another VGAM2483 host target gene. DKFZP564I0422 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP564I0422, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564I0422 BINDING SITE, designated SEQ ID:25436, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84099] Another function of VGAM2483 is therefore inhibition of DKFZP564I0422 (Accession NM_031435). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564I0422. Dedicator of Cyto-kinesis 3 (DOCK3, Accession XM_039259) is another VGAM2483 host target gene. DOCK3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DOCK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DOCK3 BINDING SITE, designated SEQ ID:33037, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84100] Another function of VGAM2483 is therefore inhibition of Dedicator of Cyto-kinesis 3 (DOCK3, Accession

XM_039259). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DOCK3. FLJ11259 (Accession NM_018370) is another VGAM2483 host target gene. FLJ11259 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ11259, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ11259 BINDING SITE, designated SEQ ID:20385, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84101] Another function of VGAM2483 is therefore inhibition of FLJ11259 (Accession NM_018370). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ11259. FLJ13197 (Accession NM_024614) is another VGAM2483 host target gene. FLJ13197 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13197, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the com-

plementarity of the nucleotide sequences of FLJ13197 BINDING SITE, designated SEQ ID:23874, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84102] Another function of VGAM2483 is therefore inhibition of FLJ13197 (Accession NM_024614). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13197. KIAA0226 (Accession XM_032901) is another VGAM2483 host target gene. KIAA0226 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0226, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0226 BINDING SITE, designated SEQ ID:31788, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84103] Another function of VGAM2483 is therefore inhibition of KIAA0226 (Accession XM_032901). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0226. KIAA1432 (Accession XM_039698) is another

VGAM2483 host target gene. KIAA1432 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KIAA1432, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1432 BINDING SITE, designated SEQ ID:33150, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84104] Another function of VGAM2483 is therefore inhibition of KIAA1432 (Accession XM_039698). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1432. KIAA1530 (Accession XM_042661) is another VGAM2483 host target gene. KIAA1530 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1530, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1530 BINDING SITE, designated SEQ ID:33736, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84105] Another function of VGAM2483 is therefore inhibition of KIAA1530 (Accession XM_042661). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1530. MGC23445 (Accession NM_144606) is another VGAM2483 host target gene. MGC23445 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC23445, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC23445 BINDING SITE, designated SEQ ID:29420, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84106] Another function of VGAM2483 is therefore inhibition of MGC23445 (Accession NM_144606). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC23445. Phosphatase, Orphan 1 (phospho1, Accession XM_091572) is another VGAM2483 host target gene. phospho1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by phospho1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of phospho1 BINDING SITE, designated SEQ ID:40064, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84107] Another function of VGAM2483 is therefore inhibition of Phosphatase, Orphan 1 (phospho1, Accession XM_091572). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with phospho1. SARM (Accession NM_015077) is another VGAM2483 host target gene. SARM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SARM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SARM BINDING SITE, designated SEQ ID:17464, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84108] Another function of VGAM2483 is therefore inhibition of SARM (Accession NM_015077). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with SARM. SSB-4 (Accession NM_080862) is another VGAM2483 host target gene. SSB-4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SSB-4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SSB-4 BINDING SITE, designated SEQ ID:28106, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84109] Another function of VGAM2483 is therefore inhibition of SSB-4 (Accession NM_080862). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SSB-4. LOC145694 (Accession XM_096838) is another VGAM2483 host target gene. LOC145694 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145694, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145694 BINDING SITE, designated SEQ ID:40558, to

the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84110] Another function of VGAM2483 is therefore inhibition of LOC145694 (Accession XM_096838). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145694. LOC256158 (Accession XM_175125) is another VGAM2483 host target gene. LOC256158 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256158, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256158 BINDING SITE, designated SEQ ID:46629, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84111] Another function of VGAM2483 is therefore inhibition of LOC256158 (Accession XM_175125). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256158. LOC57106 (Accession XM_034377) is another VGAM2483 host target gene. LOC57106 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC57106, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC57106 BINDING SITE, designated SEQ ID:32074, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84112] Another function of VGAM2483 is therefore inhibition of LOC57106 (Accession XM_034377). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC57106. LOC90133 (Accession XM_029323) is another VGAM2483 host target gene. LOC90133 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90133, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90133 BINDING SITE, designated SEQ ID:30869, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84113] Another function of VGAM2483 is therefore inhibition of LOC90133 (Accession XM_029323). Accordingly, utilities

of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90133. LOC91689 (Accession NM_033318) is another VGAM2483 host target gene. LOC91689 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC91689, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91689 BINDING SITE, designated SEQ ID:27157, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84114] Another function of VGAM2483 is therefore inhibition of LOC91689 (Accession NM_033318). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91689. LOC91974 (Accession XM_041974) is another VGAM2483 host target gene. LOC91974 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91974, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC91974 BINDING SITE, designated SEQ ID:33655, to the nucleotide sequence of VGAM2483 RNA, herein designated VGAM RNA, also designated SEQ ID:5194.

[84115] Another function of VGAM2483 is therefore inhibition of LOC91974 (Accession XM_041974). Accordingly, utilities of VGAM2483 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91974. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2484 (VGAM2484) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84116] VGAM2484 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2484 was detected is described hereinabove with reference to Figs. 1-8.

[84117] VGAM2484 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2484 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84118] VGAM2484 gene encodes a VGAM2484 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2484 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2484 precursor RNA is designated SEQ ID:2470, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2470 is located at position 183727 relative to the genome of Mouse Cytomegalovirus 1.

[84119] VGAM2484 precursor RNA folds onto itself, forming VGAM2484 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84120] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2484 folded precursor RNA into VGAM2484 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 80%) nucleotide sequence of VGAM2484 RNA is designated SEQ ID:5195, and is provided hereinbelow with reference to the sequence listing part.

[84121] VGAM2484 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2484 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2484 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84122] VGAM2484 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2484 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2484 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2484 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2484 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84123] The complementary binding of VGAM2484 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2484 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2484 host target RNA into VGAM2484 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84124] It is appreciated that VGAM2484 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2484 host target genes. The mRNA of each one of this plurality of VGAM2484 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2484 RNA, herein designated VGAM RNA, and which when bound by VGAM2484 RNA causes inhibition of translation of respective one or more VGAM2484 host target proteins.

[84125] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2484 gene, herein designated VGAM GENE, on one or more VGAM2484 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84126] It is yet further appreciated that a function of VGAM2484 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2484 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2484 correlate with, and may be deduced from, the identity of the host target genes which VGAM2484 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84127] Nucleotide sequences of the VGAM2484 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2484 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2484 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2484 are further described hereinbelow with reference to Table 1.

[84128] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2484 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2484 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84129] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2484 gene, herein designated VGAM is inhibition of expression of VGAM2484 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2484 correlate with, and may be deduced from, the identity of the target genes which VGAM2484 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84130] FLJ10565 (Accession NM_018140) is a VGAM2484 host target gene. FLJ10565 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10565, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10565 BINDING SITE, designated SEQ ID:19938, to the nucleotide sequence of VGAM2484 RNA, herein designated VGAM RNA, also designated SEQ ID:5195.

[84131] A function of VGAM2484 is therefore inhibition of

FLJ10565 (Accession NM_018140). Accordingly, utilities of VGAM2484 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10565. Neurexophilin 3 (NXPH3, Accession XM_037847) is another VGAM2484 host target gene. NXPH3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NXPH3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NXPH3 BINDING SITE, designated SEQ ID:32712, to the nucleotide sequence of VGAM2484 RNA, herein designated VGAM RNA, also designated SEQ ID:5195.

[84132] Another function of VGAM2484 is therefore inhibition of Neurexophilin 3 (NXPH3, Accession XM_037847). Accordingly, utilities of VGAM2484 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NXPH3. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2485 (VGAM2485) viral gene, which modulates expression of respective host target genes

thereof, the function and utility of which host target genes is known in the art.

[84133] VGAM2485 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2485 was detected is described hereinabove with reference to Figs. 1-8.

[84134] VGAM2485 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2485 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84135] VGAM2485 gene encodes a VGAM2485 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2485 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2485 precursor RNA is designated SEQ ID:2471, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2471 is located at position 214191 relative to the genome of Mouse Cytomegalovirus 1.

[84136] VGAM2485 precursor RNA folds onto itself, forming VGAM2485 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84137] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2485 folded precursor RNA into VGAM2485 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 49%) nucleotide sequence of VGAM2485 RNA is designated SEQ ID:5196, and is provided hereinbelow with reference to the sequence listing part.

[84138] VGAM2485 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2485 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2485 host target RNA comprises three regions, as is typical of mRNA of a pro-

tein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84139] VGAM2485 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2485 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2485 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2485 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2485 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in

the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84140] The complementary binding of VGAM2485 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2485 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2485 host target RNA into VGAM2485 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84141] It is appreciated that VGAM2485 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2485 host target genes. The mRNA of each one of this plurality of VGAM2485 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2485 RNA, herein designated VGAM RNA, and which when bound by VGAM2485 RNA causes inhibition of translation of respective one or more VGAM2485 host target proteins.

[84142] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by

VGAM2485 gene, herein designated VGAM GENE, on one or more VGAM2485 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84143] It is yet further appreciated that a function of VGAM2485 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2485 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2485 correlate with, and may be deduced from, the identity of the host target genes which VGAM2485 binds and inhibits, and the function of these host target genes, as

elaborated hereinbelow.

[84144] Nucleotide sequences of the VGAM2485 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2485 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2485 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2485 are further described hereinbelow with reference to Table 1.

[84145] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2485 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2485 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84146] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2485 gene, herein designated VGAM is inhibition of expression of VGAM2485 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2485 correlate with, and may be deduced from, the identity of the target genes which VGAM2485 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84147] Rho GDP Dissociation Inhibitor (GDI) Alpha (ARHGDIA, Accession NM_004309) is a VGAM2485 host target gene. ARHGDIA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHGDIA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGDIA BINDING SITE, designated SEQ ID:10513, to the nucleotide sequence of VGAM2485 RNA, herein designated VGAM RNA, also designated SEQ ID:5196.

[84148] A function of VGAM2485 is therefore inhibition of Rho GDP Dissociation Inhibitor (GDI) Alpha (ARHGDIA, Accession NM_004309), a gene which is a small guanine nucleotide exchange (GTP/GDP) factor. Accordingly, utilities of VGAM2485 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGDIA. The function of ARHGDIA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM435.Solute Carrier Family 20 (phosphate transporter), Member 2 (SLC20A2, Accession NM_006749) is another VGAM2485 host target gene.

SLC20A2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SLC20A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC20A2 BINDING SITE, designated SEQ ID:13600, to the nucleotide sequence of VGAM2485 RNA, herein designated VGAM RNA, also designated SEQ ID:5196.

[84149] Another function of VGAM2485 is therefore inhibition of Solute Carrier Family 20 (phosphate transporter), Member 2 (SLC20A2, Accession NM_006749), a gene which is a sodium-phosphate symporter. Accordingly, utilities of VGAM2485 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC20A2. The function of SLC20A2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM232.Chemokine (C-C motif) Receptor 5 (CCR5, Accession NM_000579) is another VGAM2485 host target gene. CCR5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CCR5, corresponding to a HOST

TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCR5 BINDING SITE, designated SEQ ID:6185, to the nucleotide sequence of VGAM2485 RNA, herein designated VGAM RNA, also designated SEQ ID:5196.

[84150] Another function of VGAM2485 is therefore inhibition of Chemokine (C-C motif) Receptor 5 (CCR5, Accession NM_000579). Accordingly, utilities of VGAM2485 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCR5. FLJ10826 (Accession NM_018233) is another VGAM2485 host target gene. FLJ10826 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10826, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10826 BINDING SITE, designated SEQ ID:20175, to the nucleotide sequence of VGAM2485 RNA, herein designated VGAM RNA, also designated SEQ ID:5196.

[84151] Another function of VGAM2485 is therefore inhibition of FLJ10826 (Accession NM_018233). Accordingly, utilities of

VGAM2485 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10826. LOC142941 (Accession XM_096363) is another VGAM2485 host target gene. LOC142941 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC142941, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC142941 BINDING SITE, designated SEQ ID:40324, to the nucleotide sequence of VGAM2485 RNA, herein designated VGAM RNA, also designated SEQ ID:5196.

[84152] Another function of VGAM2485 is therefore inhibition of LOC142941 (Accession XM_096363). Accordingly, utilities of VGAM2485 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC142941. LOC150279 (Accession XM_086820) is another VGAM2485 host target gene. LOC150279 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC150279, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC150279 BINDING SITE, designated SEQ ID:38901, to the nucleotide sequence of VGAM2485 RNA, herein designated VGAM RNA, also designated SEQ ID:5196.

[84153] Another function of VGAM2485 is therefore inhibition of LOC150279 (Accession XM_086820). Accordingly, utilities of VGAM2485 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150279. LOC152992 (Accession XM_087575) is another VGAM2485 host target gene. LOC152992 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152992, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152992 BINDING SITE, designated SEQ ID:39347, to the nucleotide sequence of VGAM2485 RNA, herein designated VGAM RNA, also designated SEQ ID:5196.

[84154] Another function of VGAM2485 is therefore inhibition of LOC152992 (Accession XM_087575). Accordingly, utilities of VGAM2485 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152992. LOC158863 (Accession XM_098999) is another VGAM2485 host target gene. LOC158863 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC158863, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC158863 BINDING SITE, designated SEQ ID:42036, to the nucleotide sequence of VGAM2485 RNA, herein designated VGAM RNA, also designated SEQ ID:5196.

[84155] Another function of VGAM2485 is therefore inhibition of LOC158863 (Accession XM_098999). Accordingly, utilities of VGAM2485 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC158863. LOC221954 (Accession XM_168349) is another VGAM2485 host target gene. LOC221954 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221954, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221954 BINDING SITE, designated SEQ ID:45121, to the nucleotide sequence of VGAM2485 RNA, herein designated VGAM RNA, also designated SEQ ID:5196.

[84156] Another function of VGAM2485 is therefore inhibition of

LOC221954 (Accession XM_168349). Accordingly, utilities of VGAM2485 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221954. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2486 (VGAM2486) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84157] VGAM2486 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2486 was detected is described hereinabove with reference to Figs. 1-8.

[84158] VGAM2486 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2486 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84159] VGAM2486 gene encodes a VGAM2486 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2486 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2486 precursor RNA is designated SEQ ID:2472, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2472 is located at position 54581 relative to the genome of Mouse Cytomegalovirus 1.

[84160] VGAM2486 precursor RNA folds onto itself, forming VGAM2486 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84161] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2486 folded precursor RNA into VGAM2486 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 41%) nucleotide se-

quence of VGAM2486 RNA is designated SEQ ID:5197, and is provided hereinbelow with reference to the sequence listing part.

[84162] VGAM2486 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2486 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2486 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84163] VGAM2486 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2486 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2486 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2486 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2486 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84164] The complementary binding of VGAM2486 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2486 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2486 host target RNA into VGAM2486 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84165] It is appreciated that VGAM2486 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2486 host target genes. The mRNA of each one of this plurality of VGAM2486 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2486 RNA, herein designated VGAM RNA, and which when bound by VGAM2486 RNA causes inhibition of translation of respective one or more VGAM2486 host target proteins.

[84166] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2486 gene, herein designated VGAM GENE, on one or more VGAM2486 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84167] It is yet further appreciated that a function of VGAM2486

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2486 correlate with, and may be deduced from, the identity of the host target genes which VGAM2486 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84168] Nucleotide sequences of the VGAM2486 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2486 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2486 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2486 are further described hereinbelow with reference to Table 1.

[84169] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2486 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2486 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84170] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2486 gene, herein designated VGAM is inhibition of expression of VGAM2486 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2486 correlate with, and may be deduced from, the identity of the target genes which VGAM2486 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84171] Cytoplasmic Linker 2 (CYLN2, Accession NM_003388) is a VGAM2486 host target gene. CYLN2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYLN2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYLN2 BINDING SITE, designated SEQ ID:9420, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84172] A function of VGAM2486 is therefore inhibition of Cytoplasmic Linker 2 (CYLN2, Accession NM_003388), a gene which associates with microtubules and dendritic lamellar bodies. Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical

conditions associated with CYLN2. The function of CYLN2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM94.Galanin Receptor 1 (GALR1, Accession NM_001480) is another VGAM2486 host target gene. GALR1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GALR1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GALR1 BINDING SITE, designated SEQ ID:7216, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84173] Another function of VGAM2486 is therefore inhibition of Galanin Receptor 1 (GALR1, Accession NM_001480), a gene which plays a role in regulating ion transport. Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GALR1. The function of GALR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1245.Heparanase (HPSE,

Accession NM_006665) is another VGAM2486 host target gene. HPSE BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HPSE, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HPSE BINDING SITE, designated SEQ ID:13477, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84174] Another function of VGAM2486 is therefore inhibition of Heparanase (HPSE, Accession NM_006665), a gene which is an endoglycosidase that cleaves heparan sulfate. Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HPSE. The function of HPSE and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM374.Interleukin 17 Receptor (IL17R, Accession NM_014339) is another VGAM2486 host target gene. IL17R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IL17R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IL17R BINDING SITE, designated SEQ ID:15660, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84175] Another function of VGAM2486 is therefore inhibition of Interleukin 17 Receptor (IL17R, Accession NM_014339). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IL17R. 2'-5'-oligoadenylate Synthetase 3, 100kDa (OAS3, Accession NM_006187) is another VGAM2486 host target gene. OAS3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by OAS3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of OAS3 BINDING SITE, designated SEQ ID:12862, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84176] Another function of VGAM2486 is therefore inhibition of 2'-5'-oligoadenylate Synthetase 3, 100kDa (OAS3, Accession NM_006187), a gene which may play a role in medi-

ating resistance to virus infection, control of cell growth, differentiation, and apoptosis. Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with OAS3. The function of OAS3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM309.Protocadherin 11 X-linked (PCDH11X, Accession NM_032967) is another VGAM2486 host target gene. PCDH11X BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCDH11X, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11X BINDING SITE, designated SEQ ID:26781, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84177] Another function of VGAM2486 is therefore inhibition of Protocadherin 11 X-linked (PCDH11X, Accession NM_032967), a gene which is thought to play a fundamental role in cell-cell recognition essential for the segmental development and function of the central nervous

system. Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11X. The function of PCDH11X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Protocadherin 11 Y-linked (PCDH11Y, Accession NM_032971) is another VGAM2486 host target gene. PCDH11Y BINDING SITE1 and PCDH11Y BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by PCDH11Y, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11Y BINDING SITE1 and PCDH11Y BINDING SITE2, designated SEQ ID:26814 and SEQ ID:26816 respectively, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84178] Another function of VGAM2486 is therefore inhibition of Protocadherin 11 Y-linked (PCDH11Y, Accession NM_032971). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11Y. Solute Carrier

Family 2 (facilitated glucose transporter), Member 6 (SLC2A6, Accession NM_017585) is another VGAM2486 host target gene. SLC2A6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC2A6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC2A6 BINDING SITE, designated SEQ ID:19031, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84179] Another function of VGAM2486 is therefore inhibition of Solute Carrier Family 2 (facilitated glucose transporter), Member 6 (SLC2A6, Accession NM_017585). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC2A6. SMG1 (Accession NM_015092) is another VGAM2486 host target gene. SMG1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMG1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMG1 BINDING SITE,

designated SEQ ID:17480, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84180] Another function of VGAM2486 is therefore inhibition of SMG1 (Accession NM_015092), a gene which acts as the target for the cell-cycle arrest and immunosuppressive effects. Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMG1. The function of SMG1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM419.Surfeit 5 (SURF5, Accession NM_006752) is another VGAM2486 host target gene. SURF5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SURF5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SURF5 BINDING SITE, designated SEQ ID:13604, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84181] Another function of VGAM2486 is therefore inhibition of

Surfeit 5 (SURF5, Accession NM_006752). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SURF5. Rho Guanine Nucleotide Exchange Factor (GEF) 15 (ARHGEF15, Accession NM_014958) is another VGAM2486 host target gene. ARHGEF15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ARHGEF15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGEF15 BINDING SITE, designated SEQ ID:17318, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84182] Another function of VGAM2486 is therefore inhibition of Rho Guanine Nucleotide Exchange Factor (GEF) 15 (ARHGEF15, Accession NM_014958). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGEF15. Fidgetin (FIGN, Accession XM_171005) is another VGAM2486 host target gene. FIGN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FIGN, corresponding to a

HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FIGN BINDING SITE, designated SEQ ID:45774, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84183] Another function of VGAM2486 is therefore inhibition of Fidgetin (FIGN, Accession XM_171005). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FIGN. FLJ10738 (Accession NM_018199) is another VGAM2486 host target gene. FLJ10738 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10738, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10738 BINDING SITE, designated SEQ ID:20070, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84184] Another function of VGAM2486 is therefore inhibition of FLJ10738 (Accession NM_018199). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with FLJ10738. FLJ12443 (Accession NM_024830) is another VGAM2486 host target gene. FLJ12443 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12443, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12443 BINDING SITE, designated SEQ ID:24222, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84185] Another function of VGAM2486 is therefore inhibition of FLJ12443 (Accession NM_024830). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12443. FLJ12684 (Accession NM_024534) is another VGAM2486 host target gene. FLJ12684 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12684, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12684 BINDING SITE, designated SEQ ID:23745, to the nucleotide

sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84186] Another function of VGAM2486 is therefore inhibition of FLJ12684 (Accession NM_024534). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12684. FLJ20139 (Accession NM_017685) is another VGAM2486 host target gene. FLJ20139 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20139, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20139 BINDING SITE, designated SEQ ID:19238, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84187] Another function of VGAM2486 is therefore inhibition of FLJ20139 (Accession NM_017685). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20139. FLJ23042 (Accession NM_025157) is another VGAM2486 host target gene. FLJ23042 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by FLJ23042, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23042 BINDING SITE, designated SEQ ID:24796, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84188] Another function of VGAM2486 is therefore inhibition of FLJ23042 (Accession NM_025157). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23042. FLJ23403 (Accession NM_022068) is another VGAM2486 host target gene. FLJ23403 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23403, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23403 BINDING SITE, designated SEQ ID:22612, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84189] Another function of VGAM2486 is therefore inhibition of FLJ23403 (Accession NM_022068). Accordingly, utilities of

VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23403. G2 (Accession XM_039515) is another VGAM2486 host target gene. G2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by G2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of G2 BINDING SITE, designated SEQ ID:33110, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84190] Another function of VGAM2486 is therefore inhibition of G2 (Accession XM_039515). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G2. HOMER-2B (Accession NM_004839) is another VGAM2486 host target gene. HOMER-2B BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HOMER-2B, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HOMER-2B BINDING

SITE, designated SEQ ID:11248, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84191] Another function of VGAM2486 is therefore inhibition of HOMER-2B (Accession NM_004839). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HOMER-2B. KIAA0889 (Accession NM_015377) is another VGAM2486 host target gene. KIAA0889 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0889, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0889 BINDING SITE, designated SEQ ID:17678, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84192] Another function of VGAM2486 is therefore inhibition of KIAA0889 (Accession NM_015377). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0889. KIAA1786 (Accession XM_038436) is another VGAM2486 host target gene. KIAA1786 BINDING SITE is

HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1786, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1786 BINDING SITE, designated SEQ ID:32845, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84193] Another function of VGAM2486 is therefore inhibition of KIAA1786 (Accession XM_038436). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1786. Testis-specific Transcript, Y-linked 2 (TTTY2, Accession XM_099029) is another VGAM2486 host target gene. TTTY2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TTTY2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TTTY2 BINDING SITE, designated SEQ ID:42068, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84194] Another function of VGAM2486 is therefore inhibition of Testis-specific Transcript, Y-linked 2 (TTTY2, Accession XM_099029). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TTTY2. Zinc Finger Protein 384 (ZNF384, Accession NM_133476) is another VGAM2486 host target gene. ZNF384 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ZNF384, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ZNF384 BINDING SITE, designated SEQ ID:28543, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84195] Another function of VGAM2486 is therefore inhibition of Zinc Finger Protein 384 (ZNF384, Accession NM_133476). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ZNF384. LOC126917 (Accession XM_059091) is another VGAM2486 host target gene. LOC126917 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by

LOC126917, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC126917 BINDING SITE, designated SEQ ID:36873, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84196] Another function of VGAM2486 is therefore inhibition of LOC126917 (Accession XM_059091). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC126917. LOC145945 (Accession XM_096908) is another VGAM2486 host target gene. LOC145945 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC145945, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC145945 BINDING SITE, designated SEQ ID:40628, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84197] Another function of VGAM2486 is therefore inhibition of LOC145945 (Accession XM_096908). Accordingly, utilities

of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145945. LOC149320 (Accession XM_047557) is another VGAM2486 host target gene. LOC149320 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149320, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149320 BINDING SITE, designated SEQ ID:35001, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84198] Another function of VGAM2486 is therefore inhibition of LOC149320 (Accession XM_047557). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149320. LOC152926 (Accession XM_087562) is another VGAM2486 host target gene. LOC152926 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152926, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC152926 BINDING SITE, designated SEQ ID:39339, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84199] Another function of VGAM2486 is therefore inhibition of LOC152926 (Accession XM_087562). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152926. LOC159148 (Accession XM_099030) is another VGAM2486 host target gene. LOC159148 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC159148, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC159148 BINDING SITE, designated SEQ ID:42075, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84200] Another function of VGAM2486 is therefore inhibition of LOC159148 (Accession XM_099030). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC159148. LOC255196 (Accession XM_173157) is another VGAM2486 host target gene. LOC255196 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255196, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255196 BINDING SITE, designated SEQ ID:46412, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84201] Another function of VGAM2486 is therefore inhibition of LOC255196 (Accession XM_173157). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255196. LOC93613 (Accession XM_052568) is another VGAM2486 host target gene. LOC93613 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC93613, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93613 BINDING SITE, designated SEQ ID:35997, to the nucleotide sequence of VGAM2486 RNA, herein designated VGAM RNA, also designated SEQ ID:5197.

[84202] Another function of VGAM2486 is therefore inhibition of

LOC93613 (Accession XM_052568). Accordingly, utilities of VGAM2486 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93613. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2487 (VGAM2487) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84203] VGAM2487 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2487 was detected is described hereinabove with reference to Figs. 1-8.

[84204] VGAM2487 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2487 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84205] VGAM2487 gene encodes a VGAM2487 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2487 precursor RNA does not encode a protein. A

nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2487 precursor RNA is designated SEQ ID:2473, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2473 is located at position 105519 relative to the genome of Mouse Cytomegalovirus 1.

[84206] VGAM2487 precursor RNA folds onto itself, forming VGAM2487 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84207] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2487 folded precursor RNA into VGAM2487 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide se-

quence of VGAM2487 RNA is designated SEQ ID:5198, and is provided hereinbelow with reference to the sequence listing part.

[84208] VGAM2487 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2487 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2487 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84209] VGAM2487 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2487 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2487 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is

meant as an illustration only, and is not meant to be limiting - VGAM2487 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2487 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84210] The complementary binding of VGAM2487 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2487 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2487 host target RNA into VGAM2487 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84211] It is appreciated that VGAM2487 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2487 host target genes. The mRNA of each one of this plurality of VGAM2487 host target genes comprises one or more host target binding sites, each

having a nucleotide sequence which is at least partly complementary to VGAM2487 RNA, herein designated VGAM RNA, and which when bound by VGAM2487 RNA causes inhibition of translation of respective one or more VGAM2487 host target proteins.

[84212] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2487 gene, herein designated VGAM GENE, on one or more VGAM2487 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84213] It is yet further appreciated that a function of VGAM2487

is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2487 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2487 correlate with, and may be deduced from, the identity of the host target genes which VGAM2487 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84214] Nucleotide sequences of the VGAM2487 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2487 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2487 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2487 are further described hereinbelow with reference to Table 1.

[84215] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2487 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2487 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84216] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2487 gene, herein designated VGAM is inhibition of expression of VGAM2487 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2487 correlate with, and may be deduced from, the identity of the target genes which VGAM2487 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84217] Giant Axonal Neuropathy (gigaxonin) (GAN, Accession NM_022041) is a VGAM2487 host target gene. GAN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by GAN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GAN BINDING SITE, designated SEQ ID:22564, to the nucleotide sequence of VGAM2487 RNA, herein designated VGAM RNA, also designated SEQ ID:5198.

[84218] A function of VGAM2487 is therefore inhibition of Giant Axonal Neuropathy (gigaxonin) (GAN, Accession NM_022041), a gene which plays an important role in neurofilament architecture. Accordingly, utilities of VGAM2487 include diagnosis, prevention and treatment

of diseases and clinical conditions associated with GAN. The function of GAN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM606.FLJ20174 (Accession NM_017699) is another VGAM2487 host target gene. FLJ20174 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20174, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20174 BINDING SITE, designated SEQ ID:19269, to the nucleotide sequence of VGAM2487 RNA, herein designated VGAM RNA, also designated SEQ ID:5198.

[84219] Another function of VGAM2487 is therefore inhibition of FLJ20174 (Accession NM_017699). Accordingly, utilities of VGAM2487 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20174. KIAA0286 (Accession XM_043118) is another VGAM2487 host target gene. KIAA0286 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0286, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0286 BINDING SITE, designated SEQ ID:33902, to the nucleotide sequence of VGAM2487 RNA, herein designated VGAM RNA, also designated SEQ ID:5198.

[84220] Another function of VGAM2487 is therefore inhibition of KIAA0286 (Accession XM_043118). Accordingly, utilities of VGAM2487 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0286. KIAA0930 (Accession XM_047214) is another VGAM2487 host target gene. KIAA0930 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0930, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0930 BINDING SITE, designated SEQ ID:34911, to the nucleotide sequence of VGAM2487 RNA, herein designated VGAM RNA, also designated SEQ ID:5198.

[84221] Another function of VGAM2487 is therefore inhibition of KIAA0930 (Accession XM_047214). Accordingly, utilities of VGAM2487 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

KIAA0930. Myosin 5C (MYO5C, Accession NM_018728) is another VGAM2487 host target gene. MYO5C BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MYO5C, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYO5C BINDING SITE, designated SEQ ID:20817, to the nucleotide sequence of VGAM2487 RNA, herein designated VGAM RNA, also designated SEQ ID:5198.

[84222] Another function of VGAM2487 is therefore inhibition of Myosin 5C (MYO5C, Accession NM_018728). Accordingly, utilities of VGAM2487 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYO5C. LOC144600 (Accession XM_096639) is another VGAM2487 host target gene. LOC144600 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144600, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144600 BINDING SITE, designated SEQ ID:40445, to the nucleotide sequence of VGAM2487 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5198.

[84223] Another function of VGAM2487 is therefore inhibition of LOC144600 (Accession XM_096639). Accordingly, utilities of VGAM2487 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144600. LOC90768 (Accession XM_033986) is another VGAM2487 host target gene. LOC90768 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC90768, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90768 BINDING SITE, designated SEQ ID:31987, to the nucleotide sequence of VGAM2487 RNA, herein designated VGAM RNA, also designated SEQ ID:5198.

[84224] Another function of VGAM2487 is therefore inhibition of LOC90768 (Accession XM_033986). Accordingly, utilities of VGAM2487 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90768. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2488 (VGAM2488) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84225] VGAM2488 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2488 was detected is described hereinabove with reference to Figs. 1-8.

[84226] VGAM2488 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2488 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84227] VGAM2488 gene encodes a VGAM2488 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2488 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2488 precursor RNA is designated SEQ ID:2474, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2474 is located at position 77638 relative to the genome of Mouse Cytomegalovirus 1.

[84228] VGAM2488 precursor RNA folds onto itself, forming

VGAM2488 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84229] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2488 folded precursor RNA into VGAM2488 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2488 RNA is designated SEQ ID:5199, and is provided hereinbelow with reference to the sequence listing part.

[84230] VGAM2488 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2488 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2488 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84231] VGAM2488 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2488 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2488 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2488 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2488 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84232] The complementary binding of VGAM2488 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2488 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2488 host target RNA into VGAM2488 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84233] It is appreciated that VGAM2488 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2488 host target genes. The mRNA of each one of this plurality of VGAM2488 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2488 RNA, herein designated VGAM RNA, and which when bound by VGAM2488 RNA causes inhibition of translation of respective one or more VGAM2488 host target proteins.

[84234] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2488 gene, herein designated VGAM GENE, on one or more VGAM2488 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84235] It is yet further appreciated that a function of VGAM2488 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2488 correlate with, and may be deduced from, the identity of the host target genes which VGAM2488 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[84236] Nucleotide sequences of the VGAM2488 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2488 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2488 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2488 are further described hereinbelow with reference to Table 1.

[84237] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2488 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2488 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84238] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2488 gene, herein designated VGAM is inhibition of expression of VGAM2488 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2488 correlate with, and may be deduced from, the identity of the target genes which VGAM2488 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[84239] ATP-binding Cassette, Sub-family B (MDR/TAP), Member 1 (ABCB1, Accession NM_000927) is a VGAM2488 host target gene. ABCB1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ABCB1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ABCB1 BINDING SITE, designated SEQ ID:6637, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84240] A function of VGAM2488 is therefore inhibition of ATP-binding Cassette, Sub-family B (MDR/TAP), Member 1 (ABCB1, Accession NM_000927), a gene which energy-dependent efflux pump responsible for decreased drug accumulation in multidrug-resistant cells. Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ABCB1. The function of ABCB1 has been established by previous studies. MDR1 encodes a large transmembrane protein that is an integral part of the blood-brain barrier and functions as a drug-transport pump trans-

porting a variety of drugs from the brain back into the blood. The development of simultaneous resistance to multiple structurally unrelated drugs is a major impediment to cancer chemotherapy. Shen et al. (1986) showed that multidrug resistance in human KB carcinoma cells selected in colchicine, vinblastine, or Adriamycin is associated with amplification of specific DNA sequences termed the multidrug resistance locus (MDR1). Increased expression and amplification of MDR1 sequences were also found in multidrug-resistant sublines of human leukemia and ovarian carcinoma cells. Overexpression of P-glycoprotein-1 appears to be a consistent feature of mammalian cells displaying resistance to multiple anticancer drugs and has been postulated to mediate resistance (Kartner et al., 1985; Riordan et al., 1985). Roninson et al. (1986) found that multidrug resistance correlated with amplification of 2 related DNA sequences, designated MDR1 and MDR2 (MDR2 OMIM Ref. No. 171060). These sequences were isolated through their homology with the Chinese hamster mdr gene. MDR1 encodes a 4.5-kb mRNA and was amplified or overexpressed in all multidrug-resistant human cell lines analyzed. No mRNA corresponding to MDR2 was detected. MDR2 DNA sequences

are coamplified with MDR1 in some but not all multidrug-resistant cell lines. Some specific subgroups of mice and dogs are exquisitely sensitive to the neurologic actions of ivermectin. Studying a subpopulation of collie dogs, Mealey et al. (2001) found that a deletion mutation of the MDR1 gene is associated with ivermectin sensitivity. The 4-bp deletion resulted in a frameshift, generating several stop codons that prematurely terminate the P-glycoprotein gene product. The homozygous normal or heterozygous animals did not display increased sensitivity. Animal model experiments lend further support to the function of ABCB1. Schinkel et al. (1994) generated mice homozygous for a disruption of the mdr1a gene. The mice were viable and fertile and appeared phenotypically normal, but they displayed an increased sensitivity to the centrally neurotoxic pesticide ivermectin (100-fold) and to the carcinostatic drug vinblastine (OMIM Ref. No. 3-fold). By comparison of the homozygous null mice with wildtype mice, they found that the mdr1a P-glycoprotein is the major P-glycoprotein in the blood-brain barrier and that its absence results in elevated drug levels in many tissues, especially in brain, and in decreased drug elimination.

[84241] It is appreciated that the abovementioned animal model

for ABCB1 is acknowledged by those skilled in the art as a scientifically valid animal model, as can be further appreciated from the publications sited hereinbelow.

[84242] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84243] Mealey, K. L.; Bentjen, S. A.; Gay, J. M.; Cantor, G. H. : Ivermectin sensitivity in collies is associated with a deletion mutation of the mdr1 gene. Pharmacogenetics 11: 727-733, 2001. ; and

[84244] Shen, D.-W.; Fojo, A.; Chin, J. E.; Roninson, I. B.; Richert, N.; Pastan, I.; Gottesman, M. M. : Human multidrug-resistant cell lines: increased mdr1 expression can precede gene amplif.

[84245] Further studies establishing the function and utilities of ABCB1 are found in John Hopkins OMIM database record ID 171050, and in sited publications numbered 11172-11181, 10830-10831, 2291-2292, 383 and 3865-3892 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.ACN (Accession NM_014977) is another VGAM2488 host target gene. ACN BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by

ACN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACN BINDING SITE, designated SEQ ID:17362, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84246] Another function of VGAM2488 is therefore inhibition of ACN (Accession NM_014977), a gene which is essential for apoptotic chromatin condensation in vitro. Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACN. The function of ACN has been established by previous studies. Apoptosis is defined by several unique morphologic nuclear changes, including chromatin condensation and nuclear fragmentation. These changes are triggered by the activation of a family of cysteine proteases called caspases (see OMIM Ref. No. 147678), and caspase-activated DNase (CAD/DFF40; 601883) and lamin protease (see OMIM Ref. No. 150330) have been implicated in some of these changes. CAD/DFF40 induces chromatin condensation in purified nuclei, but distinct caspase-activated factor(s) may be responsible for chromatin condensation. Sahara et al. (1999) used an in vitro

system to purify a nuclear factor which induces apoptotic chromatin condensation after cleavage by caspase-3 (OMIM Ref. No. 600636) without inducing DNA fragmentation from bovine thymus lysate. The name of the factor, 'acinus,' is both an acronym for 'apoptotic chromatin condensation inducer in the nucleus' and the Latin word for 'grape' or 'berry,' denotive of the grape-like appearance of the condensed chromatin. Immunodepletion experiments showed that acinus is essential for apoptotic chromatin condensation in vitro, and an antisense study revealed that acinus is also important in the induction of apoptotic chromatin condensation in cells. Ishikawa et al. (1998) found that KIAA0670 is ubiquitously expressed. Using the KIAA0670 clone, Sahara et al. (1999) obtained 3 isoforms of human acinus cDNA, the L, S, and S-prime forms, which they stated had probably been generated by alternative splicing.

[84247] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84248] Ishikawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O. : Prediction of coding sequences of unidentified human genes. X. The

complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro. DNA Res. 5: 169-176, 1998. ; and

[84249] Sahara, S.; Aoto, M.; Eguchi, Y.; Imamoto, N.; Yoneda, Y.; Tsujimoto, Y. : Acinus is a caspase-3-activated protein required for apoptotic chromatin condensation. Nature 401: 168-173, 19.

[84250] Further studies establishing the function and utilities of ACN are found in John Hopkins OMIM database record ID 604562, and in sited publications numbered 8473 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Rho GTPase Activating Protein 6 (ARHGAP6, Accession NM_006125) is another VGAM2488 host target gene. ARHGAP6 BINDING SITE1 and ARHGAP6 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by ARHGAP6, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHGAP6 BINDING SITE1 and ARHGAP6 BINDING SITE2, designated SEQ ID:12767 and SEQ ID:6845 respectively, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ

ID:5199.

[84251] Another function of VGAM2488 is therefore inhibition of Rho GTPase Activating Protein 6 (ARHGAP6, Accession NM_006125), a gene which activates the rho-type GT-Pases by converting them to an inactive GTP-bound state. Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHGAP6. The function of ARHGAP6 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Dachshund Homolog (Drosophila) (DACH, Accession NM_080759) is another VGAM2488 host target gene. DACH BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DACH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DACH BINDING SITE, designated SEQ ID:28039, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84252] Another function of VGAM2488 is therefore inhibition of Dachshund Homolog (Drosophila) (DACH, Accession

NM_080759), a gene which regulates early progenitor cell proliferation during retinogenesis and pituitary development . Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DACH. The function of DACH and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM260.Deleted In Liver Cancer 1 (DLC1, Accession NM_006094) is another VGAM2488 host target gene. DLC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DLC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DLC1 BINDING SITE, designated SEQ ID:12743, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84253] Another function of VGAM2488 is therefore inhibition of Deleted In Liver Cancer 1 (DLC1, Accession NM_006094), a gene which is a candidate tumor suppressor gene for human cancer. Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with DLC1. The function of DLC1 has been established by previous studies. To identify genes involved in hepatocellular carcinoma (HCC; 114550), Yuan et al. (1998) applied representational difference analysis (RDA), a PCR-based subtractive hybridization technique, to DNA derived from a primary HCC and adjacent noncancerous tissue from the same patient. They identified the novel gene DLC1 as a fragment that was deleted in the primary tumor. Seven of 16 primary HCCs and 10 of 11 HCC cell lines showed loss of heterozygosity (LOH) for the DLC1 gene. Northern blot analysis detected a major 7.5- and a minor 4.5-kb DLC1 transcript in all human tissues examined, including liver, but did not find DLC1 expression in 4 of 14 HCC cell lines. The authors isolated a full-length DLC1 cDNA encoding a deduced 1,091-amino acid protein. The DLC1 gene shares high sequence similarity with the rat p122 RhoGap gene (see OMIM Ref. No. 602680). By FISH, Yuan et al. (1998) mapped the DLC1 gene to 8p22-p21.3, a region frequently deleted in solid tumors. The authors suggested that DLC1 is a candidate tumor suppressor gene for human liver cancer, as well as for prostate, lung, colorectal, and breast cancers. Wilson et al. (2000) delineated the

structure of the DLC1 gene and used SSCP analysis to look for sequence variants in 126 colorectal and 33 ovarian primary tumors and cell lines. One exonic missense mutation and 3 intronic insertions/deletions were identified in primary colorectal tumors, as well as many polymorphisms present in germline DNAs. The rarity of exonic missense mutations, and the absence of protein-truncating mutations, indicated that DLC1 is not the target of the LOH frequently observed on 8p in colorectal and ovarian tumors. The delineation of gene structure allows mutation analysis of DLC1 in other tumor types for which it remains a candidate tumor suppressor gene based on its location and homology to RHOGAP (OMIM Ref. No. 602732).

[84254] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84255] Wilson, P. J.; McGlinn, E.; Marsh, A.; Evans, T.; Arnold, J.; Wright, K.; Biden, K.; Young, J.; Wainwright, B.; Wicking, C.; Chenevix-Trench, G. : Sequence variants of DLC1 in colorectal and ovarian tumours. Hum. Mutat. 15: 156-165, 2000. ; and

[84256] Yuan, B.-Z.; Miller, M. J.; Keck, C. L.; Zimonjic, D. B.;

Thorgeirsson, S. S.; Popescu, N. C. : Cloning, characterization, and chromosomal localization of a gene frequently deleted in.

[84257] Further studies establishing the function and utilities of DLC1 are found in John Hopkins OMIM database record ID 604258, and in sited publications numbered 7069-7071 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Mutated In Colorectal Cancers (MCC, Accession NM_002387) is another VGAM2488 host target gene. MCC BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MCC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MCC BINDING SITE, designated SEQ ID:8203, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84258] Another function of VGAM2488 is therefore inhibition of Mutated In Colorectal Cancers (MCC, Accession NM_002387). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MCC. Phosphoglycerate

Mutase 1 (brain) (PGAM1, Accession XM_083842) is another VGAM2488 host target gene. PGAM1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PGAM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PGAM1 BINDING SITE, designated SEQ ID:37518, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84259] Another function of VGAM2488 is therefore inhibition of Phosphoglycerate Mutase 1 (brain) (PGAM1, Accession XM_083842). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PGAM1. Phospholipase A2, Group X (PLA2G10, Accession NM_003561) is another VGAM2488 host target gene. PLA2G10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PLA2G10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PLA2G10 BINDING SITE, designated SEQ ID:9618, to the nucleotide

sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84260] Another function of VGAM2488 is therefore inhibition of Phospholipase A2, Group X (PLA2G10, Accession NM_003561). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PLA2G10. Pleckstrin and Sec7 Domain Protein (PSD, Accession NM_002779) is another VGAM2488 host target gene. PSD BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PSD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSD BINDING SITE, designated SEQ ID:8666, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84261] Another function of VGAM2488 is therefore inhibition of Pleckstrin and Sec7 Domain Protein (PSD, Accession NM_002779), a gene which promotes guanine-nucleotide exchange on arf6. Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSD. The function of

PSD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM261.SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9, Accession NM_000346) is another VGAM2488 host target gene. SOX9 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SOX9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SOX9 BINDING SITE, designated SEQ ID:5898, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84262] Another function of VGAM2488 is therefore inhibition of SRY (sex determining region Y)-box 9 (campomelic dysplasia, autosomal sex-reversal) (SOX9, Accession NM_000346), a gene which regulates the expression of other genes involved in chondrogenesis. Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SOX9. The function of SOX9 and its association with various diseases and clinical conditions, has been estab-

lished by previous studies, as described hereinabove with reference to VGAM329.Thromboxane A2 Receptor (TBXA2R, Accession NM_001060) is another VGAM2488 host target gene. TBXA2R BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TBXA2R, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TBXA2R BINDING SITE, designated SEQ ID:6724, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84263] Another function of VGAM2488 is therefore inhibition of Thromboxane A2 Receptor (TBXA2R, Accession NM_001060), a gene which activates Ca2+-activated chloride channels; stimulates platelet aggregation and smooth muscle constriction. Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TBXA2R. The function of TBXA2R and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Transcription Factor 1, Hepatic;

LF-B1, Hepatic Nuclear Factor (HNF1), Albumin Proximal Factor (TCF1, Accession NM_000545) is another VGAM2488 host target gene. TCF1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF1 BINDING SITE, designated SEQ ID:6150, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84264] Another function of VGAM2488 is therefore inhibition of Transcription Factor 1, Hepatic; LF-B1, Hepatic Nuclear Factor (HNF1), Albumin Proximal Factor (TCF1, Accession NM_000545), a gene which is required for the expression of several liver specific genes. binds to the inverted palindrome 5'-gttaatnattaac-3'. Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF1. The function of TCF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1189.Translocase of Inner Mitochondrial Mem-

brane 23 Homolog (yeast) (TIMM23, Accession XM_011891) is another VGAM2488 host target gene. TIMM23 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TIMM23, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TIMM23 BINDING SITE, designated SEQ ID:30198, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84265] Another function of VGAM2488 is therefore inhibition of Translocase of Inner Mitochondrial Membrane 23 Homolog (yeast) (TIMM23, Accession XM_011891), a gene which translocates nuclear-encoded proteins into the mitochondrion. Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TIMM23. The function of TIMM23 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1958.Diacylglycerol Kinase, Zeta 104kDa (DGKZ, Accession NM_003646) is another VGAM2488 host target

gene. DGKZ BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DGKZ, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DGKZ BINDING SITE, designated SEQ ID:9723, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84266] Another function of VGAM2488 is therefore inhibition of Diacylglycerol Kinase, Zeta 104kDa (DGKZ, Accession NM_003646). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DGKZ. FLJ14009 (Accession NM_024760) is another VGAM2488 host target gene. FLJ14009 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ14009, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14009 BINDING SITE, designated SEQ ID:24111, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84267] Another function of VGAM2488 is therefore inhibition of FLJ14009 (Accession NM_024760). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14009. FLJ20085 (Accession NM_017660) is another VGAM2488 host target gene. FLJ20085 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20085, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20085 BINDING SITE, designated SEQ ID:19183, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84268] Another function of VGAM2488 is therefore inhibition of FLJ20085 (Accession NM_017660). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20085. FLJ20359 (Accession NM_017781) is another VGAM2488 host target gene. FLJ20359 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20359, corresponding to a HOST TARGET binding site such as BINDING SITE I, BIND-

ING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20359 BINDING SITE, designated SEQ ID:19413, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84269] Another function of VGAM2488 is therefore inhibition of FLJ20359 (Accession NM_017781). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20359. FLJ22056 (Accession NM_022489) is another VGAM2488 host target gene. FLJ22056 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ22056, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22056 BINDING SITE, designated SEQ ID:22869, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84270] Another function of VGAM2488 is therefore inhibition of FLJ22056 (Accession NM_022489). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

FLJ22056. HCA4 (Accession XM_085287) is another VGAM2488 host target gene. HCA4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HCA4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HCA4 BINDING SITE, designated SEQ ID:38019, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84271] Another function of VGAM2488 is therefore inhibition of HCA4 (Accession XM_085287). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HCA4. KIAA1576 (Accession XM_038186) is another VGAM2488 host target gene. KIAA1576 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1576, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1576 BINDING SITE, designated SEQ ID:32770, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5199.

[84272] Another function of VGAM2488 is therefore inhibition of KIAA1576 (Accession XM_038186). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1576. KIAA1727 (Accession XM_034262) is another VGAM2488 host target gene. KIAA1727 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1727, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1727 BINDING SITE, designated SEQ ID:32034, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84273] Another function of VGAM2488 is therefore inhibition of KIAA1727 (Accession XM_034262). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1727. MGC11115 (Accession NM_032310) is another VGAM2488 host target gene. MGC11115 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC11115, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC11115 BINDING SITE, designated SEQ ID:26092, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84274] Another function of VGAM2488 is therefore inhibition of MGC11115 (Accession NM_032310). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC11115. MGC16703 (Accession XM_054591) is another VGAM2488 host target gene. MGC16703 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC16703, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC16703 BINDING SITE, designated SEQ ID:36181, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84275] Another function of VGAM2488 is therefore inhibition of MGC16703 (Accession XM_054591). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with MGC16703. MGC3047 (Accession NM_032348) is another VGAM2488 host target gene. MGC3047 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC3047, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC3047 BINDING SITE, designated SEQ ID:26137, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84276] Another function of VGAM2488 is therefore inhibition of MGC3047 (Accession NM_032348). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC3047. PP1665 (Accession NM_030792) is another VGAM2488 host target gene. PP1665 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PP1665, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PP1665 BINDING SITE, designated SEQ ID:25091, to the nucleotide se-

quence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84277] Another function of VGAM2488 is therefore inhibition of PP1665 (Accession NM_030792). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PP1665. SAST (Accession XM_032034) is another VGAM2488 host target gene. SAST BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SAST, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SAST BINDING SITE, designated SEQ ID:31540, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84278] Another function of VGAM2488 is therefore inhibition of SAST (Accession XM_032034). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SAST. URG4 (Accession NM_017920) is another VGAM2488 host target gene. URG4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded

by URG4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of URG4 BINDING SITE, designated SEQ ID:19578, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84279] Another function of VGAM2488 is therefore inhibition of URG4 (Accession NM_017920). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with URG4. LOC124460 (Accession XM_071892) is another VGAM2488 host target gene. LOC124460 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC124460, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC124460 BINDING SITE, designated SEQ ID:37442, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84280] Another function of VGAM2488 is therefore inhibition of LOC124460 (Accession XM_071892). Accordingly, utilities

of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC124460. LOC144483 (Accession XM_012219) is another VGAM2488 host target gene. LOC144483 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC144483, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144483 BINDING SITE, designated SEQ ID:30211, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84281] Another function of VGAM2488 is therefore inhibition of LOC144483 (Accession XM_012219). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144483. LOC145447 (Accession XM_085133) is another VGAM2488 host target gene. LOC145447 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC145447, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC145447 BINDING SITE, designated SEQ ID:37862, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84282] Another function of VGAM2488 is therefore inhibition of LOC145447 (Accession XM_085133). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC145447. LOC149706 (Accession XM_097718) is another VGAM2488 host target gene. LOC149706 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC149706, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149706 BINDING SITE, designated SEQ ID:41060, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84283] Another function of VGAM2488 is therefore inhibition of LOC149706 (Accession XM_097718). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149706. LOC151178 (Accession XM_087117) is another VGAM2488 host target gene. LOC151178 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151178, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151178 BINDING SITE, designated SEQ ID:39069, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84284] Another function of VGAM2488 is therefore inhibition of LOC151178 (Accession XM_087117). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151178. LOC155061 (Accession XM_088139) is another VGAM2488 host target gene. LOC155061 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC155061, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155061 BINDING SITE, designated SEQ ID:39537, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84285] Another function of VGAM2488 is therefore inhibition of

LOC155061 (Accession XM_088139). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155061. LOC155340 (Accession XM_055725) is another VGAM2488 host target gene. LOC155340 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC155340, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC155340 BINDING SITE, designated SEQ ID:36317, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84286] Another function of VGAM2488 is therefore inhibition of LOC155340 (Accession XM_055725). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC155340. LOC157349 (Accession XM_088298) is another VGAM2488 host target gene. LOC157349 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC157349, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC157349 BINDING SITE, designated SEQ ID:39596, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84287] Another function of VGAM2488 is therefore inhibition of LOC157349 (Accession XM_088298). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC157349. LOC196759 (Accession XM_113601) is another VGAM2488 host target gene. LOC196759 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC196759, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196759 BINDING SITE, designated SEQ ID:42292, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84288] Another function of VGAM2488 is therefore inhibition of LOC196759 (Accession XM_113601). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196759. LOC199899 (Accession XM_117153) is an-

other VGAM2488 host target gene. LOC199899 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC199899, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC199899 BINDING SITE, designated SEQ ID:43257, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84289] Another function of VGAM2488 is therefore inhibition of LOC199899 (Accession XM_117153). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC199899. LOC221495 (Accession XM_168136) is another VGAM2488 host target gene. LOC221495 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221495, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221495 BINDING SITE, designated SEQ ID:45062, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84290] Another function of VGAM2488 is therefore inhibition of LOC221495 (Accession XM_168136). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221495. LOC256598 (Accession XM_172816) is another VGAM2488 host target gene. LOC256598 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256598, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256598 BINDING SITE, designated SEQ ID:46098, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84291] Another function of VGAM2488 is therefore inhibition of LOC256598 (Accession XM_172816). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256598. LOC256867 (Accession XM_170694) is another VGAM2488 host target gene. LOC256867 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256867, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256867 BINDING SITE, designated SEQ ID:45474, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84292] Another function of VGAM2488 is therefore inhibition of LOC256867 (Accession XM_170694). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256867. LOC257054 (Accession XM_171010) is another VGAM2488 host target gene. LOC257054 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC257054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC257054 BINDING SITE, designated SEQ ID:45781, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84293] Another function of VGAM2488 is therefore inhibition of LOC257054 (Accession XM_171010). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC257054. LOC64744 (Accession XM_029830) is another VGAM2488 host target gene. LOC64744 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC64744, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC64744 BINDING SITE, designated SEQ ID:30953, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84294] Another function of VGAM2488 is therefore inhibition of LOC64744 (Accession XM_029830). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC64744. LOC90288 (Accession XM_030669) is another VGAM2488 host target gene. LOC90288 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC90288, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC90288 BINDING SITE, designated SEQ ID:31108, to the nucleotide sequence of VGAM2488 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5199.

[84295] Another function of VGAM2488 is therefore inhibition of LOC90288 (Accession XM_030669). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC90288. LOC92080 (Accession XM_042704) is another VGAM2488 host target gene. LOC92080 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC92080, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC92080 BINDING SITE, designated SEQ ID:33759, to the nucleotide sequence of VGAM2488 RNA, herein designated VGAM RNA, also designated SEQ ID:5199.

[84296] Another function of VGAM2488 is therefore inhibition of LOC92080 (Accession XM_042704). Accordingly, utilities of VGAM2488 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC92080. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2489 (VGAM2489) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84297] VGAM2489 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2489 was detected is described hereinabove with reference to Figs. 1-8.

[84298] VGAM2489 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2489 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84299] VGAM2489 gene encodes a VGAM2489 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2489 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2489 precursor RNA is designated SEQ ID:2475, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2475 is located at position 131589 relative to the genome of Mouse Cytomegalovirus 1.

[84300] VGAM2489 precursor RNA folds onto itself, forming

VGAM2489 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84301] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2489 folded precursor RNA into VGAM2489 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2489 RNA is designated SEQ ID:5200, and is provided hereinbelow with reference to the sequence listing part.

[84302] VGAM2489 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2489 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2489 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84303] VGAM2489 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2489 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2489 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2489 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2489 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84304] The complementary binding of VGAM2489 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2489 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2489 host target RNA into VGAM2489 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84305] It is appreciated that VGAM2489 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2489 host target genes. The mRNA of each one of this plurality of VGAM2489 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2489 RNA, herein designated VGAM RNA, and which when bound by VGAM2489 RNA causes inhibition of translation of respective one or more VGAM2489 host target proteins.

[84306] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2489 gene, herein designated VGAM GENE, on one or more VGAM2489 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84307] It is yet further appreciated that a function of VGAM2489 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2489 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2489 correlate with, and may be deduced from, the identity of the host target genes which VGAM2489 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[84308] Nucleotide sequences of the VGAM2489 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2489 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2489 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2489 are further described hereinbelow with reference to Table 1.

[84309] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2489 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2489 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84310] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2489 gene, herein designated VGAM is inhibition of expression of VGAM2489 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2489 correlate with, and may be deduced from, the identity of the target genes which VGAM2489 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[84311] Cadherin 1, Type 1, E-cadherin (epithelial) (CDH1, Accession NM_004360) is a VGAM2489 host target gene. CDH1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CDH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CDH1 BINDING SITE, designated SEQ ID:10567, to the nucleotide sequence of VGAM2489 RNA, herein designated VGAM RNA, also designated SEQ ID:5200.

[84312] A function of VGAM2489 is therefore inhibition of Cadherin 1, Type 1, E-cadherin (epithelial) (CDH1, Accession NM_004360). Accordingly, utilities of VGAM2489 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CDH1. Retinoblastoma Binding Protein 9 (RBBP9, Accession XM_046553) is another VGAM2489 host target gene. RBBP9 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RBBP9, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RBBP9 BIND-

ING SITE, designated SEQ ID:34744, to the nucleotide sequence of VGAM2489 RNA, herein designated VGAM RNA, also designated SEQ ID:5200.

[84313] Another function of VGAM2489 is therefore inhibition of Retinoblastoma Binding Protein 9 (RBBP9, Accession XM_046553). Accordingly, utilities of VGAM2489 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RBBP9. BRCA2 and CDKN1A Interacting Protein (BCCIP, Accession NM_078469) is another VGAM2489 host target gene. BCCIP BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by BCCIP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of BCCIP BINDING SITE, designated SEQ ID:27785, to the nucleotide sequence of VGAM2489 RNA, herein designated VGAM RNA, also designated SEQ ID:5200.

[84314] Another function of VGAM2489 is therefore inhibition of BRCA2 and CDKN1A Interacting Protein (BCCIP, Accession NM_078469). Accordingly, utilities of VGAM2489 include diagnosis, prevention and treatment of diseases and clinical conditions associated with BCCIP. Fig. 1 further pro-

vides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2490 (VGAM2490) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84315] VGAM2490 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2490 was detected is described hereinabove with reference to Figs. 1-8.

[84316] VGAM2490 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2490 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84317] VGAM2490 gene encodes a VGAM2490 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2490 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2490 precursor RNA is designated SEQ ID:2476, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2476 is located at position 47693 relative to the genome of Mouse Cytomegalovirus 1.

[84318] VGAM2490 precursor RNA folds onto itself, forming VGAM2490 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84319] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2490 folded precursor RNA into VGAM2490 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2490 RNA is designated SEQ ID:5201, and is provided hereinbelow with reference to the sequence listing part.

[84320] VGAM2490 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2490 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2490 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84321] VGAM2490 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2490 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2490 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2490 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2490 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84322] The complementary binding of VGAM2490 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2490 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2490 host target RNA into VGAM2490 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84323] It is appreciated that VGAM2490 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2490 host target genes. The mRNA of each one of this plurality of VGAM2490 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2490 RNA, herein designated VGAM RNA, and which when bound by VGAM2490 RNA causes inhibition of translation of respective one or more

VGAM2490 host target proteins.

[84324] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2490 gene, herein designated VGAM GENE, on one or more VGAM2490 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84325] It is yet further appreciated that a function of VGAM2490 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2490 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1.

Specific functions, and accordingly utilities, of VGAM2490 correlate with, and may be deduced from, the identity of the host target genes which VGAM2490 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84326] Nucleotide sequences of the VGAM2490 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2490 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2490 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2490 are further described hereinbelow with reference to Table 1.

[84327] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2490 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2490 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84328] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2490 gene, herein designated VGAM is inhibition of expression of VGAM2490 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2490 correlate with, and may be deduced from, the identity of the target genes which VGAM2490 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84329] Keratin 16 (focal non-epidermolytic palmoplantar keratoderma) (KRT16, Accession XM_170845) is a VGAM2490 host target gene. KRT16 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by KRT16, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KRT16 BINDING SITE, designated SEQ ID:45629, to the nucleotide sequence of VGAM2490 RNA, herein designated VGAM RNA, also designated SEQ ID:5201.

[84330] A function of VGAM2490 is therefore inhibition of Keratin 16 (focal non-epidermolytic palmoplantar keratoderma) (KRT16, Accession XM_170845). Accordingly, utilities of VGAM2490 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KRT16. Nescient Helix Loop Helix 1 (NHLH1, Accession NM_005598) is another VGAM2490 host target gene. NHLH1 BINDING SITE is HOST TARGET binding site found

in the 3` untranslated region of mRNA encoded by NHLH1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NHLH1 BINDING SITE, designated SEQ ID:12124, to the nucleotide sequence of VGAM2490 RNA, herein designated VGAM RNA, also designated SEQ ID:5201.

[84331] Another function of VGAM2490 is therefore inhibition of Nescient Helix Loop Helix 1 (NHLH1, Accession NM_005598), a gene which may have a role in development of the nervous system. Accordingly, utilities of VGAM2490 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NHLH1. The function of NHLH1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1923.Purinergic Receptor P2Y, G-protein Coupled, 2 (P2RY2, Accession NM_002564) is another VGAM2490 host target gene. P2RY2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by P2RY2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE

II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of P2RY2 BINDING SITE, designated SEQ ID:8414, to the nucleotide sequence of VGAM2490 RNA, herein designated VGAM RNA, also designated SEQ ID:5201.

[84332] Another function of VGAM2490 is therefore inhibition of Purinergic Receptor P2Y, G-protein Coupled, 2 (P2RY2, Accession NM_002564), a gene which mediates cellular responses to ATP. Accordingly, utilities of VGAM2490 include diagnosis, prevention and treatment of diseases and clinical conditions associated with P2RY2. The function of P2RY2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1259.Proprotein Convertase Subtilisin/kexin Type 2 (PCSK2, Accession NM_002594) is another VGAM2490 host target gene. PCSK2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PCSK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCSK2 BINDING SITE, designated SEQ ID:8454, to the nucleotide sequence of

VGAM2490 RNA, herein designated VGAM RNA, also designated SEQ ID:5201.

[84333] Another function of VGAM2490 is therefore inhibition of Proprotein Convertase Subtilisin/kexin Type 2 (PCSK2, Accession NM_002594), a gene which is involved in the processing of hormone and other protein precursors at sites comprised of pairs of basic amino acid residues. Accordingly, utilities of VGAM2490 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCSK2. The function of PCSK2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1120.FLJ22009 (Accession XM_015700) is another VGAM2490 host target gene. FLJ22009 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ22009, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ22009 BINDING SITE, designated SEQ ID:30241, to the nucleotide sequence of VGAM2490 RNA, herein designated VGAM RNA, also designated SEQ ID:5201.

[84334] Another function of VGAM2490 is therefore inhibition of FLJ22009 (Accession XM_015700). Accordingly, utilities of VGAM2490 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ22009. Interferon Regulatory Factor 7 (IRF7, Accession NM_004030) is another VGAM2490 host target gene. IRF7 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by IRF7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of IRF7 BINDING SITE, designated SEQ ID:10249, to the nucleotide sequence of VGAM2490 RNA, herein designated VGAM RNA, also designated SEQ ID:5201.

[84335] Another function of VGAM2490 is therefore inhibition of Interferon Regulatory Factor 7 (IRF7, Accession NM_004030). Accordingly, utilities of VGAM2490 include diagnosis, prevention and treatment of diseases and clinical conditions associated with IRF7. NRF (Accession NM_017544) is another VGAM2490 host target gene. NRF BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NRF, corresponding to a HOST TARGET binding site such as BINDING

SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NRF BINDING SITE, designated SEQ ID:18985, to the nucleotide sequence of VGAM2490 RNA, herein designated VGAM RNA, also designated SEQ ID:5201.

[84336] Another function of VGAM2490 is therefore inhibition of NRF (Accession NM_017544). Accordingly, utilities of VGAM2490 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NRF. LOC200317 (Accession XM_114208) is another VGAM2490 host target gene. LOC200317 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC200317, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC200317 BINDING SITE, designated SEQ ID:42801, to the nucleotide sequence of VGAM2490 RNA, herein designated VGAM RNA, also designated SEQ ID:5201.

[84337] Another function of VGAM2490 is therefore inhibition of LOC200317 (Accession XM_114208). Accordingly, utilities of VGAM2490 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC200317. LOC91408 (Accession XM_038290) is another VGAM2490 host target gene. LOC91408 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91408, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC91408 BINDING SITE, designated SEQ ID:32791, to the nucleotide sequence of VGAM2490 RNA, herein designated VGAM RNA, also designated SEQ ID:5201.

[84338] Another function of VGAM2490 is therefore inhibition of LOC91408 (Accession XM_038290). Accordingly, utilities of VGAM2490 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91408. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2491 (VGAM2491) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84339] VGAM2491 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2491 was detected is described hereinabove with reference to Figs. 1-8.

[84340] VGAM2491 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2491 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84341] VGAM2491 gene encodes a VGAM2491 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2491 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2491 precursor RNA is designated SEQ ID:2477, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2477 is located at position 198448 relative to the genome of Mouse Cytomegalovirus 1.

[84342] VGAM2491 precursor RNA folds onto itself, forming VGAM2491 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84343] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2491 folded precursor RNA into VGAM2491 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2491 RNA is designated SEQ ID:5202, and is provided hereinbelow with reference to the sequence listing part.

[84344] VGAM2491 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2491 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2491 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84345] VGAM2491 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2491 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2491 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2491 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2491 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84346] The complementary binding of VGAM2491 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2491 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2491 host target RNA into VGAM2491 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84347] It is appreciated that VGAM2491 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2491 host target genes. The mRNA of each one of this plurality of VGAM2491 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2491 RNA, herein designated VGAM RNA, and which when bound by VGAM2491 RNA causes inhibition of translation of respective one or more VGAM2491 host target proteins.

[84348] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2491 gene, herein designated VGAM GENE, on one or more VGAM2491 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84349] It is yet further appreciated that a function of VGAM2491 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2491 correlate with, and may be deduced from, the identity of the host target genes which VGAM2491 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84350] Nucleotide sequences of the VGAM2491 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2491 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2491 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2491 are further described hereinbelow with reference to Table 1.

[84351] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2491 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2491 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84352] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2491 gene, herein designated VGAM is inhibition of expression of VGAM2491 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2491 correlate with, and may be deduced from, the identity of the target genes which VGAM2491 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84353] Collagen, Type VI, Alpha 2 (COL6A2, Accession NM_058175) is a VGAM2491 host target gene. COL6A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by COL6A2,

corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of COL6A2 BINDING SITE, designated SEQ ID:27725, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84354] A function of VGAM2491 is therefore inhibition of Collagen, Type VI, Alpha 2 (COL6A2, Accession NM_058175). Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with COL6A2. Glucose-6-phosphate Dehydrogenase (G6PD, Accession NM_000402) is another VGAM2491 host target gene. G6PD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by G6PD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of G6PD BINDING SITE, designated SEQ ID:5980, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84355] Another function of VGAM2491 is therefore inhibition of

Glucose-6-phosphate Dehydrogenase (G6PD, Accession NM_000402), a gene which produces pentose sugars for nucleic acid synthesis and main producer of nadph reducing power. Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with G6PD. The function of G6PD and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1027.DQX1 (Accession NM_133637) is another VGAM2491 host target gene. DQX1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DQX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DQX1 BINDING SITE, designated SEQ ID:28596, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84356] Another function of VGAM2491 is therefore inhibition of DQX1 (Accession NM_133637). Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DQX1. ETR101 (Accession XM_051364) is another VGAM2491

host target gene. ETR101 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ETR101, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ETR101 BINDING SITE, designated SEQ ID:35830, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84357] Another function of VGAM2491 is therefore inhibition of ETR101 (Accession XM_051364). Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ETR101. FLJ14054 (Accession NM_024563) is another VGAM2491 host target gene. FLJ14054 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ14054, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ14054 BINDING SITE, designated SEQ ID:23781, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84358] Another function of VGAM2491 is therefore inhibition of FLJ14054 (Accession NM_024563). Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ14054. KIAA1884 (Accession XM_055539) is another VGAM2491 host target gene. KIAA1884 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1884, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1884 BINDING SITE, designated SEQ ID:36296, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84359] Another function of VGAM2491 is therefore inhibition of KIAA1884 (Accession XM_055539). Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1884. SEC14-like 2 (S. cerevisiae) (SEC14L2, Accession NM_012429) is another VGAM2491 host target gene. SEC14L2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SEC14L2, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC14L2 BINDING SITE, designated SEQ ID:14804, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84360] Another function of VGAM2491 is therefore inhibition of SEC14-like 2 (S. cerevisiae) (SEC14L2, Accession NM_012429). Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC14L2. LOC122769 (Accession XM_058657) is another VGAM2491 host target gene. LOC122769 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC122769, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC122769 BINDING SITE, designated SEQ ID:36695, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84361] Another function of VGAM2491 is therefore inhibition of LOC122769 (Accession XM_058657). Accordingly, utilities

of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC122769. LOC151124 (Accession XM_098006) is another VGAM2491 host target gene. LOC151124 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC151124, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151124 BINDING SITE, designated SEQ ID:41299, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84362] Another function of VGAM2491 is therefore inhibition of LOC151124 (Accession XM_098006). Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151124. LOC254016 (Accession XM_173050) is another VGAM2491 host target gene. LOC254016 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC254016, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC254016 BINDING SITE, designated SEQ ID:46309, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84363] Another function of VGAM2491 is therefore inhibition of LOC254016 (Accession XM_173050). Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC254016. LOC58509 (Accession XM_114002) is another VGAM2491 host target gene. LOC58509 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC58509, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC58509 BINDING SITE, designated SEQ ID:42612, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84364] Another function of VGAM2491 is therefore inhibition of LOC58509 (Accession XM_114002). Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC58509. LOC64150 (Accession XM_040993) is another VGAM2491 host target gene. LOC64150 BINDING SITE is

HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC64150, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC64150 BINDING SITE, designated SEQ ID:33411, to the nucleotide sequence of VGAM2491 RNA, herein designated VGAM RNA, also designated SEQ ID:5202.

[84365] Another function of VGAM2491 is therefore inhibition of LOC64150 (Accession XM_040993). Accordingly, utilities of VGAM2491 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC64150. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2492 (VGAM2492) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84366] VGAM2492 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2492 was detected is described hereinabove with reference to Figs. 1-8.

[84367] VGAM2492 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2492 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84368] VGAM2492 gene encodes a VGAM2492 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2492 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2492 precursor RNA is designated SEQ ID:2478, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2478 is located at position 124024 relative to the genome of Mouse Cytomegalovirus 1.

[84369] VGAM2492 precursor RNA folds onto itself, forming VGAM2492 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[84370] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2492 folded precursor RNA into VGAM2492 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 56%) nucleotide sequence of VGAM2492 RNA is designated SEQ ID:5203, and is provided hereinbelow with reference to the sequence listing part.

[84371] VGAM2492 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2492 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2492 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84372] VGAM2492 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2492 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2492 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2492 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2492 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84373] The complementary binding of VGAM2492 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2492 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2492 host target RNA into VGAM2492 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84374] It is appreciated that VGAM2492 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2492 host target genes. The mRNA of each one of this plurality of VGAM2492 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2492 RNA, herein designated VGAM RNA, and which when bound by VGAM2492 RNA causes inhibition of translation of respective one or more VGAM2492 host target proteins.

[84375] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2492 gene, herein designated VGAM GENE, on one or more VGAM2492 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84376] It is yet further appreciated that a function of VGAM2492 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2492 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2492 correlate with, and may be deduced from, the identity of the host target genes which VGAM2492 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84377] Nucleotide sequences of the VGAM2492 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2492 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2492 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2492 are further described hereinbelow with reference to Table 1.

[84378] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2492 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2492 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84379] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2492 gene, herein designated VGAM is inhibition of expression of VGAM2492 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2492 correlate with, and may be deduced from, the identity of the target genes which VGAM2492 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84380] AXL Receptor Tyrosine Kinase (AXL, Accession NM_001699) is a VGAM2492 host target gene. AXL BINDING SITE1 and AXL BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by AXL, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of AXL BINDING SITE1 and AXL BINDING SITE2, designated SEQ ID:7419 and SEQ ID:22440 respectively, to the nucleotide sequence of VGAM2492 RNA, herein designated VGAM RNA, also designated SEQ ID:5203.

[84381] A function of VGAM2492 is therefore inhibition of AXL Receptor Tyrosine Kinase (AXL, Accession NM_001699). Accordingly, utilities of VGAM2492 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AXL. EMILIN-2 (Accession NM_032048) is another VGAM2492 host target gene. EMILIN-2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EMILIN-2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EMILIN-2 BINDING SITE, designated SEQ ID:25766, to the nucleotide sequence of VGAM2492 RNA, herein designated VGAM RNA, also designated SEQ ID:5203.

[84382] Another function of VGAM2492 is therefore inhibition of EMILIN-2 (Accession NM_032048). Accordingly, utilities of VGAM2492 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EMILIN-

2. FLJ21742 (Accession NM_032207) is another VGAM2492 host target gene. FLJ21742 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ21742, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ21742 BINDING SITE, designated SEQ ID:25912, to the nucleotide sequence of VGAM2492 RNA, herein designated VGAM RNA, also designated SEQ ID:5203.

[84383] Another function of VGAM2492 is therefore inhibition of FLJ21742 (Accession NM_032207). Accordingly, utilities of VGAM2492 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ21742. Ring Finger Protein 24 (RNF24, Accession NM_007219) is another VGAM2492 host target gene. RNF24 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RNF24, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RNF24 BINDING SITE, designated SEQ ID:14083, to the nucleotide sequence of VGAM2492 RNA,

herein designated VGAM RNA, also designated SEQ ID:5203.

[84384] Another function of VGAM2492 is therefore inhibition of Ring Finger Protein 24 (RNF24, Accession NM_007219). Accordingly, utilities of VGAM2492 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RNF24. LOC153577 (Accession XM_098394) is another VGAM2492 host target gene. LOC153577 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153577, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153577 BINDING SITE, designated SEQ ID:41641, to the nucleotide sequence of VGAM2492 RNA, herein designated VGAM RNA, also designated SEQ ID:5203.

[84385] Another function of VGAM2492 is therefore inhibition of LOC153577 (Accession XM_098394). Accordingly, utilities of VGAM2492 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153577. LOC165140 (Accession XM_092406) is another VGAM2492 host target gene. LOC165140 BINDING

SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC165140, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC165140 BINDING SITE, designated SEQ ID:40116, to the nucleotide sequence of VGAM2492 RNA, herein designated VGAM RNA, also designated SEQ ID:5203.

[84386] Another function of VGAM2492 is therefore inhibition of LOC165140 (Accession XM_092406). Accordingly, utilities of VGAM2492 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC165140. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2493 (VGAM2493) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84387] VGAM2493 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2493 was detected is described hereinabove with reference to Figs. 1-8.

[84388] VGAM2493 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2493 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84389] VGAM2493 gene encodes a VGAM2493 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2493 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2493 precursor RNA is designated SEQ ID:2479, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2479 is located at position 160440 relative to the genome of Mouse Cytomegalovirus 1.

[84390] VGAM2493 precursor RNA folds onto itself, forming VGAM2493 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence

of the nucleotide sequence of the second half thereof.

[84391] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2493 folded precursor RNA into VGAM2493 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2493 RNA is designated SEQ ID:5204, and is provided hereinbelow with reference to the sequence listing part.

[84392] VGAM2493 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2493 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2493 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84393] VGAM2493 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2493 host target

RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2493 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2493 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2493 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84394] The complementary binding of VGAM2493 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2493 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE

II and BINDING SITE III, inhibits translation of VGAM2493 host target RNA into VGAM2493 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84395] It is appreciated that VGAM2493 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2493 host target genes. The mRNA of each one of this plurality of VGAM2493 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2493 RNA, herein designated VGAM RNA, and which when bound by VGAM2493 RNA causes inhibition of translation of respective one or more VGAM2493 host target proteins.

[84396] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2493 gene, herein designated VGAM GENE, on one or more VGAM2493 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated

only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84397] It is yet further appreciated that a function of VGAM2493 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2493 correlate with, and may be deduced from, the identity of the host target genes which VGAM2493 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84398] Nucleotide sequences of the VGAM2493 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2493 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2493 folded precursor RNA, herein designated

VGAM FOLDED PRECURSOR RNA, of VGAM2493 are further described hereinbelow with reference to Table 1.

[84399] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2493 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2493 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84400] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2493 gene, herein designated VGAM is inhibition of expression of VGAM2493 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2493 correlate with, and may be deduced from, the identity of the target genes which VGAM2493 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84401] Attractin (ATRN, Accession NM_139321) is a VGAM2493 host target gene. ATRN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATRN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity

of the nucleotide sequences of ATRN BINDING SITE, designated SEQ ID:29297, to the nucleotide sequence of VGAM2493 RNA, herein designated VGAM RNA, also designated SEQ ID:5204.

[84402] A function of VGAM2493 is therefore inhibition of Attractin (ATRN, Accession NM_139321), a gene which is involved in the initial immune cell clustering during inflammatory response. Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATRN. The function of ATRN and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM53.Cytochrome P450, Subfamily IIIA, Polypeptide 43 (CYP3A43, Accession NM_057096) is another VGAM2493 host target gene. CYP3A43 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CYP3A43, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CYP3A43 BINDING SITE, designated SEQ ID:27662, to the nucleotide sequence of VGAM2493 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5204.

[84403] Another function of VGAM2493 is therefore inhibition of Cytochrome P450, Subfamily IIIA, Polypeptide 43 (CYP3A43, Accession NM_057096), a gene which may be involved in the metabolism of insect hormones and in the breakdown of synthetic insecticides. Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CYP3A43. The function of CYP3A43 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1216.Potassium Voltage-gated Channel, Shal-related Subfamily, Member 2 (KCND2, Accession NM_012281) is another VGAM2493 host target gene. KCND2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KCND2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KCND2 BINDING SITE, designated SEQ ID:14610, to the nucleotide sequence of VGAM2493 RNA, herein designated VGAM RNA, also designated SEQ ID:5204.

[84404] Another function of VGAM2493 is therefore inhibition of Potassium Voltage-gated Channel, Shal-related Subfamily, Member 2 (KCND2, Accession NM_012281), a gene which is prominent in the repolarization phase of the action potential. Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KCND2. The function of KCND2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM449.Solute Carrier Family 22 (organic cation transporter), Member 5 (SLC22A5, Accession NM_003060) is another VGAM2493 host target gene. SLC22A5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC22A5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC22A5 BINDING SITE, designated SEQ ID:9028, to the nucleotide sequence of VGAM2493 RNA, herein designated VGAM RNA, also designated SEQ ID:5204.

[84405] Another function of VGAM2493 is therefore inhibition of Solute Carrier Family 22 (organic cation transporter),

Member 5 (SLC22A5, Accession NM_003060). Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC22A5. Transcription Factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12, Accession NM_003205) is another VGAM2493 host target gene. TCF12 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TCF12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TCF12 BINDING SITE, designated SEQ ID:9203, to the nucleotide sequence of VGAM2493 RNA, herein designated VGAM RNA, also designated SEQ ID:5204.

[84406] Another function of VGAM2493 is therefore inhibition of Transcription Factor 12 (HTF4, helix-loop-helix transcription factors 4) (TCF12, Accession NM_003205), a gene which may play important roles during development of the nervous system as well as in other organ systems. Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TCF12. The function of TCF12 and its association with various diseases and clinical conditions, has

been established by previous studies, as described hereinabove with reference to VGAM308.Tumor Protein P53 (Li-Fraumeni syndrome) (TP53, Accession NM_000546) is another VGAM2493 host target gene. TP53 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by TP53, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TP53 BINDING SITE, designated SEQ ID:6152, to the nucleotide sequence of VGAM2493 RNA, herein designated VGAM RNA, also designated SEQ ID:5204.

[84407] Another function of VGAM2493 is therefore inhibition of Tumor Protein P53 (Li-Fraumeni syndrome) (TP53, Accession NM_000546). Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TP53. MGC4172 (Accession NM_024308) is another VGAM2493 host target gene. MGC4172 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC4172, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nu-

cleotide sequences of MGC4172 BINDING SITE, designated SEQ ID:23600, to the nucleotide sequence of VGAM2493 RNA, herein designated VGAM RNA, also designated SEQ ID:5204.

[84408] Another function of VGAM2493 is therefore inhibition of MGC4172 (Accession NM_024308). Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC4172. PDZ Domain Containing 2 (PDZD2, Accession XM_087705) is another VGAM2493 host target gene. PDZD2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PDZD2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PDZD2 BINDING SITE, designated SEQ ID:39387, to the nucleotide sequence of VGAM2493 RNA, herein designated VGAM RNA, also designated SEQ ID:5204.

[84409] Another function of VGAM2493 is therefore inhibition of PDZ Domain Containing 2 (PDZD2, Accession XM_087705). Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with PDZD2. RRN3 (Accession NM_018427) is another VGAM2493 host target gene. RRN3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RRN3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RRN3 BINDING SITE, designated SEQ ID:20491, to the nucleotide sequence of VGAM2493 RNA, herein designated VGAM RNA, also designated SEQ ID:5204.

[84410] Another function of VGAM2493 is therefore inhibition of RRN3 (Accession NM_018427). Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RRN3. LOC150951 (Accession XM_097975) is another VGAM2493 host target gene. LOC150951 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150951, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150951 BINDING SITE, designated SEQ ID:41276, to the nucleotide sequence of VGAM2493 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5204.

[84411] Another function of VGAM2493 is therefore inhibition of LOC150951 (Accession XM_097975). Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150951. LOC152274 (Accession XM_087418) is another VGAM2493 host target gene. LOC152274 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152274, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152274 BINDING SITE, designated SEQ ID:39233, to the nucleotide sequence of VGAM2493 RNA, herein designated VGAM RNA, also designated SEQ ID:5204.

[84412] Another function of VGAM2493 is therefore inhibition of LOC152274 (Accession XM_087418). Accordingly, utilities of VGAM2493 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152274. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2494 (VGAM2494) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84413] VGAM2494 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2494 was detected is described hereinabove with reference to Figs. 1-8.

[84414] VGAM2494 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2494 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84415] VGAM2494 gene encodes a VGAM2494 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2494 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2494 precursor RNA is designated SEQ ID:2480, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2480 is located at position 208377 relative to the genome of Mouse Cytomegalovirus 1.

[84416] VGAM2494 precursor RNA folds onto itself, forming

VGAM2494 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84417] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2494 folded precursor RNA into VGAM2494 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2494 RNA is designated SEQ ID:5205, and is provided hereinbelow with reference to the sequence listing part.

[84418] VGAM2494 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2494 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2494 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84419] VGAM2494 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2494 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2494 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2494 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2494 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84420] The complementary binding of VGAM2494 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2494 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2494 host target RNA into VGAM2494 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84421] It is appreciated that VGAM2494 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2494 host target genes. The mRNA of each one of this plurality of VGAM2494 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2494 RNA, herein designated VGAM RNA, and which when bound by VGAM2494 RNA causes inhibition of translation of respective one or more VGAM2494 host target proteins.

[84422] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2494 gene, herein designated VGAM GENE, on one or more VGAM2494 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84423] It is yet further appreciated that a function of VGAM2494 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2494 correlate with, and may be deduced from, the identity of the host target genes which VGAM2494 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[84424] Nucleotide sequences of the VGAM2494 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2494 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2494 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2494 are further described hereinbelow with reference to Table 1.

[84425] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2494 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2494 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84426] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2494 gene, herein designated VGAM is inhibition of expression of VGAM2494 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2494 correlate with, and may be deduced from, the identity of the target genes which VGAM2494 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[84427] V-raf Murine Sarcoma 3611 Viral Oncogene Homolog 1 (ARAF1, Accession XM_033884) is a VGAM2494 host target gene. ARAF1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARAF1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARAF1 BINDING SITE, designated SEQ ID:31981, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84428] A function of VGAM2494 is therefore inhibition of V-raf Murine Sarcoma 3611 Viral Oncogene Homolog 1 (ARAF1, Accession XM_033884), a gene which may play a critical role in cell growth and development. Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARAF1. The function of ARAF1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM996.Calcium/calmodulin-dependent Protein Kinase IV (CAMK4, Accession NM_001744) is an-

other VGAM2494 host target gene. CAMK4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CAMK4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CAMK4 BINDING SITE, designated SEQ ID:7481, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84429] Another function of VGAM2494 is therefore inhibition of Calcium/calmodulin-dependent Protein Kinase IV (CAMK4, Accession NM_001744), a gene which is a heat-stable, acidic, calmodulin-binding protein. Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CAMK4. The function of CAMK4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM578.CD34 Antigen (CD34, Accession NM_001773) is another VGAM2494 host target gene. CD34 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CD34, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CD34 BINDING SITE, designated SEQ ID:7535, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84430] Another function of VGAM2494 is therefore inhibition of CD34 Antigen (CD34, Accession NM_001773), a gene which is a monomeric cell surface antigen that is selectively expressed on human hematopoietic progenitor cells. Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CD34. The function of CD34 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM55.Fibroblast Growth Factor 2 (basic) (FGF2, Accession NM_002006) is another VGAM2494 host target gene. FGF2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FGF2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FGF2 BINDING SITE, designated SEQ ID:7737, to the nucleotide sequence of

VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84431] Another function of VGAM2494 is therefore inhibition of Fibroblast Growth Factor 2 (basic) (FGF2, Accession NM_002006), a gene which probably involved in nervous system development and function. Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FGF2. The function of FGF2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM51.Frizzled Homolog 4 (Drosophila) (FZD4, Accession NM_012193) is another VGAM2494 host target gene. FZD4 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FZD4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FZD4 BINDING SITE, designated SEQ ID:14486, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84432] Another function of VGAM2494 is therefore inhibition of Frizzled Homolog 4 (Drosophila) (FZD4, Accession

NM_012193), a gene which may function in cell polarity, cell fate specification and cancer; similar to frizzled receptor family, has seven transmembrane domains. Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FZD4. The function of FZD4 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM309.Maltase-glucoamylase (alpha-glucosidase) (MGAM, Accession XM_051351) is another VGAM2494 host target gene. MGAM BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGAM, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGAM BINDING SITE, designated SEQ ID:35824, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84433] Another function of VGAM2494 is therefore inhibition of Maltase-glucoamylase (alpha-glucosidase) (MGAM, Accession XM_051351), a gene which plays a role in the final

steps of digestion of starch. Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGAM. The function of MGAM and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM791.Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 13 (SERPINB13, Accession NM_012397) is another VGAM2494 host target gene. SERPINB13 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SERPINB13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SERPINB13 BINDING SITE, designated SEQ ID:14763, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84434] Another function of VGAM2494 is therefore inhibition of Serine (or cysteine) Proteinase Inhibitor, Clade B (ovalbumin), Member 13 (SERPINB13, Accession NM_012397), a gene which plays a role in the proliferation or differentiation of keratinocytes. Accordingly, utilities of

VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SERPINB13. The function of SERPINB13 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1924.Sarcoglycan, Gamma (35kDa dystrophin-associated glycoprotein) (SGCG, Accession NM_000231) is another VGAM2494 host target gene. SGCG BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SGCG, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SGCG BINDING SITE, designated SEQ ID:5742, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84435] Another function of VGAM2494 is therefore inhibition of Sarcoglycan, Gamma (35kDa dystrophin-associated glycoprotein) (SGCG, Accession NM_000231). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SGCG. VENT-like Homeobox 2 (VENTX2, Accession NM_014468) is another VGAM2494 host target gene.

VENTX2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by VENTX2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of VENTX2 BINDING SITE, designated SEQ ID:15816, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84436] Another function of VGAM2494 is therefore inhibition of VENT-like Homeobox 2 (VENTX2, Accession NM_014468). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with VENTX2. Echinoderm Microtubule Associated Protein Like 4 (EML4, Accession NM_019063) is another VGAM2494 host target gene. EML4 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by EML4, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EML4 BINDING SITE, designated SEQ ID:21144, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA,

also designated SEQ ID:5205.

[84437] Another function of VGAM2494 is therefore inhibition of Echinoderm Microtubule Associated Protein Like 4 (EML4, Accession NM_019063). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EML4. FLJ10936 (Accession NM_018279) is another VGAM2494 host target gene. FLJ10936 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ10936, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10936 BINDING SITE, designated SEQ ID:20270, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84438] Another function of VGAM2494 is therefore inhibition of FLJ10936 (Accession NM_018279). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10936. KIAA0763 (Accession NM_014869) is another VGAM2494 host target gene. KIAA0763 BINDING SITE is HOST TARGET binding site found in the 3` untranslated

region of mRNA encoded by KIAA0763, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0763 BINDING SITE, designated SEQ ID:16970, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84439] Another function of VGAM2494 is therefore inhibition of KIAA0763 (Accession NM_014869). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0763. KIAA1297 (Accession XM_051005) is another VGAM2494 host target gene. KIAA1297 BINDING SITE1 and KIAA1297 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by KIAA1297, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1297 BINDING SITE1 and KIAA1297 BINDING SITE2, designated SEQ ID:35716 and SEQ ID:35717 respectively, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84440] Another function of VGAM2494 is therefore inhibition of KIAA1297 (Accession XM_051005). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1297. MGC2865 (Accession NM_032375) is another VGAM2494 host target gene. MGC2865 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC2865, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2865 BINDING SITE, designated SEQ ID:26167, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84441] Another function of VGAM2494 is therefore inhibition of MGC2865 (Accession NM_032375). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2865. MGC9753 (Accession NM_033419) is another VGAM2494 host target gene. MGC9753 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MGC9753, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC9753 BINDING SITE, designated SEQ ID:27242, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84442] Another function of VGAM2494 is therefore inhibition of MGC9753 (Accession NM_033419). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC9753. Methionine Sulfoxide Reductase A (MSRA, Accession NM_012331) is another VGAM2494 host target gene. MSRA BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MSRA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MSRA BINDING SITE, designated SEQ ID:14721, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84443] Another function of VGAM2494 is therefore inhibition of Methionine Sulfoxide Reductase A (MSRA, Accession NM_012331). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clini-

cal conditions associated with MSRA. Nuclear Factor of Activated T-cells 5, Tonicity-responsive (NFAT5, Accession NM_138714) is another VGAM2494 host target gene. NFAT5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by NFAT5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NFAT5 BINDING SITE, designated SEQ ID:28957, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84444] Another function of VGAM2494 is therefore inhibition of Nuclear Factor of Activated T-cells 5, Tonicity-responsive (NFAT5, Accession NM_138714). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NFAT5. PR Domain Containing 13 (PRDM13, Accession NM_021620) is another VGAM2494 host target gene. PRDM13 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRDM13, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III.

Table 2 illustrates the complementarity of the nucleotide sequences of PRDM13 BINDING SITE, designated SEQ ID:22255, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84445] Another function of VGAM2494 is therefore inhibition of PR Domain Containing 13 (PRDM13, Accession NM_021620). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRDM13. PSR (Accession XM_036784) is another VGAM2494 host target gene. PSR BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PSR, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PSR BINDING SITE, designated SEQ ID:32501, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84446] Another function of VGAM2494 is therefore inhibition of PSR (Accession XM_036784). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PSR.

LOC134689 (Accession XM_068963) is another VGAM2494 host target gene. LOC134689 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC134689, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC134689 BINDING SITE, designated SEQ ID:37383, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84447] Another function of VGAM2494 is therefore inhibition of LOC134689 (Accession XM_068963). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC134689. LOC151507 (Accession XM_087225) is another VGAM2494 host target gene. LOC151507 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC151507, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC151507 BINDING SITE, designated SEQ ID:39126, to the nucleotide sequence of VGAM2494 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5205.

[84448] Another function of VGAM2494 is therefore inhibition of LOC151507 (Accession XM_087225). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC151507. LOC164295 (Accession XM_092767) is another VGAM2494 host target gene. LOC164295 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC164295, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164295 BINDING SITE, designated SEQ ID:40142, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84449] Another function of VGAM2494 is therefore inhibition of LOC164295 (Accession XM_092767). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164295. LOC219513 (Accession XM_169166) is another VGAM2494 host target gene. LOC219513 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC219513, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219513 BINDING SITE, designated SEQ ID:45295, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84450] Another function of VGAM2494 is therefore inhibition of LOC219513 (Accession XM_169166). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219513. LOC253737 (Accession XM_171409) is another VGAM2494 host target gene. LOC253737 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC253737, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253737 BINDING SITE, designated SEQ ID:46046, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84451] Another function of VGAM2494 is therefore inhibition of LOC253737 (Accession XM_171409). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC253737. LOC51631 (Accession XM_042779) is another VGAM2494 host target gene. LOC51631 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC51631, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC51631 BINDING SITE, designated SEQ ID:33768, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84452] Another function of VGAM2494 is therefore inhibition of LOC51631 (Accession XM_042779). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC51631. LOC58509 (Accession XM_114002) is another VGAM2494 host target gene. LOC58509 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC58509, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC58509 BINDING SITE, designated SEQ ID:42613, to the

nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84453] Another function of VGAM2494 is therefore inhibition of LOC58509 (Accession XM_114002). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC58509. LOC93070 (Accession XM_049046) is another VGAM2494 host target gene. LOC93070 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC93070, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC93070 BINDING SITE, designated SEQ ID:35325, to the nucleotide sequence of VGAM2494 RNA, herein designated VGAM RNA, also designated SEQ ID:5205.

[84454] Another function of VGAM2494 is therefore inhibition of LOC93070 (Accession XM_049046). Accordingly, utilities of VGAM2494 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC93070. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Ad-

dress Messenger 2495 (VGAM2495) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84455] VGAM2495 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2495 was detected is described hereinabove with reference to Figs. 1-8.

[84456] VGAM2495 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2495 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84457] VGAM2495 gene encodes a VGAM2495 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2495 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2495 precursor RNA is designated SEQ ID:2481, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2481 is located at position 106389 relative to the genome of Mouse Cytomegalovirus 1.

[84458] VGAM2495 precursor RNA folds onto itself, forming VGAM2495 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84459] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2495 folded precursor RNA into VGAM2495 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2495 RNA is designated SEQ ID:5206, and is provided hereinbelow with reference to the sequence listing part.

[84460] VGAM2495 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2495 host target RNA, herein designated

VGAM HOST TARGET RNA. VGAM2495 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84461] VGAM2495 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2495 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2495 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2495 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2495 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding

sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84462] The complementary binding of VGAM2495 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2495 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2495 host target RNA into VGAM2495 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84463] It is appreciated that VGAM2495 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2495 host target genes. The mRNA of each one of this plurality of VGAM2495 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2495 RNA, herein designated VGAM RNA, and which when bound by VGAM2495 RNA causes inhibition of translation of respective one or more VGAM2495 host target proteins.

[84464] It is further appreciated by one skilled in the art that the

mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2495 gene, herein designated VGAM GENE, on one or more VGAM2495 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84465] It is yet further appreciated that a function of VGAM2495 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2495 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2495 correlate with, and may be deduced from, the identity of

the host target genes which VGAM2495 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84466] Nucleotide sequences of the VGAM2495 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2495 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2495 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2495 are further described hereinbelow with reference to Table 1.

[84467] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2495 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2495 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84468] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2495 gene, herein designated VGAM is inhibition of expression of VGAM2495 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2495 correlate with, and may be deduced from, the identity of the target genes which VGAM2495

binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84469] HRIHFB2436 (Accession NM_014345) is a VGAM2495 host target gene. HRIHFB2436 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by HRIHFB2436, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HRIHFB2436 BINDING SITE, designated SEQ ID:15665, to the nucleotide sequence of VGAM2495 RNA, herein designated VGAM RNA, also designated SEQ ID:5206.

[84470] A function of VGAM2495 is therefore inhibition of HRIHFB2436 (Accession NM_014345). Accordingly, utilities of VGAM2495 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HRIHFB2436. MGC12921 (Accession XM_033362) is another VGAM2495 host target gene. MGC12921 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC12921, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

MGC12921 BINDING SITE, designated SEQ ID:31899, to the nucleotide sequence of VGAM2495 RNA, herein designated VGAM RNA, also designated SEQ ID:5206.

[84471] Another function of VGAM2495 is therefore inhibition of MGC12921 (Accession XM_033362). Accordingly, utilities of VGAM2495 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC12921. LOC153579 (Accession XM_087714) is another VGAM2495 host target gene. LOC153579 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC153579, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153579 BINDING SITE, designated SEQ ID:39405, to the nucleotide sequence of VGAM2495 RNA, herein designated VGAM RNA, also designated SEQ ID:5206.

[84472] Another function of VGAM2495 is therefore inhibition of LOC153579 (Accession XM_087714). Accordingly, utilities of VGAM2495 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC153579. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the

present invention, referred to here as Viral Genomic Address Messenger 2496 (VGAM2496) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84473] VGAM2496 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2496 was detected is described hereinabove with reference to Figs. 1-8.

[84474] VGAM2496 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2496 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84475] VGAM2496 gene encodes a VGAM2496 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2496 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2496 precursor RNA is designated SEQ ID:2482, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2482 is located at position 186483 relative to the

genome of Mouse Cytomegalovirus 1.

[84476] VGAM2496 precursor RNA folds onto itself, forming VGAM2496 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84477] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2496 folded precursor RNA into VGAM2496 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 43%) nucleotide sequence of VGAM2496 RNA is designated SEQ ID:5207, and is provided hereinbelow with reference to the sequence listing part.

[84478] VGAM2496 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger

RNA, VGAM2496 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2496 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84479] VGAM2496 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2496 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2496 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2496 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2496 host target RNA, herein designated VGAM HOST TARGET RNA. It is further

appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84480] The complementary binding of VGAM2496 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2496 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2496 host target RNA into VGAM2496 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84481] It is appreciated that VGAM2496 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2496 host target genes. The mRNA of each one of this plurality of VGAM2496 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2496 RNA, herein designated VGAM RNA, and which when bound by VGAM2496 RNA causes inhibition of translation of respective one or more VGAM2496 host target proteins.

[84482] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2496 gene, herein designated VGAM GENE, on one or more VGAM2496 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84483] It is yet further appreciated that a function of VGAM2496 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2496 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2496

correlate with, and may be deduced from, the identity of the host target genes which VGAM2496 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84484] Nucleotide sequences of the VGAM2496 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2496 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2496 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2496 are further described hereinbelow with reference to Table 1.

[84485] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2496 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2496 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84486] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2496 gene, herein designated VGAM is inhibition of expression of VGAM2496 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2496 correlate with, and may be deduced

from, the identity of the target genes which VGAM2496 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84487] Podocalyxin-like (PODXL, Accession NM_005397) is a VGAM2496 host target gene. PODXL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PODXL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PODXL BINDING SITE, designated SEQ ID:11874, to the nucleotide sequence of VGAM2496 RNA, herein designated VGAM RNA, also designated SEQ ID:5207.

[84488] A function of VGAM2496 is therefore inhibition of Podocalyxin-like (PODXL, Accession NM_005397), a gene which is an antiadhesin. Accordingly, utilities of VGAM2496 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PODXL. The function of PODXL and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM247.Artemin (ARTN, Accession NM_003976) is another VGAM2496 host target gene. ARTN BINDING SITE

is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARTN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARTN BINDING SITE, designated SEQ ID:10110, to the nucleotide sequence of VGAM2496 RNA, herein designated VGAM RNA, also designated SEQ ID:5207.

[84489] Another function of VGAM2496 is therefore inhibition of Artemin (ARTN, Accession NM_003976). Accordingly, utilities of VGAM2496 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARTN. FLJ23191 (Accession NM_024574) is another VGAM2496 host target gene. FLJ23191 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ23191, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23191 BINDING SITE, designated SEQ ID:23804, to the nucleotide sequence of VGAM2496 RNA, herein designated VGAM RNA, also designated SEQ ID:5207.

[84490] Another function of VGAM2496 is therefore inhibition of

FLJ23191 (Accession NM_024574). Accordingly, utilities of VGAM2496 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23191. FLJ23323 (Accession NM_024654) is another VGAM2496 host target gene. FLJ23323 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ23323, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ23323 BINDING SITE, designated SEQ ID:23955, to the nucleotide sequence of VGAM2496 RNA, herein designated VGAM RNA, also designated SEQ ID:5207.

[84491] Another function of VGAM2496 is therefore inhibition of FLJ23323 (Accession NM_024654). Accordingly, utilities of VGAM2496 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ23323. Neuron Navigator 3 (NAV3, Accession NM_014903) is another VGAM2496 host target gene. NAV3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NAV3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2

illustrates the complementarity of the nucleotide sequences of NAV3 BINDING SITE, designated SEQ ID:17091, to the nucleotide sequence of VGAM2496 RNA, herein designated VGAM RNA, also designated SEQ ID:5207.

[84492] Another function of VGAM2496 is therefore inhibition of Neuron Navigator 3 (NAV3, Accession NM_014903). Accordingly, utilities of VGAM2496 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NAV3. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2497 (VGAM2497) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84493] VGAM2497 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2497 was detected is described hereinabove with reference to Figs. 1-8.

[84494] VGAM2497 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2497 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the

human genome.

[84495] VGAM2497 gene encodes a VGAM2497 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2497 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2497 precursor RNA is designated SEQ ID:2483, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2483 is located at position 212016 relative to the genome of Mouse Cytomegalovirus 1.

[84496] VGAM2497 precursor RNA folds onto itself, forming VGAM2497 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84497] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2497 folded precursor RNA into VGAM2497 RNA, herein designated VGAM RNA, a single stranded ~22

nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 46%) nucleotide sequence of VGAM2497 RNA is designated SEQ ID:5208, and is provided hereinbelow with reference to the sequence listing part.

[84498] VGAM2497 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2497 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2497 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84499] VGAM2497 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2497 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2497 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide se-

quence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2497 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2497 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84500] The complementary binding of VGAM2497 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2497 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2497 host target RNA into VGAM2497 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84501] It is appreciated that VGAM2497 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2497 host target genes. The mRNA of each one of this plurality of VGAM2497 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2497 RNA, herein designated VGAM RNA, and which when bound by VGAM2497 RNA causes inhibition of translation of respective one or more VGAM2497 host target proteins.

[84502] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2497 gene, herein designated VGAM GENE, on one or more VGAM2497 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84503] It is yet further appreciated that a function of VGAM2497 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2497 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2497 correlate with, and may be deduced from, the identity of the host target genes which VGAM2497 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84504] Nucleotide sequences of the VGAM2497 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2497 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2497 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2497 are further described hereinbelow with reference to Table 1.

[84505] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2497 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2497 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84506] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2497 gene, herein designated VGAM is inhibition of expression of VGAM2497 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2497 correlate with, and may be deduced from, the identity of the target genes which VGAM2497 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84507] Fanconi Anemia, Complementation Group A (FANCA, Accession NM_000135) is a VGAM2497 host target gene. FANCA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FANCA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FANCA BINDING SITE, designated SEQ ID:5629, to the nucleotide sequence of VGAM2497 RNA, herein designated VGAM RNA, also designated SEQ

ID:5208.

[84508] A function of VGAM2497 is therefore inhibition of Fanconi Anemia, Complementation Group A (FANCA, Accession NM_000135). Accordingly, utilities of VGAM2497 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FANCA. Myelin Basic Protein (MBP, Accession XM_117096) is another VGAM2497 host target gene. MBP BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MBP, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MBP BINDING SITE, designated SEQ ID:43222, to the nucleotide sequence of VGAM2497 RNA, herein designated VGAM RNA, also designated SEQ ID:5208.

[84509] Another function of VGAM2497 is therefore inhibition of Myelin Basic Protein (MBP, Accession XM_117096), a gene which Myelin basic protein; a constituent of myelin, plays a role in nerve function. Accordingly, utilities of VGAM2497 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MBP. The function of MBP and its association with various dis-

eases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1959.Myosin ID (MYO1D, Accession XM_050041) is another VGAM2497 host target gene. MYO1D BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MYO1D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MYO1D BINDING SITE, designated SEQ ID:35549, to the nucleotide sequence of VGAM2497 RNA, herein designated VGAM RNA, also designated SEQ ID:5208.

[84510] Another function of VGAM2497 is therefore inhibition of Myosin ID (MYO1D, Accession XM_050041), a gene which is an unconventional myosin. Accordingly, utilities of VGAM2497 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MYO1D. The function of MYO1D and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM126.MGC2817 (Accession XM_046613) is another VGAM2497 host target gene. MGC2817 BINDING SITE is HOST TARGET binding site found in the 5` un-

translated region of mRNA encoded by MGC2817, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC2817 BINDING SITE, designated SEQ ID:34764, to the nucleotide sequence of VGAM2497 RNA, herein designated VGAM RNA, also designated SEQ ID:5208.

[84511] Another function of VGAM2497 is therefore inhibition of MGC2817 (Accession XM_046613). Accordingly, utilities of VGAM2497 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC2817. SEC24 Related Gene Family, Member D (S. cerevisiae) (SEC24D, Accession NM_014822) is another VGAM2497 host target gene. SEC24D BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by SEC24D, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SEC24D BINDING SITE, designated SEQ ID:16799, to the nucleotide sequence of VGAM2497 RNA, herein designated VGAM RNA, also designated SEQ ID:5208.

[84512] Another function of VGAM2497 is therefore inhibition of

SEC24 Related Gene Family, Member D (S. cerevisiae) (SEC24D, Accession NM_014822). Accordingly, utilities of VGAM2497 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SEC24D. Ubiquitin Specific Protease 2 (USP2, Accession NM_004205) is another VGAM2497 host target gene. USP2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by USP2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USP2 BINDING SITE, designated SEQ ID:10402, to the nucleotide sequence of VGAM2497 RNA, herein designated VGAM RNA, also designated SEQ ID:5208.

[84513] Another function of VGAM2497 is therefore inhibition of Ubiquitin Specific Protease 2 (USP2, Accession NM_004205). Accordingly, utilities of VGAM2497 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USP2. XPO5 (Accession XM_166042) is another VGAM2497 host target gene. XPO5 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by XPO5, corresponding to a HOST TARGET binding site such as

BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of XPO5 BINDING SITE, designated SEQ ID:43841, to the nucleotide sequence of VGAM2497 RNA, herein designated VGAM RNA, also designated SEQ ID:5208.

[84514] Another function of VGAM2497 is therefore inhibition of XPO5 (Accession XM_166042). Accordingly, utilities of VGAM2497 include diagnosis, prevention and treatment of diseases and clinical conditions associated with XPO5. LOC153603 (Accession XM_087715) is another VGAM2497 host target gene. LOC153603 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC153603, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC153603 BINDING SITE, designated SEQ ID:39406, to the nucleotide sequence of VGAM2497 RNA, herein designated VGAM RNA, also designated SEQ ID:5208.

[84515] Another function of VGAM2497 is therefore inhibition of LOC153603 (Accession XM_087715). Accordingly, utilities of VGAM2497 include diagnosis, prevention and treatment of diseases and clinical conditions associated with

LOC153603. LOC164714 (Accession XM_104657) is another VGAM2497 host target gene. LOC164714 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC164714, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC164714 BINDING SITE, designated SEQ ID:42178, to the nucleotide sequence of VGAM2497 RNA, herein designated VGAM RNA, also designated SEQ ID:5208.

[84516] Another function of VGAM2497 is therefore inhibition of LOC164714 (Accession XM_104657). Accordingly, utilities of VGAM2497 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC164714. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2498 (VGAM2498) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84517] VGAM2498 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene.

The method by which VGAM2498 was detected is described hereinabove with reference to Figs. 1-8.

[84518] VGAM2498 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2498 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84519] VGAM2498 gene encodes a VGAM2498 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2498 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2498 precursor RNA is designated SEQ ID:2484, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2484 is located at position 211848 relative to the genome of Mouse Cytomegalovirus 1.

[84520] VGAM2498 precursor RNA folds onto itself, forming VGAM2498 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide

sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84521] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2498 folded precursor RNA into VGAM2498 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 61%) nucleotide sequence of VGAM2498 RNA is designated SEQ ID:5209, and is provided hereinbelow with reference to the sequence listing part.

[84522] VGAM2498 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2498 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2498 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84523] VGAM2498 RNA, herein designated VGAM RNA, binds

complementarily to one or more host target binding sites located in untranslated regions of VGAM2498 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2498 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2498 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2498 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84524] The complementary binding of VGAM2498 RNA, herein designated VGAM RNA, to host target binding sites on

VGAM2498 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2498 host target RNA into VGAM2498 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84525] It is appreciated that VGAM2498 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2498 host target genes. The mRNA of each one of this plurality of VGAM2498 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2498 RNA, herein designated VGAM RNA, and which when bound by VGAM2498 RNA causes inhibition of translation of respective one or more VGAM2498 host target proteins.

[84526] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2498 gene, herein designated VGAM GENE, on one or more VGAM2498 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove

with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84527] It is yet further appreciated that a function of VGAM2498 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2498 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2498 correlate with, and may be deduced from, the identity of the host target genes which VGAM2498 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84528] Nucleotide sequences of the VGAM2498 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2498 RNA, herein designated VGAM RNA,

and a schematic representation of the secondary folding of VGAM2498 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2498 are further described hereinbelow with reference to Table 1.

[84529] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2498 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2498 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84530] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2498 gene, herein designated VGAM is inhibition of expression of VGAM2498 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2498 correlate with, and may be deduced from, the identity of the target genes which VGAM2498 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84531] Cas-Br-M (murine) Ecotropic Retroviral Transforming Sequence B (CBLB, Accession NM_004351) is a VGAM2498 host target gene. CBLB BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA

encoded by CBLB, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CBLB BINDING SITE, designated SEQ ID:10552, to the nucleotide sequence of VGAM2498 RNA, herein designated VGAM RNA, also designated SEQ ID:5209.

[84532] A function of VGAM2498 is therefore inhibition of Cas-Br-M (murine) Ecotropic Retroviral Transforming Sequence B (CBLB, Accession NM_004351), a gene which SH3 binding protein with similarity to human CBL; interacts and regulates signal transduction proteins. Accordingly, utilities of VGAM2498 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CBLB. The function of CBLB and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM401.Cadherin, EGF LAG Seven-pass G-type Receptor 1 (flamingo homolog, Drosophila) (CELSR1, Accession NM_014246) is another VGAM2498 host target gene. CELSR1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CELSR1, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CELSR1 BINDING SITE, designated SEQ ID:15515, to the nucleotide sequence of VGAM2498 RNA, herein designated VGAM RNA, also designated SEQ ID:5209.

[84533] Another function of VGAM2498 is therefore inhibition of Cadherin, EGF LAG Seven-pass G-type Receptor 1 (flamingo homolog, Drosophila) (CELSR1, Accession NM_014246), a gene which is involved in contact-mediated communication. Accordingly, utilities of VGAM2498 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CELSR1. The function of CELSR1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM459.Protein Kinase C, Eta (PRKCH, Accession NM_006255) is another VGAM2498 host target gene. PRKCH BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PRKCH, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide

sequences of PRKCH BINDING SITE, designated SEQ ID:12934, to the nucleotide sequence of VGAM2498 RNA, herein designated VGAM RNA, also designated SEQ ID:5209.

[84534] Another function of VGAM2498 is therefore inhibition of Protein Kinase C, Eta (PRKCH, Accession NM_006255), a gene which is calcium-independent, phospholipid-dependent, serine- and threonine-specific enzyme. Accordingly, utilities of VGAM2498 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PRKCH. The function of PRKCH has been established by previous studies. Protein kinase C (PKC) is involved in one of the major signal transduction systems, which is activated upon external stimulation of cells by various ligands. For further background information on the PKC family, see PRKCA (OMIM Ref. No. 176960). By screening a human keratinocyte cDNA library using PRKCA fragments as probes, Bacher et al. (1991) isolated a cDNA encoding PRKCH, which they called PKCL. The predicted PRKCH protein contains 680 amino acids and shows highest homology with PRKCE (OMIM Ref. No. 176975). PRKCH has a consensus ATP-binding site, a catalytic kinase domain, and a conserved cysteine-rich domain. Northern blot

analysis of rat tissues detected a 4.2-kb transcript at highest levels in lung, with lower levels in heart and skin. The PRKCH transcript was also detected in the human skin carcinoma cell line SCL-1, the human epidermoid carcinoma cell line A431, and in HaCaT human skin keratinocytes. Transfection of COS cells with a PRKCH expression vector determined that this protein has phorbol ester-binding ability and kinase activity. By FISH, Quan and Fisher (1999) mapped the PRKCH gene to 14q22-q23

[84535] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84536] Bacher, N.; Zisman, Y.; Berent, E.; Livneh, E. : Isolation and characterization of PKC-L, a new member of the protein kinase C-related gene family specifically expressed in lung, skin, and heart. Molec. Cell. Biol. 11: 126-133, 1991. ; and

[84537] Quan, T.; Fisher, G. J. : Cloning and characterization of the human protein kinase C-eta promoter. J. Biol. Chem. 274: 28566-28574, 1999.

[84538] Further studies establishing the function and utilities of PRKCH are found in John Hopkins OMIM database record ID 605437, and in sited publications numbered

4429-4430 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Retinoid X Receptor, Alpha (RXRA, Accession NM_002957) is another VGAM2498 host target gene. RXRA BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RXRA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RXRA BINDING SITE, designated SEQ ID:8870, to the nucleotide sequence of VGAM2498 RNA, herein designated VGAM RNA, also designated SEQ ID:5209.

[84539] Another function of VGAM2498 is therefore inhibition of Retinoid X Receptor, Alpha (RXRA, Accession NM_002957), a gene which activates genes required for vitamin A metabolism, binds 9-cis retinoic acid. Accordingly, utilities of VGAM2498 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RXRA. The function of RXRA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM349.A Kinase (PRKA) Anchor Protein (gravin) 12 (AKAP12, Accession NM_144497) is another

VGAM2498 host target gene. AKAP12 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by AKAP12, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of AKAP12 BINDING SITE, designated SEQ ID:29313, to the nucleotide sequence of VGAM2498 RNA, herein designated VGAM RNA, also designated SEQ ID:5209.

[84540] Another function of VGAM2498 is therefore inhibition of A Kinase (PRKA) Anchor Protein (gravin) 12 (AKAP12, Accession NM_144497). Accordingly, utilities of VGAM2498 include diagnosis, prevention and treatment of diseases and clinical conditions associated with AKAP12. KIAA0644 (Accession NM_014817) is another VGAM2498 host target gene. KIAA0644 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0644, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0644 BINDING SITE, designated SEQ ID:16784, to the nucleotide sequence of VGAM2498 RNA, herein designated VGAM RNA, also designated SEQ

ID:5209.

[84541] Another function of VGAM2498 is therefore inhibition of KIAA0644 (Accession NM_014817). Accordingly, utilities of VGAM2498 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0644. LOC152345 (Accession XM_087442) is another VGAM2498 host target gene. LOC152345 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC152345, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC152345 BINDING SITE, designated SEQ ID:39266, to the nucleotide sequence of VGAM2498 RNA, herein designated VGAM RNA, also designated SEQ ID:5209.

[84542] Another function of VGAM2498 is therefore inhibition of LOC152345 (Accession XM_087442). Accordingly, utilities of VGAM2498 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152345. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2499 (VGAM2499) viral gene, which

modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84543] VGAM2499 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2499 was detected is described hereinabove with reference to Figs. 1-8.

[84544] VGAM2499 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2499 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84545] VGAM2499 gene encodes a VGAM2499 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2499 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2499 precursor RNA is designated SEQ ID:2485, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2485 is located at position 88282 relative to the genome of Mouse Cytomegalovirus 1.

[84546] VGAM2499 precursor RNA folds onto itself, forming

VGAM2499 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84547] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2499 folded precursor RNA into VGAM2499 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 45%) nucleotide sequence of VGAM2499 RNA is designated SEQ ID:5210, and is provided hereinbelow with reference to the sequence listing part.

[84548] VGAM2499 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2499 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2499 host target RNA

comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84549] VGAM2499 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2499 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2499 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2499 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2499 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example

only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84550] The complementary binding of VGAM2499 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2499 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2499 host target RNA into VGAM2499 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84551] It is appreciated that VGAM2499 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2499 host target genes. The mRNA of each one of this plurality of VGAM2499 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2499 RNA, herein designated VGAM RNA, and which when bound by VGAM2499 RNA causes inhibition of translation of respective one or more VGAM2499 host target proteins.

[84552] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with

specific reference to translational inhibition exerted by VGAM2499 gene, herein designated VGAM GENE, on one or more VGAM2499 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84553] It is yet further appreciated that a function of VGAM2499 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2499 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2499 correlate with, and may be deduced from, the identity of the host target genes which VGAM2499 binds and in-

hibits, and the function of these host target genes, as elaborated hereinbelow.

[84554] Nucleotide sequences of the VGAM2499 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2499 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2499 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2499 are further described hereinbelow with reference to Table 1.

[84555] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2499 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2499 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84556] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2499 gene, herein designated VGAM is inhibition of expression of VGAM2499 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2499 correlate with, and may be deduced from, the identity of the target genes which VGAM2499 binds and inhibits, and the function of these target genes,

as elaborated hereinbelow.

[84557] GASC1 (Accession XM_034624) is a VGAM2499 host target gene. GASC1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GASC1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GASC1 BINDING SITE, designated SEQ ID:32124, to the nucleotide sequence of VGAM2499 RNA, herein designated VGAM RNA, also designated SEQ ID:5210.

[84558] A function of VGAM2499 is therefore inhibition of GASC1 (Accession XM_034624), a gene which may play an important role in the development and/or progression of various types of cancer . Accordingly, utilities of VGAM2499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GASC1. The function of GASC1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1671.Insulinoma-associated 1 (INSM1, Accession NM_002196) is another VGAM2499 host target gene. INSM1 BINDING SITE is HOST TARGET binding site found in

the 3` untranslated region of mRNA encoded by INSM1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of INSM1 BINDING SITE, designated SEQ ID:7951, to the nucleotide sequence of VGAM2499 RNA, herein designated VGAM RNA, also designated SEQ ID:5210.

[84559] Another function of VGAM2499 is therefore inhibition of Insulinoma-associated 1 (INSM1, Accession NM_002196). Accordingly, utilities of VGAM2499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with INSM1. Chromosome 17 Open Reading Frame 26 (C17orf26, Accession NM_139177) is another VGAM2499 host target gene. C17orf26 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by C17orf26, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C17orf26 BINDING SITE, designated SEQ ID:29187, to the nucleotide sequence of VGAM2499 RNA, herein designated VGAM RNA, also designated SEQ ID:5210.

[84560] Another function of VGAM2499 is therefore inhibition of

Chromosome 17 Open Reading Frame 26 (C17orf26, Accession NM_139177). Accordingly, utilities of VGAM2499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C17orf26. KIAA0416 (Accession NM_015564) is another VGAM2499 host target gene. KIAA0416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0416 BINDING SITE, designated SEQ ID:17836, to the nucleotide sequence of VGAM2499 RNA, herein designated VGAM RNA, also designated SEQ ID:5210.

[84561] Another function of VGAM2499 is therefore inhibition of KIAA0416 (Accession NM_015564). Accordingly, utilities of VGAM2499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0416. LOC255082 (Accession XM_172843) is another VGAM2499 host target gene. LOC255082 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255082, corresponding to a HOST TARGET binding site such as BINDING SITE I,

BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC255082 BINDING SITE, designated SEQ ID:46119, to the nucleotide sequence of VGAM2499 RNA, herein designated VGAM RNA, also designated SEQ ID:5210.

[84562] Another function of VGAM2499 is therefore inhibition of LOC255082 (Accession XM_172843). Accordingly, utilities of VGAM2499 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255082. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2500 (VGAM2500) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84563] VGAM2500 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2500 was detected is described hereinabove with reference to Figs. 1-8.

[84564] VGAM2500 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2500 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[84565] VGAM2500 gene encodes a VGAM2500 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2500 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2500 precursor RNA is designated SEQ ID:2486, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2486 is located at position 173739 relative to the genome of Mouse Cytomegalovirus 1.

[84566] VGAM2500 precursor RNA folds onto itself, forming VGAM2500 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84567] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2500 folded precursor RNA into VGAM2500

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2500 RNA is designated SEQ ID:5211, and is provided hereinbelow with reference to the sequence listing part.

[84568] VGAM2500 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2500 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2500 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84569] VGAM2500 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2500 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2500 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2500 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2500 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84570] The complementary binding of VGAM2500 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2500 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2500 host target RNA into VGAM2500 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[84571] It is appreciated that VGAM2500 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2500 host target genes. The mRNA of each one of this plurality of VGAM2500 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2500 RNA, herein designated VGAM RNA, and which when bound by VGAM2500 RNA causes inhibition of translation of respective one or more VGAM2500 host target proteins.

[84572] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2500 gene, herein designated VGAM GENE, on one or more VGAM2500 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate ex-

pression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84573] It is yet further appreciated that a function of VGAM2500 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2500 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2500 correlate with, and may be deduced from, the identity of the host target genes which VGAM2500 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84574] Nucleotide sequences of the VGAM2500 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2500 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2500 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2500 are further described hereinbelow with reference to Table 1.

[84575] Nucleotide sequences of host target binding sites, such as

BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2500 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2500 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84576] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2500 gene, herein designated VGAM is inhibition of expression of VGAM2500 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2500 correlate with, and may be deduced from, the identity of the target genes which VGAM2500 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84577] CAAX Box 1 (CXX1, Accession NM_003928) is a VGAM2500 host target gene. CXX1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CXX1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CXX1 BINDING SITE, designated SEQ ID:10025, to the nucleotide sequence of VGAM2500 RNA, herein designated VGAM RNA, also des-

ignated SEQ ID:5211.

[84578] A function of VGAM2500 is therefore inhibition of CAAX Box 1 (CXX1, Accession NM_003928). Accordingly, utilities of VGAM2500 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CXX1. Solute Carrier Family 25 (mitochondrial carrier; ornithine transporter) Member 15 (SLC25A15, Accession NM_014252) is another VGAM2500 host target gene. SLC25A15 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SLC25A15, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SLC25A15 BINDING SITE, designated SEQ ID:15529, to the nucleotide sequence of VGAM2500 RNA, herein designated VGAM RNA, also designated SEQ ID:5211.

[84579] Another function of VGAM2500 is therefore inhibition of Solute Carrier Family 25 (mitochondrial carrier; ornithine transporter) Member 15 (SLC25A15, Accession NM_014252), a gene which participates theornithine transport across inner mitochondrial membrane, from the cytoplasm to the matrix. Accordingly, utilities of

VGAM2500 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC25A15. The function of SLC25A15 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM172.DKFZP564B147 (Accession XM_088745) is another VGAM2500 host target gene. DKFZP564B147 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DKFZP564B147, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP564B147 BINDING SITE, designated SEQ ID:39936, to the nucleotide sequence of VGAM2500 RNA, herein designated VGAM RNA, also designated SEQ ID:5211.

[84580] Another function of VGAM2500 is therefore inhibition of DKFZP564B147 (Accession XM_088745). Accordingly, utilities of VGAM2500 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP564B147. KIAA1856 (Accession XM_166549) is another VGAM2500 host target gene. KIAA1856 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by KIAA1856, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1856 BINDING SITE, designated SEQ ID:44527, to the nucleotide sequence of VGAM2500 RNA, herein designated VGAM RNA, also designated SEQ ID:5211.

[84581] Another function of VGAM2500 is therefore inhibition of KIAA1856 (Accession XM_166549). Accordingly, utilities of VGAM2500 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1856. Serum/glucocorticoid Regulated Kinase-like (SGKL, Accession NM_013257) is another VGAM2500 host target gene. SGKL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SGKL, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SGKL BINDING SITE, designated SEQ ID:14928, to the nucleotide sequence of VGAM2500 RNA, herein designated VGAM RNA, also designated SEQ ID:5211.

[84582] Another function of VGAM2500 is therefore inhibition of

Serum/glucocorticoid Regulated Kinase-like (SGKL, Accession NM_013257). Accordingly, utilities of VGAM2500 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SGKL. LOC165246 (Accession XM_092473) is another VGAM2500 host target gene. LOC165246 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC165246, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC165246 BINDING SITE, designated SEQ ID:40127, to the nucleotide sequence of VGAM2500 RNA, herein designated VGAM RNA, also designated SEQ ID:5211.

[84583] Another function of VGAM2500 is therefore inhibition of LOC165246 (Accession XM_092473). Accordingly, utilities of VGAM2500 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC165246. LOC196337 (Accession XM_113696) is another VGAM2500 host target gene. LOC196337 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC196337, corresponding to a HOST TARGET binding site such as BIND-

ING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC196337 BINDING SITE, designated SEQ ID:42357, to the nucleotide sequence of VGAM2500 RNA, herein designated VGAM RNA, also designated SEQ ID:5211.

[84584] Another function of VGAM2500 is therefore inhibition of LOC196337 (Accession XM_113696). Accordingly, utilities of VGAM2500 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC196337. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2501 (VGAM2501) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84585] VGAM2501 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2501 was detected is described hereinabove with reference to Figs. 1-8.

[84586] VGAM2501 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2501 host target gene, herein designated VGAM

HOST TARGET GENE, is a human gene contained in the human genome.

[84587] VGAM2501 gene encodes a VGAM2501 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2501 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2501 precursor RNA is designated SEQ ID:2487, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2487 is located at position 72060 relative to the genome of Mouse Cytomegalovirus 1.

[84588] VGAM2501 precursor RNA folds onto itself, forming VGAM2501 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84589] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2501 folded precursor RNA into VGAM2501

RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 47%) nucleotide sequence of VGAM2501 RNA is designated SEQ ID:5212, and is provided hereinbelow with reference to the sequence listing part.

[84590] VGAM2501 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2501 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2501 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84591] VGAM2501 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2501 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2501 RNA is an accurate or a

partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2501 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2501 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84592] The complementary binding of VGAM2501 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2501 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2501 host target RNA into VGAM2501 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM

host target protein is therefore outlined by a broken line.

[84593] It is appreciated that VGAM2501 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2501 host target genes. The mRNA of each one of this plurality of VGAM2501 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2501 RNA, herein designated VGAM RNA, and which when bound by VGAM2501 RNA causes inhibition of translation of respective one or more VGAM2501 host target proteins.

[84594] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2501 gene, herein designated VGAM GENE, on one or more VGAM2501 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, al-

though specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84595] It is yet further appreciated that a function of VGAM2501 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2501 correlate with, and may be deduced from, the identity of the host target genes which VGAM2501 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84596] Nucleotide sequences of the VGAM2501 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2501 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2501 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2501 are further described hereinbelow with reference to Table 1.

[84597] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of

Fig. 1, found on VGAM2501 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2501 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84598] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2501 gene, herein designated VGAM is inhibition of expression of VGAM2501 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2501 correlate with, and may be deduced from, the identity of the target genes which VGAM2501 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84599] UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 5 (B4GALT5, Accession NM_004776) is a VGAM2501 host target gene. B4GALT5 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by B4GALT5, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of B4GALT5 BINDING SITE, designated SEQ ID:11168, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM

RNA, also designated SEQ ID:5212.

[84600] A function of VGAM2501 is therefore inhibition of UDP-Gal:betaGlcNAc Beta 1,4- Galactosyltransferase, Polypeptide 5 (B4GALT5, Accession NM_004776). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with B4GALT5. Growth Factor Receptor-bound Protein 10 (GRB10, Accession NM_005311) is another VGAM2501 host target gene. GRB10 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by GRB10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of GRB10 BINDING SITE, designated SEQ ID:11787, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84601] Another function of VGAM2501 is therefore inhibition of Growth Factor Receptor-bound Protein 10 (GRB10, Accession NM_005311), a gene which plays a functional role in insulin and IGF-I signaling. Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with GRB10.

The function of GRB10 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM441.LIM Domain Binding 2 (LDB2, Accession NM_001290) is another VGAM2501 host target gene. LDB2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LDB2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LDB2 BINDING SITE, designated SEQ ID:6970, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84602] Another function of VGAM2501 is therefore inhibition of LIM Domain Binding 2 (LDB2, Accession NM_001290), a gene which physically interacts with the LIM domains of nuclear proteins. Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LDB2. The function of LDB2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM2325.Pregnancy-associated Plasma Protein A

(PAPPA, Accession NM_002581) is another VGAM2501 host target gene. PAPPA BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by PAPPA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PAPPA BINDING SITE, designated SEQ ID:8442, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84603] Another function of VGAM2501 is therefore inhibition of Pregnancy-associated Plasma Protein A (PAPPA, Accession NM_002581), a gene which is a putative metalloprotease. Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PAPPA. The function of PAPPA and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1324.Protocadherin 11 X-linked (PCDH11X, Accession NM_032968) is another VGAM2501 host target gene. PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2 are HOST TARGET binding sites found in untranslated regions

of mRNA encoded by PCDH11X, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PCDH11X BINDING SITE1 and PCDH11X BINDING SITE2, designated SEQ ID:26791 and SEQ ID:26806 respectively, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84604] Another function of VGAM2501 is therefore inhibition of Protocadherin 11 X-linked (PCDH11X, Accession NM_032968), a gene which is thought to play a fundamental role in cell-cell recognition essential for the segmental development and function of the central nervous system. Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PCDH11X. The function of PCDH11X and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM433.Retina and Anterior Neural Fold Homeobox (RAX, Accession NM_013435) is another VGAM2501 host target gene. RAX BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded

by RAX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RAX BINDING SITE, designated SEQ ID:15093, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84605] Another function of VGAM2501 is therefore inhibition of Retina and Anterior Neural Fold Homeobox (RAX, Accession NM_013435), a gene which activates PKR in a dsRNA-independent manner. Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RAX. The function of RAX has been established by previous studies. The double-stranded RNA (dsRNA)-activated protein kinase PKR (OMIM Ref. No. 176871) is a mediator of the effects of interferon (see OMIM Ref. No. 107470), particularly its antiviral activities. PKR has also been implicated in the onset of differentiation. Based on its interaction with PKR, Patel and Sen (1998) cloned PACT cDNA. The PACT cDNA encodes a deduced 313-amino acid polypeptide that contains 3 motifs resembling the dimerization motifs present in PKR and other dsRNA-binding proteins. Northern blot

analysis revealed that PACT is expressed as a 2.0-kb mRNA in a variety of human cell lines. Ito et al. (1999) cloned the mouse homolog, which they called RAX, from a mouse Il3 (OMIM Ref. No. 147740)-dependent cell cDNA library using the yeast 2-hybrid interactive cloning system. They showed that the mouse and human sequences share 98% identity. Northern blot analysis detected expression of RAX in all tissues tested. Western blot analysis showed a 35-kD protein expressed in cell lines derived from several mammalian species.

[84606] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84607] Patel, R. C.; Sen, G. C. : PACT, a protein activator of the interferon-induced protein kinase, PKR. EMBO J. 17: 4379-4390, 1998. ; and

[84608] Ito, T.; Yang, M.; May, W. S. : RAX, a cellular activator for double-stranded RNA-dependent protein kinase during stress signaling. J. Biol. Chem. 274: 15427-15432, 1999.

[84609] Further studies establishing the function and utilities of RAX are found in John Hopkins OMIM database record ID 603424, and in sited publications numbered 8188-8190 listed in the bibliography section hereinbelow, which are

also hereby incorporated by reference.Short Stature Homeobox (SHOX, Accession NM_000451) is another VGAM2501 host target gene. SHOX BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SHOX, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SHOX BINDING SITE, designated SEQ ID:6056, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84610] Another function of VGAM2501 is therefore inhibition of Short Stature Homeobox (SHOX, Accession NM_000451). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SHOX. Solute Carrier Family 6 (neurotransmitter transporter, dopamine), Member 3 (SLC6A3, Accession NM_001044) is another VGAM2501 host target gene. SLC6A3 BINDING SITE1 through SLC6A3 BINDING SITE5 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by SLC6A3, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illus-

trates the complementarity of the nucleotide sequences of SLC6A3 BINDING SITE1 through SLC6A3 BINDING SITE5, designated SEQ ID:6710, SEQ ID:6709, SEQ ID:6708, SEQ ID:6711 and SEQ ID:6707 respectively, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84611] Another function of VGAM2501 is therefore inhibition of Solute Carrier Family 6 (neurotransmitter transporter, dopamine), Member 3 (SLC6A3, Accession NM_001044), a gene which terminates the action of dopamine by its high affinity sodium-dependent reuptake into presynaptic terminals. Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SLC6A3. The function of SLC6A3 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1753.Chromosome 17 Open Reading Frame 31 (C17orf31, Accession NM_017575) is another VGAM2501 host target gene. C17orf31 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C17orf31, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or

BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C17orf31 BINDING SITE, designated SEQ ID:19005, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84612] Another function of VGAM2501 is therefore inhibition of Chromosome 17 Open Reading Frame 31 (C17orf31, Accession NM_017575). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C17orf31. Frequently Rearranged In Advanced T-cell Lymphomas (FRAT1, Accession NM_005479) is another VGAM2501 host target gene. FRAT1 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FRAT1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FRAT1 BINDING SITE, designated SEQ ID:11981, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84613] Another function of VGAM2501 is therefore inhibition of Frequently Rearranged In Advanced T-cell Lymphomas

(FRAT1, Accession NM_005479). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FRAT1. KIAA0153 (Accession NM_015140) is another VGAM2501 host target gene. KIAA0153 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0153, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0153 BINDING SITE, designated SEQ ID:17499, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84614] Another function of VGAM2501 is therefore inhibition of KIAA0153 (Accession NM_015140). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0153. KIAA0469 (Accession NM_014851) is another VGAM2501 host target gene. KIAA0469 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0469, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of KIAA0469 BINDING SITE, designated SEQ ID:16894, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84615] Another function of VGAM2501 is therefore inhibition of KIAA0469 (Accession NM_014851). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0469. KIAA1363 (Accession XM_045056) is another VGAM2501 host target gene. KIAA1363 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1363, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1363 BINDING SITE, designated SEQ ID:34334, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84616] Another function of VGAM2501 is therefore inhibition of KIAA1363 (Accession XM_045056). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1363. KIAA1951 (Accession XM_057401) is another

VGAM2501 host target gene. KIAA1951 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1951, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1951 BINDING SITE, designated SEQ ID:36512, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84617] Another function of VGAM2501 is therefore inhibition of KIAA1951 (Accession XM_057401). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1951. Paternally Expressed 10 (PEG10, Accession NM_015068) is another VGAM2501 host target gene. PEG10 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PEG10, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PEG10 BINDING SITE, designated SEQ ID:17430, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ

ID:5212.

[84618] Another function of VGAM2501 is therefore inhibition of Paternally Expressed 10 (PEG10, Accession NM_015068). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PEG10. LOC128989 (Accession XM_059310) is another VGAM2501 host target gene. LOC128989 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC128989, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC128989 BINDING SITE, designated SEQ ID:36944, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84619] Another function of VGAM2501 is therefore inhibition of LOC128989 (Accession XM_059310). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC128989. LOC137964 (Accession XM_059933) is another VGAM2501 host target gene. LOC137964 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC137964, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC137964 BINDING SITE, designated SEQ ID:37112, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84620] Another function of VGAM2501 is therefore inhibition of LOC137964 (Accession XM_059933). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC137964. LOC148397 (Accession XM_086171) is another VGAM2501 host target gene. LOC148397 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC148397, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC148397 BINDING SITE, designated SEQ ID:38529, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84621] Another function of VGAM2501 is therefore inhibition of LOC148397 (Accession XM_086171). Accordingly, utilities

of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC148397. LOC149127 (Accession XM_097584) is another VGAM2501 host target gene. LOC149127 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC149127, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC149127 BINDING SITE, designated SEQ ID:40948, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84622] Another function of VGAM2501 is therefore inhibition of LOC149127 (Accession XM_097584). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC149127. LOC152860 (Accession XM_087539) is another VGAM2501 host target gene. LOC152860 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC152860, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences

of LOC152860 BINDING SITE, designated SEQ ID:39324, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84623] Another function of VGAM2501 is therefore inhibition of LOC152860 (Accession XM_087539). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC152860. LOC197408 (Accession XM_117031) is another VGAM2501 host target gene. LOC197408 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC197408, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC197408 BINDING SITE, designated SEQ ID:43207, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84624] Another function of VGAM2501 is therefore inhibition of LOC197408 (Accession XM_117031). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC197408. LOC205095 (Accession XM_119820) is another VGAM2501 host target gene. LOC205095 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC205095, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC205095 BINDING SITE, designated SEQ ID:43604, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84625] Another function of VGAM2501 is therefore inhibition of LOC205095 (Accession XM_119820). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC205095. LOC219688 (Accession XM_167568) is another VGAM2501 host target gene. LOC219688 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC219688, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC219688 BINDING SITE, designated SEQ ID:44700, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84626] Another function of VGAM2501 is therefore inhibition of

LOC219688 (Accession XM_167568). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC219688. LOC253897 (Accession XM_171187) is another VGAM2501 host target gene. LOC253897 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC253897, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC253897 BINDING SITE, designated SEQ ID:45968, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84627] Another function of VGAM2501 is therefore inhibition of LOC253897 (Accession XM_171187). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC253897. LOC255423 (Accession XM_174498) is another VGAM2501 host target gene. LOC255423 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC255423, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 il-

lustrates the complementarity of the nucleotide sequences of LOC255423 BINDING SITE, designated SEQ ID:46594, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84628] Another function of VGAM2501 is therefore inhibition of LOC255423 (Accession XM_174498). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC255423. LOC256222 (Accession XM_173177) is another VGAM2501 host target gene. LOC256222 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256222, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256222 BINDING SITE, designated SEQ ID:46427, to the nucleotide sequence of VGAM2501 RNA, herein designated VGAM RNA, also designated SEQ ID:5212.

[84629] Another function of VGAM2501 is therefore inhibition of LOC256222 (Accession XM_173177). Accordingly, utilities of VGAM2501 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256222. Fig. 1 further provides a conceptual descrip-

tion of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2502 (VGAM2502) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84630] VGAM2502 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2502 was detected is described hereinabove with reference to Figs. 1-8.

[84631] VGAM2502 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2502 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84632] VGAM2502 gene encodes a VGAM2502 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2502 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2502 precursor RNA is designated SEQ ID:2488, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence

SEQ ID:2488 is located at position 192021 relative to the genome of Mouse Cytomegalovirus 1.

[84633] VGAM2502 precursor RNA folds onto itself, forming VGAM2502 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84634] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2502 folded precursor RNA into VGAM2502 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 40%) nucleotide sequence of VGAM2502 RNA is designated SEQ ID:5213, and is provided hereinbelow with reference to the sequence listing part.

[84635] VGAM2502 host target gene, herein designated VGAM

HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2502 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2502 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84636] VGAM2502 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2502 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2502 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2502 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2502 host target RNA,

herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84637] The complementary binding of VGAM2502 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2502 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2502 host target RNA into VGAM2502 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84638] It is appreciated that VGAM2502 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2502 host target genes. The mRNA of each one of this plurality of VGAM2502 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2502 RNA, herein designated VGAM RNA, and which when bound by VGAM2502 RNA causes inhibition of translation of respective one or more

VGAM2502 host target proteins.

[84639] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2502 gene, herein designated VGAM GENE, on one or more VGAM2502 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84640] It is yet further appreciated that a function of VGAM2502 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2502 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1.

Specific functions, and accordingly utilities, of VGAM2502 correlate with, and may be deduced from, the identity of the host target genes which VGAM2502 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84641] Nucleotide sequences of the VGAM2502 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2502 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2502 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2502 are further described hereinbelow with reference to Table 1.

[84642] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2502 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2502 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84643] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2502 gene, herein designated VGAM is inhibition of expression of VGAM2502 target genes. It is appreciated that specific functions, and accordingly utili-

ties, of VGAM2502 correlate with, and may be deduced from, the identity of the target genes which VGAM2502 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84644] Dual Specificity Phosphatase 7 (DUSP7, Accession XM_037430) is a VGAM2502 host target gene. DUSP7 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by DUSP7, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DUSP7 BINDING SITE, designated SEQ ID:32614, to the nucleotide sequence of VGAM2502 RNA, herein designated VGAM RNA, also designated SEQ ID:5213.

[84645] A function of VGAM2502 is therefore inhibition of Dual Specificity Phosphatase 7 (DUSP7, Accession XM_037430), a gene which is a member of the dual specificity protein phosphatase family . Accordingly, utilities of VGAM2502 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DUSP7. The function of DUSP7 has been established by previous studies. Members of the mitogen-activated protein (MAP) kinase family play a pivotal role in cellular signal transduction.

The dual-specificity phosphatases can reverse MAP kinase activation by dephosphorylating critical phosphotyrosine and phosphothreonine residues. Muda et al. (1996) identified rat superior cervical ganglion cDNAs encoding 2 dual-specificity phosphatases that they designated MKP3 (OMIM Ref. No. 602748) and MKPX. The predicted 280-amino acid sequence of the partial MKPX cDNA was 76% identical to that of MKP3. Groom et al. (1996) identified cDNAs encoding the human MKP3 and MKPX homologs, which they called PYST1 and PYST2, respectively. The predicted amino acid sequence of the partial PYST2 cDNA was 73% identical to that of PYST1. Northern analysis revealed that the 3.5-kb PYST2 mRNA was expressed at low levels in several tissues. In liver, Groom et al. (1996) observed strong expression of a 2.5-kb transcript and much weaker expression of a 5-kb transcript.

[84646] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84647] Groom, L. A.; Sneddon, A. A.; Alessi, D. R.; Dowd, S.; Keyse, S. M. : Differential regulation of the MAP, SAP and Rk/p38 kinases by Pyst1, a novel cytosolic dual-specificity phosphatase. EMBO J. 15: 3621-3632, 1996. ; and

[84648] Muda, M.; Boschert, U.; Dickinson, R.; Martinou, J.-C.; Martinou, I.; Camps, M.; Schlegel, W.; Arkinstall, S. : MKP-3, a novel cytosolic protein-tyrosine phosphatase that exemplifies a.

[84649] Further studies establishing the function and utilities of DUSP7 are found in John Hopkins OMIM database record ID 602749, and in sited publications numbered 2411-2413 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Myeloid/lymphoid Or Mixed-lineage Leukemia (trithorax homolog, Drosophila); Translocated To, 2 (MLLT2, Accession NM_005935) is another VGAM2502 host target gene. MLLT2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by MLLT2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MLLT2 BINDING SITE, designated SEQ ID:12567, to the nucleotide sequence of VGAM2502 RNA, herein designated VGAM RNA, also designated SEQ ID:5213.

[84650] Another function of VGAM2502 is therefore inhibition of Myeloid/lymphoid Or Mixed-lineage Leukemia (trithorax

homolog, Drosophila); Translocated To, 2 (MLLT2, Accession NM_005935), a gene which is a Putative transcription factor. Accordingly, utilities of VGAM2502 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MLLT2. The function of MLLT2 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM57.FLJ12132 (Accession NM_024980) is another VGAM2502 host target gene. FLJ12132 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by FLJ12132, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ12132 BINDING SITE, designated SEQ ID:24541, to the nucleotide sequence of VGAM2502 RNA, herein designated VGAM RNA, also designated SEQ ID:5213.

[84651] Another function of VGAM2502 is therefore inhibition of FLJ12132 (Accession NM_024980). Accordingly, utilities of VGAM2502 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ12132. FLJ20306 (Accession NM_017756) is another

VGAM2502 host target gene. FLJ20306 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ20306, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ20306 BINDING SITE, designated SEQ ID:19367, to the nucleotide sequence of VGAM2502 RNA, herein designated VGAM RNA, also designated SEQ ID:5213.

[84652] Another function of VGAM2502 is therefore inhibition of FLJ20306 (Accession NM_017756). Accordingly, utilities of VGAM2502 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ20306. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2503 (VGAM2503) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84653] VGAM2503 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2503 was detected is de-

scribed hereinabove with reference to Figs. 1-8.

[84654] VGAM2503 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2503 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84655] VGAM2503 gene encodes a VGAM2503 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2503 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2503 precursor RNA is designated SEQ ID:2489, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2489 is located at position 125983 relative to the genome of Mouse Cytomegalovirus 1.

[84656] VGAM2503 precursor RNA folds onto itself, forming VGAM2503 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA

gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84657] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2503 folded precursor RNA into VGAM2503 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 81%) nucleotide sequence of VGAM2503 RNA is designated SEQ ID:5214, and is provided hereinbelow with reference to the sequence listing part.

[84658] VGAM2503 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2503 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2503 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84659] VGAM2503 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites

located in untranslated regions of VGAM2503 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2503 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2503 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2503 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84660] The complementary binding of VGAM2503 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2503 host target RNA, herein designated VGAM

HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2503 host target RNA into VGAM2503 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84661] It is appreciated that VGAM2503 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2503 host target genes. The mRNA of each one of this plurality of VGAM2503 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2503 RNA, herein designated VGAM RNA, and which when bound by VGAM2503 RNA causes inhibition of translation of respective one or more VGAM2503 host target proteins.

[84662] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2503 gene, herein designated VGAM GENE, on one or more VGAM2503 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a spe-

cific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84663] It is yet further appreciated that a function of VGAM2503 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2503 correlate with, and may be deduced from, the identity of the host target genes which VGAM2503 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84664] Nucleotide sequences of the VGAM2503 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2503 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding

of VGAM2503 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2503 are further described hereinbelow with reference to Table 1.

[84665] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2503 host target RNA, and schematic representation of the complementarity of each of these host target binding sites to VGAM2503 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84666] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2503 gene, herein designated VGAM is inhibition of expression of VGAM2503 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2503 correlate with, and may be deduced from, the identity of the target genes which VGAM2503 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84667] Carboxyl Ester Lipase-like (bile salt-stimulated lipase-like) (CELL, Accession NM_001808) is a VGAM2503 host target gene. CELL BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CELL, corresponding to a HOST TARGET binding site

such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CELL BINDING SITE, designated SEQ ID:7558, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84668] A function of VGAM2503 is therefore inhibition of Carboxyl Ester Lipase-like (bile salt-stimulated lipase-like) (CELL, Accession NM_001808), a gene which is a Carboxyl ester lipase-like protein. Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CELL. The function of CELL has been established by previous studies. The human lactating mammary gland and pancreas produce a lipolytic enzyme, carboxyl ester lipase (CEL; 114840), earlier called bile salt-stimulated lipase. The enzyme exerts its function in duodenal juice, is activated when mixed with bile salts, and plays an important role in the digestion of milk fat in newborn infants. Lidberg et al. (1992) described the genomic organization of the CEL gene and proposed the presence of a transcribed pseudogene, designated carboxyl ester lipase-like gene (CELL). The existence of the CELL gene was confirmed by Kumar et al. (1992). The main difference between CEL and

CELL is that the latter lacks a 4.8-kb fragment, including exons 2-7. Furthermore, in the coding sequence, several differences are found in exons 10 and 11. The remaining coding regions are identical in the 2 genes. The intron sequences of the genes show a 97.5% homology. The CELL gene does not include exon 5, in which the active serine is located, indicating that the product of this gene cannot be a lipase. Nilsson et al. (1993) found that in contrast to the CEL gene, CELL is expressed in low amounts in all tissues analyzed. They found that the average length of the cDNA for CELL is 1,214 bases. This sequence includes several termination codons in all 3 reading frames. The longest open reading frame with the same start of translation as that of the CEL transcript could encode a 59-amino acid-long peptide, presumably without any function. The CELL gene may have arisen as a result of gene duplication of the CEL gene followed by deletions and point mutations. A hypervariable region was characterized in the last exon of the CELL gene. Nilsson et al. (1993) suggested that this polymorphism would be useful for linkage analysis. Taylor et al. (1991) suggested that the CEL gene contains a hypervariable region, according to results obtained by Southern blotting. Most processed pseudogenes (Vanin,

1985) are transcriptionally silent; transcribed pseudogenes are rare because once the coding information of a particular gene is inactivated by a mutational event, further mutation of promoter sequences would not be selected against. Two known pseudogenes that retained their ability to be transcribed are the high-affinity dopamine receptor pseudogene (Weinshank et al., 1991) and the murine glyceraldhyde-3-phosphate dehydrogenase pseudogene (Galland et al., 1990). These genes may have arisen through gene duplication followed by several mutations. Thus, even though these genes are expressed, they will not give rise to functional protein. Nilsson et al. (1993) stated that 'the CEL gene and the CELL gene were mapped to the same region of chromosome 9,' namely, 9q34.3.

[84669] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84670] Lidberg, U.; Nilsson, J.; Stromberg, K.; Stenman, G.; Sahlin, P.; Enerback, S.; Bjursell, G. : Genomic organization, sequence analysis, and chromosomal localization of the human carboxyl ester lipase (CEL) gene and a CEL-like (CELL) gene. Genomics 13: 630-640, 1992. ; and

[84671] Lidmer, A.-S.; Kannius, M.; Lundberg, L.; Bjursell, G.; Nilsson, J. : Molecular cloning and characterization of the mouse carboxyl ester lipase gene and evidence for expression in the l.

[84672] Further studies establishing the function and utilities of CELL are found in John Hopkins OMIM database record ID 114841, and in sited publications numbered 4230-4229, 4231-423 and 2037 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.Lamin A/C (LMNA, Accession NM_005572) is another VGAM2503 host target gene. LMNA BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LMNA, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LMNA BINDING SITE, designated SEQ ID:12099, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84673] Another function of VGAM2503 is therefore inhibition of Lamin A/C (LMNA, Accession NM_005572), a gene which is thought to provide a framework for the nuclear envelope and may also interact with chromatin. Accordingly,

utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LMNA. The function of LMNA has been established by previous studies. The nuclear lamina is a proteinaceous layer apposed to the inner nuclear membrane. It is composed of a family of polypeptides, the lamins, highly conserved in evolution (Krohne and Benavente, 1986). In mammals, 3 lamins, A, B, and C, have been described, with molecular weights ranging from 60,000 to 78,000. Lamins A and C but not lamin B have close sequence homology. During mitosis, the lamina meshwork is reversibly disassembled in parallel with phosphorylation of the lamins. Lamins can be classified with the intermediate filament (IF) polypeptides. Guilly et al. (1987) demonstrated that lamin B was the only lamin present in T lymphoblasts. The mRNAs of lamins A and C were detected in HeLa cells. The transport of newly-synthesized proteins from the cytoplasm into the nucleus differs from the transport of proteins into other organelles such as mitochondria by 1 important feature: sequences are not cleaved but remain a permanent feature of the mature polypeptide. One exception to this rule, however, appears to be lamin A. Lebel and Raymond (1987) concluded that

lamin A is not synthesized as a large precursor polypeptide Complementary DNA cloning and sequencing showed that human lamins A and C are identical for the first 566 amino acids (McKeon et al., 1986; Fisher et al., 1986). Pre-lamin A, from which the last 18 amino acids are proteolytically removed to yield lamin A, has 98 unique carboxy-terminal amino acids. Lamin C has 6 unique carboxy-terminal amino acids. Because pre-lamin A contains a CAAX (cysteine-aliphatic-aliphatic-any amino acid) box at its carboxyl terminus, it can be modified by farnesylation, whereas lamin C cannot. The sequence similarities and data obtained from Southern blotting (McKeon et al., 1986) suggested that lamin A and lamin C arise from 1 gene by alternative splicing. Lin and Worman (1993) demonstrated that the coding region of the lamin A/C gene spans approximately 24 kb and contains 12 exons. Alternative splicing within exon 10 gives rise to 2 different mRNAs that code for pre-lamin A and lamin C

[84674] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84675] Lebel, S.; Raymond, Y. : Lamin A is not synthesized as a larger precursor polypeptide. Biochem. Biophys. Res.

Commun. 149: 417-423, 1987. ; and

[84676] Lin, F.; Worman, H. J. : Structural organization of the human gene encoding nuclear lamin A and nuclear lamin C. J. Biol. Chem. 268: 16321-16326, 1993.

[84677] Further studies establishing the function and utilities of LMNA are found in John Hopkins OMIM database record ID 150330, and in sited publications numbered 3843, 12466-1248 and 12699 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.NHP2 Non-histone Chromosome Protein 2-like 1 (S. cerevisiae) (NHP2L1, Accession NM_005008) is another VGAM2503 host target gene. NHP2L1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by NHP2L1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of NHP2L1 BINDING SITE, designated SEQ ID:11444, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84678] Another function of VGAM2503 is therefore inhibition of NHP2 Non-histone Chromosome Protein 2-like 1 (S. cerevisiae) (NHP2L1, Accession NM_005008), a gene which

may play a role in the late stage of spliceosome assembly. Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with NHP2L1. The function of NHP2L1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM1923.RAN Binding Protein 3 (RANBP3, Accession NM_003624) is another VGAM2503 host target gene. RANBP3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by RANBP3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of RANBP3 BINDING SITE, designated SEQ ID:9689, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84679] Another function of VGAM2503 is therefore inhibition of RAN Binding Protein 3 (RANBP3, Accession NM_003624). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with RANBP3. Usher Syndrome 3A (USH3A, Accession NM_052995) is another VGAM2503

host target gene. USH3A BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by USH3A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of USH3A BINDING SITE, designated SEQ ID:27564, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84680] Another function of VGAM2503 is therefore inhibition of Usher Syndrome 3A (USH3A, Accession NM_052995). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with USH3A. Chromosome 20 Open Reading Frame 121 (C20orf121, Accession NM_024331) is another VGAM2503 host target gene. C20orf121 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by C20orf121, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of C20orf121 BINDING SITE, designated SEQ ID:23634, to the nucleotide sequence of VGAM2503 RNA, herein desig-

nated VGAM RNA, also designated SEQ ID:5214.

[84681] Another function of VGAM2503 is therefore inhibition of Chromosome 20 Open Reading Frame 121 (C20orf121, Accession NM_024331). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with C20orf121. DKFZP434K028 (Accession XM_167745) is another VGAM2503 host target gene. DKFZP434K028 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DKFZP434K028, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DKFZP434K028 BINDING SITE, designated SEQ ID:44772, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84682] Another function of VGAM2503 is therefore inhibition of DKFZP434K028 (Accession XM_167745). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DKFZP434K028. FLJ10847 (Accession NM_018242) is another VGAM2503 host target gene. FLJ10847 BINDING

SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ10847, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ10847 BINDING SITE, designated SEQ ID:20202, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84683] Another function of VGAM2503 is therefore inhibition of FLJ10847 (Accession NM_018242). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ10847. FLJ13490 (Accession NM_024942) is another VGAM2503 host target gene. FLJ13490 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by FLJ13490, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of FLJ13490 BINDING SITE, designated SEQ ID:24487, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84684] Another function of VGAM2503 is therefore inhibition of

FLJ13490 (Accession NM_024942). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with FLJ13490. MDS006 (Accession NM_020233) is another VGAM2503 host target gene. MDS006 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MDS006, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MDS006 BINDING SITE, designated SEQ ID:21503, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84685] Another function of VGAM2503 is therefore inhibition of MDS006 (Accession NM_020233). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MDS006. MGC15873 (Accession NM_032920) is another VGAM2503 host target gene. MGC15873 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC15873, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the

complementarity of the nucleotide sequences of MGC15873 BINDING SITE, designated SEQ ID:26743, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84686] Another function of VGAM2503 is therefore inhibition of MGC15873 (Accession NM_032920). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC15873. SCAM-1 (Accession NM_005775) is another VGAM2503 host target gene. SCAM-1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SCAM-1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SCAM-1 BINDING SITE, designated SEQ ID:12351, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84687] Another function of VGAM2503 is therefore inhibition of SCAM-1 (Accession NM_005775). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SCAM-1. SMOC2 (Accession XM_051452) is another VGAM2503

host target gene. SMOC2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by SMOC2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of SMOC2 BINDING SITE, designated SEQ ID:35837, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84688] Another function of VGAM2503 is therefore inhibition of SMOC2 (Accession XM_051452). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with SMOC2. Tousled-like Kinase 2 (TLK2, Accession XM_085650) is another VGAM2503 host target gene. TLK2 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by TLK2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of TLK2 BINDING SITE, designated SEQ ID:38275, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84689] Another function of VGAM2503 is therefore inhibition of Tousled-like Kinase 2 (TLK2, Accession XM_085650). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with TLK2. LOC144587 (Accession XM_040195) is another VGAM2503 host target gene. LOC144587 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC144587, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC144587 BINDING SITE, designated SEQ ID:33270, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84690] Another function of VGAM2503 is therefore inhibition of LOC144587 (Accession XM_040195). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC144587. LOC146802 (Accession XM_085595) is another VGAM2503 host target gene. LOC146802 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC146802, cor-

responding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC146802 BINDING SITE, designated SEQ ID:38247, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84691] Another function of VGAM2503 is therefore inhibition of LOC146802 (Accession XM_085595). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC146802. LOC147841 (Accession XM_085924) is another VGAM2503 host target gene. LOC147841 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC147841, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC147841 BINDING SITE, designated SEQ ID:38398, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84692] Another function of VGAM2503 is therefore inhibition of LOC147841 (Accession XM_085924). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with LOC147841. LOC202986 (Accession XM_117489) is another VGAM2503 host target gene. LOC202986 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC202986, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC202986 BINDING SITE, designated SEQ ID:43471, to the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84693] Another function of VGAM2503 is therefore inhibition of LOC202986 (Accession XM_117489). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC202986. LOC221474 (Accession XM_166464) is another VGAM2503 host target gene. LOC221474 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC221474, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221474 BINDING SITE, designated SEQ ID:44377, to

the nucleotide sequence of VGAM2503 RNA, herein designated VGAM RNA, also designated SEQ ID:5214.

[84694] Another function of VGAM2503 is therefore inhibition of LOC221474 (Accession XM_166464). Accordingly, utilities of VGAM2503 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221474. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2504 (VGAM2504) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84695] VGAM2504 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2504 was detected is described hereinabove with reference to Figs. 1-8.

[84696] VGAM2504 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2504 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84697] VGAM2504 gene encodes a VGAM2504 precursor RNA,

herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2504 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2504 precursor RNA is designated SEQ ID:2490, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2490 is located at position 179418 relative to the genome of Mouse Cytomegalovirus 1.

[84698] VGAM2504 precursor RNA folds onto itself, forming VGAM2504 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84699] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2504 folded precursor RNA into VGAM2504 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a hairpin structured RNA precursor product into a short

~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 79%) nucleotide sequence of VGAM2504 RNA is designated SEQ ID:5215, and is provided hereinbelow with reference to the sequence listing part.

[84700] VGAM2504 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2504 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2504 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84701] VGAM2504 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2504 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2504 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an illustration, Fig. 1 shows three such host target binding

sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2504 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2504 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84702] The complementary binding of VGAM2504 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2504 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2504 host target RNA into VGAM2504 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84703] It is appreciated that VGAM2504 host target gene, herein designated VGAM HOST TARGET GENE, in fact represents

a plurality of VGAM2504 host target genes. The mRNA of each one of this plurality of VGAM2504 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2504 RNA, herein designated VGAM RNA, and which when bound by VGAM2504 RNA causes inhibition of translation of respective one or more VGAM2504 host target proteins.

[84704] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2504 gene, herein designated VGAM GENE, on one or more VGAM2504 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these other miRNA genes have not yet been found (Ruvkun G.,

`Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84705] It is yet further appreciated that a function of VGAM2504 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2504 correlate with, and may be deduced from, the identity of the host target genes which VGAM2504 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84706] Nucleotide sequences of the VGAM2504 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2504 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2504 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2504 are further described hereinbelow with reference to Table 1.

[84707] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2504 host target RNA, and schematic representation of the complementarity of each

of these host target binding sites to VGAM2504 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84708] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2504 gene, herein designated VGAM is inhibition of expression of VGAM2504 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2504 correlate with, and may be deduced from, the identity of the target genes which VGAM2504 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84709] ATPase, Cu++ Transporting, Alpha Polypeptide (Menkes syndrome) (ATP7A, Accession NM_000052) is a VGAM2504 host target gene. ATP7A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP7A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP7A BINDING SITE, designated SEQ ID:5500, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84710] A function of VGAM2504 is therefore inhibition of ATPase,

Cu++ Transporting, Alpha Polypeptide (Menkes syndrome) (ATP7A, Accession NM_000052). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ATP7A. Dipeptidylpeptidase VI (DPP6, Accession NM_130797) is another VGAM2504 host target gene. DPP6 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DPP6, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DPP6 BINDING SITE, designated SEQ ID:28283, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84711] Another function of VGAM2504 is therefore inhibition of Dipeptidylpeptidase VI (DPP6, Accession NM_130797), a gene which may be involved in the physiological processes of brain function. Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DPP6. The function of DPP6 has been established by previous studies. Wada et al. (1992) isolated cDNA clones for a dipeptidyl peptidase IV-related protein from bovine and

rat brain libraries. Unlike dipeptidyl peptidase IV (OMIM Ref. No. 102720) which belongs to a family in which a serine, an aspartate, and a histidine form a catalytic triad, the DPPIV-related protein does not show the first serine residue. Yokotani et al. (1993) isolated the human homolog. Using a fragment of the bovine DPPX clone as a probe, Yokotani et al. (1993) mapped the human DPP6 gene to chromosome 7 by PCR analysis of somatic cell hybrids. Wada et al. (1993) showed that the mouse Dpp6 gene is linked to markers in the proximal end of chromosome 5 in a region of conserved synteny.

[84712] Full details of the abovementioned studies are described in the following publications, the disclosure of which are hereby incorporated by reference:

[84713] Wada, K.; Yokotani, N.; Hunter, C.; Doi, K.; Wenthold, R. J.; Shimasaki, S. : Differential expression of two distinct forms of mRNA encoding members of a dipeptidyl aminopeptidase family. Proc. Nat. Acad. Sci. 89: 197-201, 1992. ; and

[84714] Yokotani, N.; Doi, K.; Wenthold, R. J.; Wada, K. : Non-conservation of a catalytic residue in a depeptidyl aminopeptidase IV-related protein encoded by a gene on human chromosome 7. Hum.

[84715] Further studies establishing the function and utilities of DPP6 are found in John Hopkins OMIM database record ID 126141, and in sited publications numbered 4320-4322 listed in the bibliography section hereinbelow, which are also hereby incorporated by reference.EphA8 (EPHA8, Accession NM_020526) is another VGAM2504 host target gene. EPHA8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by EPHA8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of EPHA8 BINDING SITE, designated SEQ ID:21748, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84716] Another function of VGAM2504 is therefore inhibition of EphA8 (EPHA8, Accession NM_020526), a gene which Eph-related receptor tyrosine kinase A8. Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with EPHA8. The function of EPHA8 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove

with reference to VGAM494.Huntingtin (Huntington disease) (HD, Accession NM_002111) is another VGAM2504 host target gene. HD BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by HD, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of HD BINDING SITE, designated SEQ ID:7890, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84717] Another function of VGAM2504 is therefore inhibition of Huntingtin (Huntington disease) (HD, Accession NM_002111). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with HD. MAX Interacting Protein 1 (MXI1, Accession NM_005962) is another VGAM2504 host target gene. MXI1 BINDING SITE1 and MXI1 BINDING SITE2 are HOST TARGET binding sites found in untranslated regions of mRNA encoded by MXI1, corresponding to HOST TARGET binding sites such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MXI1

BINDING SITE1 and MXI1 BINDING SITE2, designated SEQ ID:12583 and SEQ ID:28193 respectively, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84718] Another function of VGAM2504 is therefore inhibition of MAX Interacting Protein 1 (MXI1, Accession NM_005962), a gene which acts as a tumor suppressor in vivo, engages the MYC network in a functionally relevant manner. Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MXI1. The function of MXI1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM128.ARP1 Actin-related Protein 1 Homolog A, Centractin Alpha (yeast) (ACTR1A, Accession XM_031949) is another VGAM2504 host target gene. ACTR1A BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ACTR1A, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ACTR1A BINDING SITE, designated SEQ ID:31530, to the nucleotide sequence of VGAM2504 RNA,

herein designated VGAM RNA, also designated SEQ ID:5215.

[84719] Another function of VGAM2504 is therefore inhibition of ARP1 Actin-related Protein 1 Homolog A, Centractin Alpha (yeast) (ACTR1A, Accession XM_031949). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ACTR1A. Chemokine (C-C motif) Receptor 8 (CCR8, Accession NM_005201) is another VGAM2504 host target gene. CCR8 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by CCR8, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CCR8 BINDING SITE, designated SEQ ID:11701, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84720] Another function of VGAM2504 is therefore inhibition of Chemokine (C-C motif) Receptor 8 (CCR8, Accession NM_005201). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CCR8. CIZ1 (Accession NM_012127) is another VGAM2504 host target gene. CIZ1

BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by CIZ1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of CIZ1 BINDING SITE, designated SEQ ID:14442, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84721] Another function of VGAM2504 is therefore inhibition of CIZ1 (Accession NM_012127). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with CIZ1. Dedicator of Cyto-kinesis 3 (DOCK3, Accession XM_039259) is another VGAM2504 host target gene. DOCK3 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by DOCK3, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of DOCK3 BINDING SITE, designated SEQ ID:33040, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84722] Another function of VGAM2504 is therefore inhibition of Dedicator of Cyto-kinesis 3 (DOCK3, Accession XM_039259). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with DOCK3. KIAA0894 (Accession NM_014896) is another VGAM2504 host target gene. KIAA0894 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA0894, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA0894 BINDING SITE, designated SEQ ID:17053, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84723] Another function of VGAM2504 is therefore inhibition of KIAA0894 (Accession NM_014896). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA0894. KIAA1364 (Accession XM_032997) is another VGAM2504 host target gene. KIAA1364 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1364, corresponding to

a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1364 BINDING SITE, designated SEQ ID:31811, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84724] Another function of VGAM2504 is therefore inhibition of KIAA1364 (Accession XM_032997). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with KIAA1364. KIAA1416 (Accession XM_098762) is another VGAM2504 host target gene. KIAA1416 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by KIAA1416, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of KIAA1416 BINDING SITE, designated SEQ ID:41809, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84725] Another function of VGAM2504 is therefore inhibition of KIAA1416 (Accession XM_098762). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treat-

ment of diseases and clinical conditions associated with KIAA1416. MGC21675 (Accession NM_052861) is another VGAM2504 host target gene. MGC21675 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by MGC21675, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of MGC21675 BINDING SITE, designated SEQ ID:27445, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84726] Another function of VGAM2504 is therefore inhibition of MGC21675 (Accession NM_052861). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with MGC21675. PIPPIN (Accession XM_086825) is another VGAM2504 host target gene. PIPPIN BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by PIPPIN, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of PIPPIN BINDING SITE, designated SEQ ID:38910, to the nucleotide sequence of

VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84727] Another function of VGAM2504 is therefore inhibition of PIPPIN (Accession XM_086825). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with PIPPIN. LOC150685 (Accession XM_103563) is another VGAM2504 host target gene. LOC150685 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC150685, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC150685 BINDING SITE, designated SEQ ID:42154, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84728] Another function of VGAM2504 is therefore inhibition of LOC150685 (Accession XM_103563). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC150685. LOC201522 (Accession XM_113978) is another VGAM2504 host target gene. LOC201522 BINDING SITE is HOST TARGET binding site found in the 3` un-

translated region of mRNA encoded by LOC201522, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC201522 BINDING SITE, designated SEQ ID:42584, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84729] Another function of VGAM2504 is therefore inhibition of LOC201522 (Accession XM_113978). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC201522. LOC221398 (Accession XM_165762) is another VGAM2504 host target gene. LOC221398 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by LOC221398, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC221398 BINDING SITE, designated SEQ ID:43748, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84730] Another function of VGAM2504 is therefore inhibition of LOC221398 (Accession XM_165762). Accordingly, utilities

of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC221398. LOC256250 (Accession XM_173171) is another VGAM2504 host target gene. LOC256250 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC256250, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of LOC256250 BINDING SITE, designated SEQ ID:46424, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84731] Another function of VGAM2504 is therefore inhibition of LOC256250 (Accession XM_173171). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC256250. LOC91040 (Accession XM_035641) is another VGAM2504 host target gene. LOC91040 BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by LOC91040, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of

LOC91040 BINDING SITE, designated SEQ ID:32313, to the nucleotide sequence of VGAM2504 RNA, herein designated VGAM RNA, also designated SEQ ID:5215.

[84732] Another function of VGAM2504 is therefore inhibition of LOC91040 (Accession XM_035641). Accordingly, utilities of VGAM2504 include diagnosis, prevention and treatment of diseases and clinical conditions associated with LOC91040. Fig. 1 further provides a conceptual description of a novel bioinformatically detected viral gene of the present invention, referred to here as Viral Genomic Address Messenger 2505 (VGAM2505) viral gene, which modulates expression of respective host target genes thereof, the function and utility of which host target genes is known in the art.

[84733] VGAM2505 is a novel bioinformatically detected regulatory, non protein coding, viral micro RNA (miRNA) gene. The method by which VGAM2505 was detected is described hereinabove with reference to Figs. 1-8.

[84734] VGAM2505 gene, herein designated VGAM GENE, is a viral gene contained in the genome of Mouse Cytomegalovirus 1. VGAM2505 host target gene, herein designated VGAM HOST TARGET GENE, is a human gene contained in the human genome.

[84735] VGAM2505 gene encodes a VGAM2505 precursor RNA, herein designated VGAM PRECURSOR RNA. Similar to other miRNA genes, and unlike most ordinary genes, VGAM2505 precursor RNA does not encode a protein. A nucleotide sequence identical or highly similar to the nucleotide sequence of VGAM2505 precursor RNA is designated SEQ ID:2491, and is provided hereinbelow with reference to the sequence listing part. Nucleotide sequence SEQ ID:2491 is located at position 75695 relative to the genome of Mouse Cytomegalovirus 1.

[84736] VGAM2505 precursor RNA folds onto itself, forming VGAM2505 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, which has a two-dimensional `hairpin structure`. As is well known in the art, this `hairpin structure`, is typical of RNA encoded by miRNA genes, and is due to the fact that the nucleotide sequence of the first half of the RNA encoded by a miRNA gene is an accurate or partial inversed-reversed sequence of the nucleotide sequence of the second half thereof.

[84737] An enzyme complex designated DICER COMPLEX, `dices` the VGAM2505 folded precursor RNA into VGAM2505 RNA, herein designated VGAM RNA, a single stranded ~22 nt long RNA segment. As is known in the art, `dicing` of a

hairpin structured RNA precursor product into a short ~22nt RNA segment is catalyzed by an enzyme complex comprising an enzyme called Dicer together with other necessary proteins. A probable (over 44%) nucleotide sequence of VGAM2505 RNA is designated SEQ ID:5216, and is provided hereinbelow with reference to the sequence listing part.

[84738] VGAM2505 host target gene, herein designated VGAM HOST TARGET GENE, encodes a corresponding messenger RNA, VGAM2505 host target RNA, herein designated VGAM HOST TARGET RNA. VGAM2505 host target RNA comprises three regions, as is typical of mRNA of a protein coding gene: a 5` untranslated region, a protein coding region and a 3` untranslated region, designated 5`UTR, PROTEIN CODING and 3`UTR respectively.

[84739] VGAM2505 RNA, herein designated VGAM RNA, binds complementarily to one or more host target binding sites located in untranslated regions of VGAM2505 host target RNA, herein designated VGAM HOST TARGET RNA. This complementary binding is due to the fact that the nucleotide sequence of VGAM2505 RNA is an accurate or a partial inversed-reversed sequence of the nucleotide sequence of each of the host target binding sites. As an il-

lustration, Fig. 1 shows three such host target binding sites, designated BINDING SITE I, BINDING SITE II and BINDING SITE III respectively. It is appreciated that the number of host target binding sites shown in Fig. 1 is meant as an illustration only, and is not meant to be limiting - VGAM2505 RNA, herein designated VGAM RNA, may have a different number of host target binding sites in untranslated regions of a VGAM2505 host target RNA, herein designated VGAM HOST TARGET RNA. It is further appreciated that while Fig. 1 depicts host target binding sites in the 3`UTR region, this is meant as an example only - these host target binding sites may be located in the 3`UTR region, the 5`UTR region, or in both 3`UTR and 5`UTR regions.

[84740] The complementary binding of VGAM2505 RNA, herein designated VGAM RNA, to host target binding sites on VGAM2505 host target RNA, herein designated VGAM HOST TARGET RNA, such as BINDING SITE I, BINDING SITE II and BINDING SITE III, inhibits translation of VGAM2505 host target RNA into VGAM2505 host target protein, herein designated VGAM HOST TARGET PROTEIN. VGAM host target protein is therefore outlined by a broken line.

[84741] It is appreciated that VGAM2505 host target gene, herein

designated VGAM HOST TARGET GENE, in fact represents a plurality of VGAM2505 host target genes. The mRNA of each one of this plurality of VGAM2505 host target genes comprises one or more host target binding sites, each having a nucleotide sequence which is at least partly complementary to VGAM2505 RNA, herein designated VGAM RNA, and which when bound by VGAM2505 RNA causes inhibition of translation of respective one or more VGAM2505 host target proteins.

[84742] It is further appreciated by one skilled in the art that the mode of translational inhibition illustrated by Fig. 1 with specific reference to translational inhibition exerted by VGAM2505 gene, herein designated VGAM GENE, on one or more VGAM2505 host target gene, herein designated VGAM HOST TARGET GENE, is in fact common to other known non-viral miRNA genes. As mentioned hereinabove with reference to the background section, although a specific complementary binding site has been demonstrated only for some of the known miRNA genes (primarily Lin-4 and Let-7), all other recently discovered miRNA genes are also believed by those skilled in the art to modulate expression of other genes by complementary binding, although specific complementary binding sites of these

other miRNA genes have not yet been found (Ruvkun G., `Perspective: Glimpses of a tiny RNA world`, Science 294,779 (2001)).

[84743] It is yet further appreciated that a function of VGAM2505 is inhibition of expression of host target genes, as part of a novel viral mechanism of attacking a host. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of viral infection by Mouse Cytomegalovirus 1. Specific functions, and accordingly utilities, of VGAM2505 correlate with, and may be deduced from, the identity of the host target genes which VGAM2505 binds and inhibits, and the function of these host target genes, as elaborated hereinbelow.

[84744] Nucleotide sequences of the VGAM2505 precursor RNA, herein designated VGAM PRECURSOR RNA, and of the `diced` VGAM2505 RNA, herein designated VGAM RNA, and a schematic representation of the secondary folding of VGAM2505 folded precursor RNA, herein designated VGAM FOLDED PRECURSOR RNA, of VGAM2505 are further described hereinbelow with reference to Table 1.

[84745] Nucleotide sequences of host target binding sites, such as BINDING SITE-I, BINDING SITE-II and BINDING SITE-III of Fig. 1, found on VGAM2505 host target RNA, and

schematic representation of the complementarity of each of these host target binding sites to VGAM2505 RNA, herein designated VGAM RNA, are described hereinbelow with reference to Table 2.

[84746] As mentioned hereinabove with reference to Fig. 1, a function of VGAM2505 gene, herein designated VGAM is inhibition of expression of VGAM2505 target genes. It is appreciated that specific functions, and accordingly utilities, of VGAM2505 correlate with, and may be deduced from, the identity of the target genes which VGAM2505 binds and inhibits, and the function of these target genes, as elaborated hereinbelow.

[84747] Adrenergic, Beta, Receptor Kinase 1 (ADRBK1, Accession NM_001619) is a VGAM2505 host target gene. ADRBK1 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ADRBK1, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ADRBK1 BINDING SITE, designated SEQ ID:7329, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84748] A function of VGAM2505 is therefore inhibition of Adrenergic, Beta, Receptor Kinase 1 (ADRBK1, Accession NM_001619), a gene which regulates desensitization of b-adrenergic receptors and related GPCRs. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ADRBK1. The function of ADRBK1 and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM626.Ras Homolog Gene Family, Member C (ARHC, Accession NM_005167) is another VGAM2505 host target gene. ARHC BINDING SITE is HOST TARGET binding site found in the 5` untranslated region of mRNA encoded by ARHC, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ARHC BINDING SITE, designated SEQ ID:11662, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84749] Another function of VGAM2505 is therefore inhibition of Ras Homolog Gene Family, Member C (ARHC, Accession NM_005167), a gene which remodels of the actin cy-

toskeleton during cell morphogenesis and motility. Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with ARHC. The function of ARHC and its association with various diseases and clinical conditions, has been established by previous studies, as described hereinabove with reference to VGAM885.ATPase, Na+/K+ Transporting, Alpha 2 (+) Polypeptide (ATP1A2, Accession NM_000702) is another VGAM2505 host target gene. ATP1A2 BINDING SITE is HOST TARGET binding site found in the 3` untranslated region of mRNA encoded by ATP1A2, corresponding to a HOST TARGET binding site such as BINDING SITE I, BINDING SITE II or BINDING SITE III. Table 2 illustrates the complementarity of the nucleotide sequences of ATP1A2 BINDING SITE, designated SEQ ID:6364, to the nucleotide sequence of VGAM2505 RNA, herein designated VGAM RNA, also designated SEQ ID:5216.

[84750] Another function of VGAM2505 is therefore inhibition of ATPase, Na+/K+ Transporting, Alpha 2 (+) Polypeptide (ATP1A2, Accession NM_000702). Accordingly, utilities of VGAM2505 include diagnosis, prevention and treatment of diseases and clinical conditions associated with